

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**

PCTWORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C12Q 1/68	A2	(11) International Publication Number: WO 98/20165 (43) International Publication Date: 14 May 1998 (14.05.98)
(21) International Application Number: PCT/US97/20313 (22) International Filing Date: 5 November 1997 (05.11.97) (30) Priority Data: 60/030,455 6 November 1996 (06.11.96) US (71) Applicant (for all designated States except US): WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH [US/US]; Nine Cambridge Center, Cambridge, MA 02142 (US). (72) Inventors; and (75) Inventors/Applicants (for US only): LANDER, Eric, S. [US/US]; 151 Bishop Allen Drive, Cambridge, MA 02138 (US). WANG, David [CN/US]; Apartment 314, 276 Mass- achusetts Avenue, Arlington, MA 02173 (US). HUDSON, Thomas [CA/US]; 361 Metcalfe Avenue, Westmount, Quebec H3Z 2J2 (CA). (74) Agents: GRANAHAN, Patricia et al.; Hamilton, Brook, Smith & Reynolds, Two Militia Drive, Lexington, MA 02173 (US).		(81) Designated States: JP, US, European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE). Published <i>Without international search report and to be republished upon receipt of that report.</i>
(54) Title: BIALLELIC MARKERS (57) Abstract The invention provides nucleic acid segments of the human genome including polymorphic sites. Allele-specific primers and probes hybridizing to regions flanking these sites are also provided. The nucleic acids, primers and probes are used in applications such as forensics, paternity testing, medicine and genetic analysis.		

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
AU	Australia	GA	Gabon	LV	Latvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav Republic of Macedonia	TM	Turkmenistan
BF	Burkina Faso	GR	Greece	ML	Mali	TR	Turkey
BG	Bulgaria	HU	Hungary	MN	Mongolia	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MR	Mauritania	UA	Ukraine
BR	Brazil	IL	Israel	MW	Malawi	UG	Uganda
BY	Belarus	IS	Iceland	MX	Mexico	US	United States of America
CA	Canada	IT	Italy	NE	Niger	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NL	Netherlands	VN	Viet Nam
CG	Congo	KE	Kenya	NO	Norway	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NZ	New Zealand	ZW	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's Republic of Korea	PL	Poland		
CM	Cameroon	KR	Republic of Korea	PT	Portugal		
CN	China	KZ	Kazakstan	RO	Romania		
CU	Cuba	LC	Saint Lucia	RU	Russian Federation		
CZ	Czech Republic	LI	Liechtenstein	SD	Sudan		
DE	Germany	LK	Sri Lanka	SE	Sweden		
DK	Denmark	LR	Liberia	SG	Singapore		
EE	Estonia						

-1-

BIALLELIC MARKERS

RELATED APPLICATIONS

This application claims priority to U.S. provisional application Serial No. 60/030,455, filed November 6, 1996, the entire teachings of which are incorporated herein by reference.

BACKGROUND OF THE INVENTION

The genomes of all organisms undergo spontaneous mutation in the course of their continuing evolution, generating variant forms of progenitor sequences (Gusella, *Ann. Rev. Biochem.* 55, 831-854 (1986)). The variant form may confer an evolutionary advantage or disadvantage relative to a progenitor form or may be neutral. In some instances, a variant form confers a lethal disadvantage and is not transmitted to subsequent generations of the organism. In other instances, a variant form confers an evolutionary advantage to the species and is eventually incorporated into the DNA of many or most members of the species and effectively becomes the progenitor form. In many instances, both progenitor and variant form(s) survive and co-exist in a species population. The coexistence of multiple forms of a sequence gives rise to polymorphisms.

Several different types of polymorphism have been reported. A restriction fragment length polymorphism (RFLP) is a variation in DNA sequence that alters the length of a restriction fragment (Botstein et al., *Am. J. Hum. Genet.* 32, 314-331 (1980)). The restriction fragment length polymorphism may create or delete a restriction site, thus changing the length of the restriction fragment.

-2-

RFLPs have been widely used in human and animal genetic analyses (see WO 90/13668; W090/11369; Donis-Keller, *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 85-99 (1989)). When a heritable trait can be linked to a particular RFLP, the presence of the RFLP in an individual can be used to predict the likelihood that the animal will also exhibit the trait.

Other polymorphisms take the form of short tandem repeats (STRs) that include tandem di-, tri- and tetra-nucleotide repeated motifs. These tandem repeats are also referred to as variable number tandem repeat (VNTR) polymorphisms. VNTRs have been used in identity and paternity analysis (US 5,075,217; Armour et al., *FEBS Lett.* 307, 113-115 (1992); Horn et al., WO 91/14003; Jeffreys, EP 370,719), and in a large number of genetic mapping studies.

Other polymorphisms take the form of single nucleotide variations between individuals of the same species. Such polymorphisms are far more frequent than RFLPs, STRs and VNTRs. Some single nucleotide polymorphisms occur in protein-coding sequences, in which case, one of the polymorphic forms may give rise to the expression of a defective or other variant protein and, potentially, a genetic disease. Examples of genes, in which polymorphisms within coding sequences give rise to genetic disease include β -globin (sickle cell anemia) and CFTR (cystic fibrosis). Other single nucleotide polymorphisms occur in noncoding regions. Some of these polymorphisms may also result in defective protein expression (e.g., as a result of defective splicing). Other single nucleotide polymorphisms have no phenotypic effects.

Single nucleotide polymorphisms can be used in the same manner as RFLPs and VNTRs, but offer several advantages. Single nucleotide polymorphisms occur with greater

-3-

frequency and are spaced more uniformly throughout the genome than other forms of polymorphism. The greater frequency and uniformity of single nucleotide polymorphisms means that there is a greater probability that such a

5 polymorphism will be found in close proximity to a genetic locus of interest than would be the case for other polymorphisms. The different forms of characterized single nucleotide polymorphisms are often easier to distinguish than other types of polymorphism (e.g., by use of assays

10 employing allele-specific hybridization probes or primers).

Only a small percentage of the total repository of polymorphisms in humans and other organisms has been identified. The limited number of polymorphisms identified to date is due to the large amount of work required for

15 their detection by conventional methods. For example, a conventional approach to identifying polymorphisms might be to sequence the same stretch of DNA in a population of individuals by dideoxy sequencing. In this type of approach, the amount of work increases in proportion to

20 both the length of sequence and the number of individuals in a population and becomes impractical for large stretches of DNA or large numbers of persons.

-4-

SUMMARY OF THE INVENTION

The invention provides nucleic acid sequences comprising nucleic acid segments of from about 10 to about 200 bases as shown in the Table, column 7, including a polymorphic site. Complements of these segments are also included. The segments can be DNA or RNA, and can be double- or single-stranded. Segments can be, for example, 10-20, 10-50 or 10-100 bases long. Preferred segments include a biallelic polymorphic site. The base occupying the polymorphic site in the segments can be the reference (Table, column 3) or an alternative base (Table, column 4).

The invention further provides allele-specific oligonucleotides that hybridize to a segment of a fragment shown in the Table, column 7, or its complement. These oligonucleotides can be probes or primers. Also provided are isolated nucleic acids comprising a sequence shown in the Table, column 7, or the complement thereto, in which the polymorphic site within the sequence is occupied by a base other than the reference base shown in the Table, column 3.

The invention further provides a method of analyzing a nucleic acid from an individual. The method determines which base is present at any one of the polymorphic sites shown in the Table. Optionally, a set of bases occupying a set of the polymorphic sites shown in the Table is determined. This type of analysis can be performed on a number of individuals, who are tested for the presence of a disease phenotype. The presence or absence of disease phenotype is then correlated with a base or set of bases present at the polymorphic sites in the individuals tested.

-5-

DETAILED DESCRIPTION OF THE INVENTION
DEFINITIONS

An oligonucleotide can be DNA or RNA, and single- or double-stranded. Oligonucleotides can be naturally occurring or synthetic, but are typically prepared by synthetic means. The oligonucleotides of the present invention can comprise all of an oligonucleotide sequence presented in column 7 of the Table or a segment of such an oligonucleotide which includes a polymorphic site.

Oligonucleotides can be all of a nucleic acid segment as represented in column 7 of the Table; a nucleic acid sequence which comprises a nucleic acid segment represented in column 7 of the Table and additional nucleic acids (present at either or both ends of a nucleic acid segment of column 7); or a portion (fragment) of a nucleic acid segment represented in column 7 of the Table which includes a polymorphic site. Preferred oligonucleotides of the invention include segments of DNA, or their complements, which include any one of the polymorphic sites shown in the Table. The segments can be between 5 and 250 bases, and, in specific embodiments, are between 5-10, 5-20, 10-20, 10-50, 20-50 or 10-100 bases. The polymorphic site can occur within any position of the segment. The segments can be from any of the allelic forms of DNA shown in the Table.

Hybridization probes are oligonucleotides which bind in a base-specific manner to a complementary strand of nucleic acid. Such probes include peptide nucleic acids, as described in Nielsen et al., *Science* 254, 1497-1500 (1991).

As used herein, the term primer refers to a single-stranded oligonucleotide which acts as a point of initiation of template-directed DNA synthesis under appropriate conditions (e.g., in the presence of four different nucleoside triphosphates and an agent for

-6-

polymerization, such as, DNA or RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer, but typically ranges from 15 to 30 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer need not reflect the exact sequence of the template, but must be sufficiently complementary to hybridize with a template.

The term primer site refers to the area of the target DNA to which a primer hybridizes. The term primer pair refers to a set of primers including a 5' (upstream) primer that hybridizes with the 5' end of the DNA sequence to be amplified and a 3' (downstream) primer that hybridizes with the complement of the 3' end of the sequence to be amplified.

As used herein, linkage describes the tendency of genes, alleles, loci or genetic markers to be inherited together as a result of their location on the same chromosome. It can be measured by percent recombination between the two genes, alleles, loci or genetic markers.

As used herein, polymorphism refers to the occurrence of two or more genetically determined alternative sequences or alleles in a population. A polymorphic marker or site is the locus at which divergence occurs. Preferred markers have at least two alleles, each occurring at frequency of greater than 1%, and more preferably greater than 10% or 20% of a selected population. A polymorphic locus may be as small as one base pair. Polymorphic markers include restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple sequence repeats,

-7-

and insertion elements such as Alu. The first identified allelic form is arbitrarily designated as the reference form and other allelic forms are designated as alternative or variant alleles. The allelic form occurring most frequently in a selected population is sometimes referred to as the wildtype form. Diploid organisms may be homozygous or heterozygous for allelic forms. A diallelic or biallelic polymorphism has two forms. A triallelic polymorphism has three forms.

10 A single nucleotide polymorphism occurs at a polymorphic site occupied by a single nucleotide, which is the site of variation between allelic sequences. The site is usually preceded by and followed by highly conserved sequences of the allele (e.g., sequences that vary in less than 1/100 or 1/1000 members of the populations).

15 A single nucleotide polymorphism usually arises due to substitution of one nucleotide for another at the polymorphic site. A transition is the replacement of one purine by another purine or one pyrimidine by another pyrimidine. A transversion is the replacement of a purine by a pyrimidine or vice versa. Single nucleotide polymorphisms can also arise from a deletion of a nucleotide or an insertion of a nucleotide relative to a reference allele. Typically the polymorphic site is occupied by a base other than the reference base. For example, where the reference allele contains the base "T" at the polymorphic site, the altered allele can contain a "C", "G" or "A" at the polymorphic site.

25 Hybridizations are usually performed under stringent conditions, for example, at a salt concentration of no more than 1 M and a temperature of at least 25°C. For example, conditions of 5X SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C, or equivalent

-8-

conditions, are suitable for allele-specific probe hybridizations. Equivalent conditions can be determined by varying one or more of the parameters given as an example, as known in the art, while maintaining a similar degree of identity or similarity between the target nucleotide sequence and the primer or probe used.

The term "isolated" is used herein to indicate that the material in question exists in a physical milieu distinct from that in which it occurs in nature. For example, an isolated nucleic acid of the invention may be substantially isolated with respect to the complex cellular milieu in which it naturally occurs. In some instances, the isolated material will form part of a composition (for example, a crude extract containing other substances), buffer system or reagent mix. In other circumstance, the material may be purified to essential homogeneity, for example as determined by PAGE or column chromatography such as HPLC. Preferably, an isolated nucleic acid comprises at least about 50, 80 or 90 percent (on a molar basis) of all macromolecular species present.

I. Novel Polymorphisms of the Invention

The novel polymorphisms of the invention are listed in the Table. The first column of the Table lists the names assigned to the fragments in which the polymorphisms occur. The fragments are all human genomic fragments. The sequence of one allelic form of each of the fragments (arbitrarily referred to as the prototypical or reference form) has been previously published. These sequences are listed at <http://www-genome.wi.mit.edu/> (all STS's (sequence tag sites)); <http://shgc.stanford.edu> (Stanford STS's); and <http://ww.tigr.org/> (TIGR STS's). The Web sites also list primers for amplification of the fragments,

-9-

and the genomic location of fragments. Some fragments are expressed sequence tags, and some are random genomic fragments. All information in the websites concerning the fragments listed in the Table is incorporated by reference
5 in its entirety for all purposes.

The second column lists the position in the fragment in which a polymorphic site has been found. Positions are numbered consecutively with the first base of the fragment sequence as listed in one of the above databases being
10 assigned the number one. The third column lists the base occupying the polymorphic site in the sequence in the data base. This base is arbitrarily designated the reference or prototypical form, but it is not necessarily the most frequently occurring form. The fourth column in the Table
15 lists the alternative base(s) at the polymorphic site. The fifth column of the Table lists a 5' (upstream or forward) primer that hybridizes with the 5' end of the DNA sequence to be amplified. The sixth column of the Table lists a 3' (downstream or reverse) primer that hybridizes with the
20 complement of the 3' end of the sequence to be amplified. The seventh column of the Table lists a number of bases of sequence on either side of the polymorphic site in each fragment. The indicated sequences can be either DNA or RNA. In the latter, the T's shown in the Table are
25 replaced by U's. The base occupying the polymorphic site is indicated in EUPAC-IUB ambiguity code.

II. Analysis of Polymorphisms

A. Preparation of Samples

Polymorphisms are detected in a target nucleic acid
30 from an individual being analyzed. For assay of genomic DNA, virtually any biological sample (other than pure red blood cells) is suitable. For example, convenient tissue

-10-

samples include whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair. For assay of cDNA or mRNA, the tissue sample must be obtained from an organ in which the target nucleic acid is expressed. For
5 example, if the target nucleic acid is a cytochrome P450, the liver is a suitable source.

Many of the methods described below require amplification of DNA from target samples. This can be accomplished by e.g., PCR. See generally *PCR Technology: Principles and Applications for DNA Amplification* (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); *PCR Protocols: A Guide to Methods and Applications* (eds. Innis, et al., Academic Press, San Diego, CA, 1990); Mattila et al., *Nucleic Acids Res.* 19, 4967 (1991); Eckert et al., *PCR Methods and Applications* 1, 17 (1991); *PCR* (eds. McPherson et al., IRL Press, Oxford); and U.S. Patent 4,683,202.

Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics* 4, 560 (1989), Landegren et al., *Science* 241, 1077 (1988),
20 transcription amplification (Kwoh et al., *Proc. Natl. Acad. Sci. USA* 86, 1173 (1989)), and self-sustained sequence replication (Guatelli et al., *Proc. Nat. Acad. Sci. USA*, 87, 1874 (1990)) and nucleic acid based sequence amplification (NASBA). The latter two amplification
25 methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the amplification products in a ratio of about 30 or 100 to 1, respectively.

30 B. Detection of Polymorphisms in Target DNA

There are two distinct types of analysis of target DNA for detecting polymorphisms. The first type of analysis,

-11-

sometimes referred to as de novo characterization, is carried out to identify polymorphic sites not previously characterized (i.e., to identify new polymorphisms). This analysis compares target sequences in different individuals to identify points of variation, i.e., polymorphic sites. By analyzing groups of individuals representing the greatest ethnic diversity among humans and greatest breed and species variety in plants and animals, patterns characteristic of the most common alleles/haplotypes of the locus can be identified, and the frequencies of such alleles/haplotypes in the population can be determined. Additional allelic frequencies can be determined for subpopulations characterized by criteria such as geography, race, or gender. The de novo identification of polymorphisms of the invention is described in the Examples section. The second type of analysis determines which form(s) of a characterized (known) polymorphism are present in individuals under test. There are a variety of suitable procedures, which are discussed in turn.

1. Allele-Specific Probes

The design and use of allele-specific probes for analyzing polymorphisms is described by e.g., Saiki et al., *Nature* 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki, WO 89/11548. Allele-specific probes can be designed that hybridize to a segment of target DNA from one individual but do not hybridize to the corresponding segment from another individual due to the presence of different polymorphic forms in the respective segments from the two individuals. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary response, whereby a probe

-12-

hybridizes to only one of the alleles. Some probes are designed to hybridize to a segment of target DNA such that the polymorphic site aligns with a central position (e.g., in a 15-mer at the 7 position; in a 16-mer, at either the 8 or 9 position) of the probe. This design of probe achieves good discrimination in hybridization between different allelic forms.

Allele-specific probes are often used in pairs, one member of a pair showing a perfect match to a reference form of a target sequence and the other member showing a perfect match to a variant form. Several pairs of probes can then be immobilized on the same support for simultaneous analysis of multiple polymorphisms within the same target sequence.

2. Tiling Arrays

The polymorphisms can also be identified by hybridization to nucleic acid arrays, some examples of which are described in WO 95/11995. One form of such arrays is described in the Examples section in connection with de novo identification of polymorphisms. The same array or a different array can be used for analysis of characterized polymorphisms. WO 95/11995 also describes subarrays that are optimized for detection of a variant form of a precharacterized polymorphism. Such a subarray contains probes designed to be complementary to a second reference sequence, which is an allelic variant of the first reference sequence. The second group of probes is designed by the same principles as described in the Examples, except that the probes exhibit complementarity to the second reference sequence. The inclusion of a second group (or further groups) can be particularly useful for analyzing short subsequences of the primary reference

-13-

sequence in which multiple mutations are expected to occur within a short distance commensurate with the length of the probes (e.g., two or more mutations within 9 to 21 bases).

3. Allele-Specific Primers

5 An allele-specific primer hybridizes to a site on target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, *Nucleic Acid Res.* 17, 2427-2448 (1989). This primer is used in
10 conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two-primers, resulting in a detectable product which indicates the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows
15 a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of
20 the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer (see, e.g., WO 93/22456).

4. Direct-Sequencing

The direct analysis of the sequence of polymorphisms of
25 the present invention can be accomplished using either the dideoxy chain termination method or the Maxam Gilbert method (see Sambrook et al., *Molecular Cloning, A Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind et al., *Recombinant DNA Laboratory Manual*, (Acad. Press,
30 1988)).

-14-

5. Denaturing Gradient Gel Electrophoresis

Amplification products generated using the polymerase chain reaction can be analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. Erlich, ed., *PCR Technology, Principles and Applications for DNA Amplification*, (W.H. Freeman and Co, New York, 1992), Chapter 7.

6. Single-Strand Conformation Polymorphism Analysis

Alleles of target sequences can be differentiated using single-strand conformation polymorphism analysis, which identifies base differences by alteration in electrophoretic migration of single stranded PCR products, as described in Orita et al., *Proc. Nat. Acad. Sci.* 86, 2766-2770 (1989). Amplified PCR products can be generated as described above, and heated or otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids may refold or form secondary structures which are partially dependent on the base sequence. The different electrophoretic mobilities of single-stranded amplification products can be related to base-sequence differences between alleles of target sequences.

III. Methods of Use

After determining polymorphic form(s) present in an individual at one or more polymorphic sites, this information can be used in a number of methods.

-15-

A. Forensics

Determination of which polymorphic forms occupy a set of polymorphic sites in an individual identifies a set of polymorphic forms that distinguishes the individual. See
5 generally National Research Council, *The Evaluation of Forensic DNA Evidence* (Eds. Pollard et al., National Academy Press, DC, 1996). The more sites that are analyzed, the lower the probability that the set of polymorphic forms in one individual is the same as that in
10 an unrelated individual. Preferably, if multiple sites are analyzed, the sites are unlinked. Thus, polymorphisms of the invention are often used in conjunction with polymorphisms in distal genes. Preferred polymorphisms for use in forensics are biallelic because the population
15 frequencies of two polymorphic forms can usually be determined with greater accuracy than those of multiple polymorphic forms at multi-allelic loci.

The capacity to identify a distinguishing or unique set of forensic markers in an individual is useful for forensic
20 analysis. For example, one can determine whether a blood sample from a suspect matches a blood or other tissue sample from a crime scene by determining whether the set of polymorphic forms occupying selected polymorphic sites is the same in the suspect and the sample. If the set of
25 polymorphic markers does not match between a suspect and a sample, it can be concluded (barring experimental error) that the suspect was not the source of the sample. If the set of markers does match, one can conclude that the DNA from the suspect is consistent with that found at the crime
30 scene. If frequencies of the polymorphic forms at the loci tested have been determined (e.g., by analysis of a suitable population of individuals), one can perform a statistical analysis to determine the probability that a

-16-

match of suspect and crime scene sample would occur by chance.

$p(\text{ID})$ is the probability that two random individuals have the same polymorphic or allelic form at a given polymorphic site. In biallelic loci, four genotypes are possible: AA, AB, BA, and BB. If alleles A and B occur in a haploid genome of the organism with frequencies x and y , the probability of each genotype in a diploid organism is (see WO 95/12607):

- 10 Homozygote: $p(\text{AA}) = x^2$
 Homozygote: $p(\text{BB}) = y^2 = (1-x)^2$
 Single Heterozygote: $p(\text{AB}) = p(\text{BA}) = xy = x(1-x)$
 Both Heterozygotes: $p(\text{AB}+\text{BA}) = 2xy = 2x(1-x)$

The probability of identity at one locus (i.e., the probability that two individuals, picked at random from a population will have identical polymorphic forms at a given locus) is given by the equation:

15 $p(\text{ID}) = (x^2)^2 + (2xy)^2 + (y^2)^2$.

These calculations can be extended for any number of polymorphic forms at a given locus. For example, the probability of identity $p(\text{ID})$ for a 3-allele system where the alleles have the frequencies in the population of x , y and z , respectively, is equal to the sum of the squares of the genotype frequencies:

25 $p(\text{ID}) = x^4 + (2xy)^2 + (2yz)^2 + (2xz)^2 + z^4 + y^4$

In a locus of n alleles, the appropriate binomial expansion is used to calculate $p(\text{ID})$ and $p(\text{exc})$.

The cumulative probability of identity ($\text{cum } p(\text{ID})$) for each of multiple unlinked loci is determined by multiplying the probabilities provided by each locus.

30

$$\text{cum } p(\text{ID}) = p(\text{ID}_1)p(\text{ID}_2)p(\text{ID}_3)\dots p(\text{ID}_n)$$

-17-

The cumulative probability of non-identity for n loci (i.e. the probability that two random individuals will be different at 1 or more loci) is given by the equation:

$$\text{cum } p(\text{nonID}) = 1 - \text{cum } p(\text{ID}).$$

- 5 If several polymorphic loci are tested, the cumulative probability of non-identity for random individuals becomes very high (e.g., one billion to one). Such probabilities can be taken into account together with other evidence in determining the guilt or innocence of the suspect.

10 B. Paternity Testing

The object of paternity testing is usually to determine whether a male is the father of a child. In most cases, the mother of the child is known and thus, the mother's contribution to the child's genotype can be traced.

- 15 Paternity testing investigates whether the part of the child's genotype not attributable to the mother is consistent with that of the putative father. Paternity testing can be performed by analyzing sets of polymorphisms in the putative father and the child.

- 20 If the set of polymorphisms in the child attributable to the father does not match the set of polymorphisms of the putative father, it can be concluded, barring experimental error, that the putative father is not the real father. If the set of polymorphisms in the child
25 attributable to the father does match the set of polymorphisms of the putative father, a statistical calculation can be performed to determine the probability of coincidental match.

- 30 The probability of parentage exclusion (representing the probability that a random male will have a polymorphic form at a given polymorphic site that makes him

-18-

incompatible as the father) is given by the equation (see WO 95/12607):

$$p(\text{exc}) = xy(1-xy)$$

where x and y are the population frequencies of alleles A and B of a biallelic polymorphic site.

(At a triallelic site $p(\text{exc}) = xy(1-xy) + yz(1-yz) + xz(1-xz) + 3xyz(1-xyz)$), where x, y and z are the respective population frequencies of alleles A, B and C).

The probability of non-exclusion is

$$p(\text{non-exc}) = 1 - p(\text{exc})$$

The cumulative probability of non-exclusion (representing the value obtained when n loci are used) is thus:

$$\text{cum } p(\text{non-exc}) = p(\text{non-exc1})p(\text{non-exc2})p(\text{non-exc3})\dots$$

$$p(\text{non-excn})$$

The cumulative probability of exclusion for n loci (representing the probability that a random male will be excluded)

$$\text{cum } p(\text{exc}) = 1 - \text{cum } p(\text{non-exc}).$$

If several polymorphic loci are included in the analysis, the cumulative probability of exclusion of a random male is very high. This probability can be taken into account in assessing the liability of a putative father whose polymorphic marker set matches the child's polymorphic marker set attributable to his/her father.

C. Correlation of Polymorphisms with Phenotypic Traits

The polymorphisms of the invention may contribute to the phenotype of an organism in different ways. Some polymorphisms occur within a protein coding sequence and contribute to phenotype by affecting protein structure. The effect may be neutral, beneficial or detrimental, or both beneficial and detrimental, depending on the

-19-

circumstances. For example, a heterozygous sickle cell mutation confers resistance to malaria, but a homozygous sickle cell mutation is usually lethal. Other polymorphisms occur in noncoding regions but may exert phenotypic effects indirectly via influence on replication, transcription, and translation. A single polymorphism may affect more than one phenotypic trait. Likewise, a single phenotypic trait may be affected by polymorphisms in different genes. Further, some polymorphisms predispose an individual to a distinct mutation that is causally related to a certain phenotype.

Phenotypic traits include diseases that have known but hitherto unmapped genetic components (e.g., agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria). Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, leukemia, liver, lung, oral cavity, ovary, pancreas, prostate, skin, stomach and uterus. Phenotypic traits also include characteristics such as longevity, appearance

-20-

(e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Correlation is performed for a population of
5 individuals who have been tested for the presence or
absence of a phenotypic trait of interest and for
polymorphic markers sets. To perform such analysis, the
presence or absence of a set of polymorphisms (i.e. a
polymorphic set) is determined for a set of the
10 individuals, some of whom exhibit a particular trait, and
some of which exhibit lack of the trait. The alleles of
each polymorphism of the set are then reviewed to determine
whether the presence or absence of a particular allele is
associated with the trait of interest. Correlation can be
15 performed by standard statistical methods such as a χ^2 -
squared test and statistically significant correlations
between polymorphic form(s) and phenotypic characteristics
are noted. For example, it might be found that the
presence of allele A1 at polymorphism A correlates with
20 heart disease. As a further example, it might be found
that the combined presence of allele A1 at polymorphism A
and allele B1 at polymorphism B correlates with increased
milk production of a farm animal.

Such correlations can be exploited in several ways. In
25 the case of a strong correlation between a set of one or
more polymorphic forms and a disease for which treatment is
available, detection of the polymorphic form set in a human
or animal patient may justify immediate administration of
treatment, or at least the institution of regular
30 monitoring of the patient. Detection of a polymorphic form
correlated with serious disease in a couple contemplating a
family may also be valuable to the couple in their
reproductive decisions. For example, the female partner

-21-

might elect to undergo in vitro fertilization to avoid the possibility of transmitting such a polymorphism from her husband to her offspring. In the case of a weaker, but still statistically significant correlation between a polymorphic set and human disease, immediate therapeutic intervention or monitoring may not be justified. Nevertheless, the patient can be motivated to begin simple life-style changes (e.g., diet, exercise) that can be accomplished at little cost to the patient but confer potential benefits in reducing the risk of conditions to which the patient may have increased susceptibility by virtue of variant alleles. Identification of a polymorphic set in a patient correlated with enhanced receptiveness to one of several treatment regimes for a disease indicates that this treatment regime should be followed.

For animals and plants, correlations between characteristics and phenotype are useful for breeding for desired characteristics. For example, Beitz et al., US 5,292,639 discuss use of bovine mitochondrial polymorphisms in a breeding program to improve milk production in cows. To evaluate the effect of mtDNA D-loop sequence polymorphism on milk production, each cow was assigned a value of 1 if variant or 0 if wildtype with respect to a prototypical mitochondrial DNA sequence at each of 17 locations considered. Each production trait was analyzed individually with the following animal model:

$$Y_{ijkpn} = \mu + YS_i + P_j + X_k + \beta_1 + \dots \beta_{17} + PE_n + a_n + e_p$$

where Y_{ijkpn} is the milk, fat, fat percentage, SNF, SNF percentage, energy concentration, or lactation energy record; μ is an overall mean; YS_i is the effect common to all cows calving in year-season; X_k is the effect common to cows in either the high or average selection line; β_1 to β_{17} are the binomial regressions of production record on mtDNA

-22-

D-loop sequence polymorphisms; PE_n is permanent environmental effect common to all records of cow n ; a_n is effect of animal n and is composed of the additive genetic contribution of sire and dam breeding values and a Mendelian sampling effect; and e_p is a random residual. It was found that eleven of seventeen polymorphisms tested influenced at least one production trait. Bovines having the best polymorphic forms for milk production at these eleven loci are used as parents for breeding the next generation of the herd.

D. Genetic Mapping of Phenotypic Traits

The previous section concerns identifying correlations between phenotypic traits and polymorphisms that directly or indirectly contribute to those traits. The present section describes identification of a physical linkage between a genetic locus associated with a trait of interest and polymorphic markers that are not associated with the trait, but are in physical proximity with the genetic locus responsible for the trait and co-segregate with it. Such analysis is useful for mapping a genetic locus associated with a phenotypic trait to a chromosomal position, and thereby cloning gene(s) responsible for the trait. See Lander et al., *Proc. Natl. Acad. Sci. (USA)* 83, 7353-7357 (1986); Lander et al., *Proc. Natl. Acad. Sci. (USA)* 84, 2363-2367 (1987); Donis-Keller et al., *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 185-199 (1989)). Genes localized by linkage can be cloned by a process known as directional cloning. See Wainwright, *Med. J. Australia* 159, 170-174 (1993); Collins, *Nature Genetics* 1, 3-6 (1992).

Linkage studies are typically performed on members of a family. Available members of the family are characterized

-23-

for the presence or absence of a phenotypic trait and for a set of polymorphic markers. The distribution of polymorphic markers in an informative meiosis is then analyzed to determine which polymorphic markers co-

5 segregate with a phenotypic trait. See, e.g., Kerem et al., *Science* 245, 1073-1080 (1989); Monaco et al., *Nature* 316, 842 (1985); Yamoka et al., *Neurology* 40, 222-226 (1990); Rossiter et al., *FASEB Journal* 5, 21-27 (1991).

Linkage is analyzed by calculation of LOD (log of the

10 odds) values. A lod value is the relative likelihood of obtaining observed segregation data for a marker and a genetic locus when the two are located at a recombination fraction θ , versus the situation in which the two are not linked, and thus segregating independently (Thompson &

15 Thompson, *Genetics in Medicine* (5th ed, W.B. Saunders Company, Philadelphia, 1991); Strachan, "Mapping the human genome" in *The Human Genome* (BIOS Scientific Publishers Ltd, Oxford), Chapter 4). A series of likelihood ratios are calculated at various recombination fractions (θ),

20 ranging from $\theta = 0.0$ (coincident loci) to $\theta = 0.50$ (unlinked). Thus, the likelihood at a given value of θ is: probability of data if loci linked at θ to probability of data if loci unlinked. The computed likelihoods are usually expressed as the \log_{10} of this ratio (i.e., a lod

25 score). For example, a lod score of 3 indicates 1000:1 odds against an apparent observed linkage being a coincidence. The use of logarithms allows data collected from different families to be combined by simple addition. Computer programs are available for the calculation of lod

30 scores for differing values of θ (e.g., LIPED, MLINK (Lathrop, *Proc. Nat. Acad. Sci. (USA)* 81, 3443-3446 (1984)). For any particular lod score, a recombination fraction may be determined from mathematical tables. See

-24-

Smith et al., *Mathematical tables for research workers in human genetics* (Churchill, London, 1961); Smith, *Ann. Hum. Genet.* 32, 127-150 (1968). The value of θ at which the lod score is the highest is considered to be the best estimate
5 of the recombination fraction.

Positive lod score values suggest that the two loci are linked, whereas negative values suggest that linkage is less likely (at that value of θ) than the possibility that the two loci are unlinked. By convention, a combined lod
10 score of +3 or greater (equivalent to greater than 1000:1 odds in favor of linkage) is considered definitive evidence that two loci are linked. Similarly, by convention, a negative lod score of -2 or less is taken as definitive evidence against linkage of the two loci being compared.
15 Negative linkage data are useful in excluding a chromosome or a segment thereof from consideration. The search focuses on the remaining non-excluded chromosomal locations.

IV. Modified Polypeptides and Gene Sequences

20 The invention further provides variant forms of nucleic acids and corresponding proteins. The nucleic acids comprise one of the sequences described in the Table, column 8, in which the polymorphic position is occupied by one of the alternative bases for that position. Some
25 nucleic acids encode full-length variant forms of proteins. Similarly, variant proteins have the prototypical amino acid sequences encoded by nucleic acid sequences shown in the Table, column 8, (read so as to be in-frame with the full-length coding sequence of which it is a component)
30 except at an amino acid encoded by a codon including one of the polymorphic positions shown in the Table. That position is occupied by the amino acid coded by the

-25-

corresponding codon in any of the alternative forms shown in the Table.

Variant genes can be expressed in an expression vector in which a variant gene is operably linked to a native or other promoter. Usually, the promoter is a eukaryotic promoter for expression in a mammalian cell. The transcription regulation sequences typically include a heterologous promoter and optionally an enhancer which is recognized by the host. The selection of an appropriate promoter, for example trp, lac, phage promoters, glycolytic enzyme promoters and tRNA promoters, depends on the host selected. Commercially available expression vectors can be used. Vectors can include host-recognized replication systems, amplifiable genes, selectable markers, host sequences useful for insertion into the host genome, and the like.

The means of introducing the expression construct into a host cell varies depending upon the particular construction and the target host. Suitable means include fusion, conjugation, transfection, transduction, electroporation or injection, as described in Sambrook, *supra*. A wide variety of host cells can be employed for expression of the variant gene, both prokaryotic and eukaryotic. Suitable host cells include bacteria such as *E. coli*, yeast, filamentous fungi, insect cells, mammalian cells, typically immortalized, e.g., mouse, CHO, human and monkey cell lines and derivatives thereof. Preferred host cells are able to process the variant gene product to produce an appropriate mature polypeptide. Processing includes glycosylation, ubiquitination, disulfide bond formation, general post-translational modification, and the like.

-26-

The protein may be isolated by conventional means of protein biochemistry and purification to obtain a substantially pure product, i.e., 80, 95 or 99% free of cell component contaminants, as described in Jacoby,
5 *Methods in Enzymology* Volume 104, Academic Press, New York (1984); Scopes, *Protein Purification, Principles and Practice*, 2nd Edition, Springer-Verlag, New York (1987); and Deutscher (ed), *Guide to Protein Purification, Methods in Enzymology*, Vol. 182 (1990). If the protein is
10 secreted, it can be isolated from the supernatant in which the host cell is grown. If not secreted, the protein can be isolated from a lysate of the host cells.

The invention further provides transgenic nonhuman animals capable of expressing an exogenous variant gene
15 and/or having one or both alleles of an endogenous variant gene inactivated. Expression of an exogenous variant gene is usually achieved by operably linking the gene to a promoter and optionally an enhancer, and microinjecting the construct into a zygote. See Hogan et al., "Manipulating
20 the Mouse Embryo, A Laboratory Manual," Cold Spring Harbor Laboratory. Inactivation of endogenous variant genes can be achieved by forming a transgene in which a cloned variant gene is inactivated by insertion of a positive selection marker. See Capecchi, *Science* 244, 1288-1292
25 (1989). The transgene is then introduced into an embryonic stem cell, where it undergoes homologous recombination with an endogenous variant gene. Mice and other rodents are preferred animals. Such animals provide useful drug screening systems.

30 In addition to substantially full-length polypeptides expressed by variant genes, the present invention includes biologically active fragments of the polypeptides, or analogs thereof, including organic molecules which simulate

-27-

the interactions of the peptides. Biologically active fragments include any portion of the full-length polypeptide which confers a biological function on the variant gene product, including ligand binding, and
5 antibody binding. Ligand binding includes binding by nucleic acids, proteins or polypeptides, small biologically active molecules, or large cellular structures.

Polyclonal and/or monoclonal antibodies that specifically bind to variant gene products but not to
10 corresponding prototypical gene products are also provided. Antibodies can be made by injecting mice or other animals with the variant gene product or synthetic peptide fragments thereof. Monoclonal antibodies are screened as are described, for example, in Harlow & Lane, *Antibodies, A*
15 *Laboratory Manual*, Cold Spring Harbor Press, New York (1988); Goding, *Monoclonal antibodies, Principles and Practice* (2d ed.) Academic Press, New York (1986). Monoclonal antibodies are tested for specific immunoreactivity with a variant gene product and lack of
20 immunoreactivity to the corresponding prototypical gene product. These antibodies are useful in diagnostic assays for detection of the variant form, or as an active ingredient in a pharmaceutical composition.

V. Kits

25 The invention further provides kits comprising at least one allele-specific oligonucleotide as described above. Often, the kits contain one or more pairs of allele-specific oligonucleotides hybridizing to different forms of a polymorphism. In some kits, the allele-specific
30 oligonucleotides are provided immobilized to a substrate. For example, the same substrate can comprise allele-specific oligonucleotide probes for detecting at least 10,

-28-

100 or all of the polymorphisms shown in the Table. Optional additional components of the kit include, for example, restriction enzymes, reverse-transcriptase or polymerase, the substrate nucleoside triphosphates, means
5 used to label (for example, an avidin-enzyme conjugate and enzyme substrate and chromogen if the label is biotin), and the appropriate buffers for reverse transcription, PCR, or hybridization reactions. Usually, the kit also contains instructions for carrying out the methods.

10 The following Examples are offered for the purpose of illustrating the present invention and are not to be construed to limit the scope of this invention. The teachings of all references cited herein are hereby incorporated herein by reference.

15

EXAMPLES

The polymorphisms shown in the Table were identified by resequencing of target sequences from three to ten unrelated individuals of diverse ethnic and geographic backgrounds by hybridization to probes immobilized to
20 microfabricated arrays or conventional sequencing. The strategy and principles for design and use of such arrays are generally described in WO 95/11995. The strategy provides arrays of probes for analysis of target sequences showing a high degree of sequence identity to the reference
25 sequences of the fragments shown in the Table, column 1.

The reference sequences were sequence-tagged sites (STSs) developed in the course of the Human Genome Project (see, e.g., *Science* 270, 1945-1954 (1995); *Nature* 380, 152-154 (1996)). Most STS's ranged from 100 bp to 300 bp in size.

30 A typical probe array used in this analysis has two groups of four sets of probes that respectively tile both strands of a reference sequence. A first probe set

-29-

comprises a plurality of probes exhibiting perfect complementarily with one of the reference sequences. Each probe in the first probe set has an interrogation position that corresponds to a nucleotide in the reference sequence.

5 That is, the interrogation position is aligned with the corresponding nucleotide in the reference sequence, when the probe and reference sequence are aligned to maximize complementarily between the two. For each probe in the first set, there are three corresponding probes from three

10 additional probe sets. Thus, there are four probes corresponding to each nucleotide in the reference sequence. The probes from the three additional probe sets are identical to the corresponding probe from the first probe set except at the interrogation position, which occurs in

15 the same position in each of the four corresponding probes from the four probe sets, and is occupied by a different nucleotide in the four probe sets. In the present analysis, probes were 25 nucleotides long. Arrays tiled for multiple different references sequences were included

20 on the same substrate.

Multiple target sequences from an individual were amplified from human genomic DNA using primers for the fragments indicated in the listed Web sites. The amplified target sequences were fluorescently labelled during or

25 after PCR. The labelled target sequences were hybridized with a substrate bearing immobilized arrays of probes. The amount of label bound to probes was measured. Analysis of the pattern of label revealed the nature and position of differences between the target and reference sequence. For

30 example, comparison of the intensities of four corresponding probes reveals the identity of a corresponding nucleotide in the target sequences aligned with the interrogation position of the probes. The

-30-

corresponding nucleotide is the complement of the nucleotide occupying the interrogation position of the probe showing the highest intensity (see WO 95/11995). The existence of a polymorphism is also manifested by

5 differences in normalized hybridization intensities of probes flanking the polymorphism when the probes hybridized to corresponding targets from different individuals. For example, relative loss of hybridization intensity in a "footprint" of probes flanking a polymorphism signals a

10 difference between the target and reference (i.e., a polymorphism) (see EP 717,113). Additionally, hybridization intensities for corresponding targets from different individuals can be classified into groups or clusters suggested by the data, not defined *a priori*, such

15 that isolates in a give cluster tend to be similar and isolates in different clusters tend to be dissimilar. Hybridizations to samples from different individuals were performed separately. The Table summarizes the data obtained for target sequences in comparison with a

20 reference sequence for the individuals tested.

From the foregoing, it is apparent that the invention includes a number of general uses that can be expressed concisely as follows. The invention provides for the use of any of the nucleic acid segments described above in the

25 diagnosis or monitoring of diseases, such as cancer, inflammation, heart disease, diseases of the CNS, and susceptibility to infection by microorganisms. The invention further provides for the use of any of the nucleic acid segments in the manufacture of a medicament

30 for the treatment or prophylaxis of such diseases. The invention further provides for the use of any of the DNA segments as a pharmaceutical.

-31-

All publications and patent applications cited above are incorporated by reference in their entirety for all purposes to the same extent as if each individual publication or patent application were specifically and
5 individually indicated to be so incorporated by reference.

1	2	3	4	5	6	7
WI-7070	226	C T	---			TGTGAACCTCCACTTGAAGCCAAAGAAAGAACTCACACTTAAACACATGCCAGTTGGGAAGGCTCT GAAACTCAGTGCATAATAGGAACACTTGAGACTAATGAAGAGAGAGATTGAGACCAATCTTTATTT GTACTGGCCAAATACTGAATAACAGTTGAAGGAAAGACATTGGAAAAAGCTTTTGAGGATAATGT TACTAGACTTTATGCCATGGTCTTTC/TAGTTTAATGCTGTCTCTGTCTG
WI-10744	61	G C	---			AAGCCATTGACGTAACTCTCAGAGGTTATTTGCATGGATTGACTCTCTGGGACAAAAGGAC[G/C]AA AAACACTCTTCTGTGGATATCTGTGCAGATAGATGACCCAAAGATCAGATGCTACCCAGATGTGTTTT GATAATACATAAGCCCCCTAGGATTTAGATACAATCTTGAAGAAACTGAGACAGATAATCTCTGAATT AAATGAGGTAAGTTTCAGGCACCTCA
WI-9975	126	C T	---			GGGCAAAATACCAGCAAAAAGTCAAAATACCAGCATCAAAAGTCAGGTGCAAGGAGGTAGAACA TTACAGTAACATATGTCAATCTTTTGTATATTAGTATTATCTGCCAATGCCTAGAATAC/TAGTG GGTCCCTAATAGTTATTAGTTCCTTTTCTCCCTCTCTCAATCTCTGAATTTATTTTATACTTAA GGGATTAGTTACCACCAAAAATGTGTATGATCAATTTGATCTTACTGAA
WI-8010	247	G T	---			GCTAGGTTTGTCTGTGGCTGTCTTCACTAGACTTTGAGATGACTTGATTACAGTATCCCTATGT GATGTAACAGTGTAGACCTTCCCTTCTCCGCAATCCAGCTCCAGGTTTCAGAAAGTATGCCACAG TCAACCCCTCTCTCCAGTTCATCCTGTATTAAATTTCTCCCATATTAAATTCAAAGGAGTGGACAGGT CCCTGGCTGAAAAGAAATAAAGAGATCCCAAGTGGTGGGG[G/T]CTT
WI-5222b	85	G C	---			GCCGGCCTATCTTTAATTTAACTTGTATCTTTGGTGTCTCCATCCTAGGATTCGCCTTATAAT CTTTGTCTGTCTGTG[G/C]ATTACCTGATCTACTTTTGATACACAAGGCTGATGGCTCACAATGT AGTAGGCCAATCTTCAGGTCTCTTTGAATTTTCTCTGCTATTGAGGACATTTCCACTTTCTACTTA TCTCGACTCTATAACAACCTCCAACAGAA
WI-5222	52	G C	---			GCCGGCCTATCTTTAATTTAACTTGTATCTTTGGTGTCTCCATCCTAG[G/C]GATTCTGCCTTAT AATCTTTGCTCTGTGTAGATTACCTGATCTACTTTTGATACACAAGGCTGATGGCTCACAATGT AGTAGGCCAATCTTCAGGTCTCTTTGAATTTTCTCTGCTATTGAGGACATTTCCACTTTCTACTTA TCTCGACTCTATAACAACCTCCAACAGAA
WI-8007	242	C A	---			TATGCATCTCCACAAAAGGATATAATTTAAAAGTTTTTTTCATTAGAAAATAAATGTATAAAAATAA ATATGTTATTATAGGCATTTATTACTACTATAGTCTCTTGGAAAGGAACACCCCAACCAATACTT ATAAAGTACATGTAAATTTATAGTAACATATTTACTATATACATATGGAATAAATCATATCTCACA GAAGAGCTGAACAGACATTCACCAGGATACGACTGTGGAC[C/A]AGCTGCTG
WI-9823	97	C T	---			TCAGTTGCAAAAATGCTGCCATAAACATGCTTTTGCTTATCTCTGTGCATATGTATGTTTTGTTAG TCTATATTCACACATATGAGTGAATTT[C/T]GGGGCATGGGAAATACATCTTTATGAGACATTTGA ACTGCTCACCACACTATCATAGTATCCATTTAAACAGACCAACAATGTATAGAATTCCTTTGTTTTAC ATGCTTCCAACTGATTTGTATGACTATTGTATGCACAGTTGGATCACC

WI-9651b	105	A T ---	---	---	TCCTACATTCTATGGACAACCTCCATGCCCTTTGCACATGCTGATCCCTCCTCCTGGAATTCCTTTCCCT ACTTGCTCCTCATGTACAAATTTTCTGCTGCTCCTTCA/TJGGGGCAGCTTGCAAGCCTCCCTTTAGAC ACCTCTACAGGTACAGCCGACCATGCCCTACCTCCATGGCACTGCCAGGGACCCCTTATAGGCTCTG TCTTTAAACCTGTAAATGGTATATTAATCCTTGGTGTTGAATGCTCTC
WI-9651	139	T C ---	---	---	TCCTACATTCTATGGACAACCTCCATGCCCTTTGCACATGCTGATCCCTCCTCCTGGAATTCCTTTCCCT ACTTGCTCCTCATGTACAAATTTTCTGCTGCTCCTTCAAGGGCAGCTTGCAAGCCTCCCTTTAGACACCT CT/CACAGGTACAGCCGACCATGCCCTACCTCCATGGCACTGCCAGGGACCCCTTATAGGCTCTGT CTTTAAACCTGTAAATGGTATATTAATCCTTGGTGTTGAATGCTCTC
WI-7676b	309	A C ---	---	---	GTGACCTTCCTGCAGCGTGAGATGGCACATCCTTGCTGCTGGGACTTGGCCCTGCTATTATTTTG TATTTATGCTTAATCTCTCCACTGATGCATCCTCCAAAGGTAGATGGGAGGGTCTGTGTGAAGGG GCCGCTCTCTTGGTCTGCTGGGTGCAGGGGCAGGAAGCGTGTGGACTGCAGCTTCTGCTGGTGC TCCCCCGCTCCTCCTGGAGGCAGTATAGGAGAGAGAGCAAGGATTGAGT
WI-7676	139	C T ---	---	---	GTGACCTTCCTGCAGCGTGAGATGGCACATCCTTGCTGCTGGGACTTGGCCCTGCTATTATTTTG TATTTATGCTTAATCTCTCCACTGATGCATCCTCCAAAGGTAGATGGGAGGGTCTGTGTGAAGGG GC/TJGGCTCTCTTGGTGCCTGCTGGGTGCAGGGGCAGGAAGCGTGTGGACTGCAGCTTCTGCTG GTGCTCCCCCGCTCCTCCTGGAGGCAGTATAGGAGAGAGAGCAAGGATT
WI-10072	105	G A ---	---	---	CATTATCTTGCTGGTCTGTTCAATTCATCTTCCCTCTCCTCCAAATGAAGAGGATATTTAAGCATCAT CATCTGGCCCTTTTGGTGTGAATATTTTGTG/AJTGACTCCTATGCACATGATAAATTTGTTA TGCTTGCTCTATCTATCTTTTGTATAGGAGTTTGGCCCATGACCCCTTTATGAGGAGAAAAGGA TCACCCCTTTTGGCTCTACAACCTTATAGATATTTAAATATCTTT
WI-9986	42	T C ---	---	---	TTGGTGTGAACCTCAGAATATAGGGAAAATAAGACAAATTTGAAT/A,CJGTACCCAGGAAACAAGAG CCCTGCACTTGACTCCAAAAGGAGTTCTATTTCTGGCTGTTCCAGACTTTATGTATCTTGAGAA GAGAACTGTTTCCCTCTAAATCAGTTTCATCATCTGTATCCAGGGTAGTACTCACAAGAACAATGTCA ATATCAATAGCATGCATATGGGTGTGGATTCTTAGAACTTATTGCAATT
WI-7041	174	C A ---	---	---	GTCTATTGCAGGAGAAACGTCCCTTGCCACTCCCTCCTCATCAGGCCAAGTGGAGGACTGGCCAGA GGCCCTGCACATGCAAACTCCAGTCCCTGCCCTTCAGAGAGCTGAAAAGGGTCCCTCGGTCTTTTATTT CAGGGCTTGCATGGCTCTATCCCTCTATCCCTCTGCTG/AJCCACCTTCTTTGGAGCAAGGAGATGC AGCTGTATTGTGTAAACAGCTCATTGTACAGTGTCTGTTCAATAA
WI-7224	134	T C ---	---	---	ATAAACCTTGTTGTATGTATCACCCCAACTCAATAATTATCAACTTATGTGCTATCAGATATCCTCTCT ACCCCTCACGTTATTTGAAGAAAATCCTTAACATCAAACTTATCATCCATAAAAATGTCAGCATTT /CJATTTAAAAACAATAAATCTTTTAAAGAAACATAAGGACACATTTTCAAAATTAATAAAAAATAAAG GCATTTTAAAGGATGGCCTGTGATTATCTTTGGGAAGCAGAGTGATTCATGCTAG

WI-10826	132	A C ---			TCATTATGCAATTCACAGTAGCCCATGAAGTAGGTAAACCAGCCTCTATTTAACATGAGAAGAT GGAGGCCCTTTCCAAATGGACTAAGTAATGTGTCTCAGGTTTTCCTAATAAGCAAAGACCTGCA/C JCCCTGGCTTCCTGACTCCAAAGCTTATCCCTTCATGCTGTGCTGTCAGCCAGGACCCCATGGCA GAAAGCCCAAGCCTCTCCATCCCCAC
TIGR- A004S25	145	GA ---			AGATCTGCCATTAGTATTTATCTTTGAAGATACCTTTGGAGATTCAATTTCTTGAGTGGCACTGCAT GCTCATTCACTGAAACCTTGTGGGTATAGAAATGGAATGGAGAGTTTCAACACAGCTTTGCTGAAAC TGACTTTGGG/GA/CTCCAGACTTCACCTGCTTGGCATTGAACCATCACCTGGTTTGCAATCTTC ATGACTGAGGTTAACTTAAATGACTGAGGTTAACTTAAAC
WI-1021	24	A T --			AAACACACAGAAATCATCAAGCAC/GA/CTGTGTTTGAGATAAATGATAGCTGAGTCACCTATG TAAGAACTAACTCTGAAATAGTAGGATAGTATATCAATTCCTGTAAATAGATTCACCTCTCAGCAAT TGGTCTGTTTCACTTATGGAACCTCCTGACTGTAAATTTTCAATCTATGGAACTCCCCATACTGT AATTGGACAGTTTGGTTCCAC
WI-4687	121	GT ---			TAGTATGTCACCTGCCATGGTAAGGACTTTGATCACTAGGAATAAGAACACCTTTGAATGGCTTGTC TTTCAATAAAGAGAGTGACATGATTGAACATGTGTTTAGATAAAGGGCACTT/G/TCAGGAGTGT TTAGGATGAAGAGAGAGAGATTAAAGGAAGATCAGGAAGAAAGTAGCAATGGGAATGAAATAG GAGGCCCTGAGATCCACTGGATAATCTAAAAACCAAGAGAAAGAACTTGAT
WI-4719b	107	T G ---			TTCAATTCCTTCCAAATCCTTAGGAAATTTACATTATGGGCTAGTGTGTTGGGTGAGCGGATT ATGCTGACGCCATGGGTGTTTATAAGTACTTGAAGTGTGAGAGTACTGTAGAGGCTACACAGAAATCT CTGTGAGGGGCAIGTAATTGTATTCAATTCACAAATTCGTCTGCTATGCTCTCAGATTGCAGAAAAATCAC TGCTCAAAATCCCCACTTGTCAACTTATCCTTAAGACATTTTTCACAGGA
WI-4719	70	GA ---			TTCAATTCCTTCCAAATCCTTAGGAAATTTACATTATGGGCTAGTGTGTTGGGTGAGCGGATT AT/GA/CTGACGCCATGGGTGTTTATAAGTACTTGAAGTGTGAGAGTACTGTAGAGGCTACACAGAAATCT CTGTGAGGGGCAIGTAATTGTATTCAATTCACAAATTCGTCTGCTATGCTCTCAGATTGCAGAAAAATCAC TGCTCAAAATCCCCACTTGTCAACTTATCCTTAAGACATTTTTCACAGGA
WI-9484b	216	GC ---			TCAACACGCTTTATTGCCACTTCTGGCTCCCCCTCGTCCCAGCAAGATTCTACCTCTACCCCTGAGG AATACTGAGCTCCGATGCAGGGGAATGGGTGGGGGTGTACCACTTCTCCTCTGCACACTGCCAAGT TAAAGAAACCCCTGCTTGTGAGAGGGAGGGCCAGACAGGGAGGAATTCAGGGGCATGTATGGCTC AGTCCCACCTTCT/G/GA/CTGCAGAGTATAGGGACCAGGGTTCCAACTTT
WI-9484	178	G A ---			TCAACACGCTTTATTGCCACTTCTGGCTCCCCCTCGTCCCAGCAAGATTCTACCTCTACCCCTGAGG AATACTGAGCTCCGATGCAGGGGAATGGGTGGGGGTGTACCACTTCTCCTCTGCACACTGCCAAGT TAAAGAAACCCCTGCTTGTGAGAGGGAGGGCCAGACAGGGAGGAATTCAGGGGCATGTATG GCTCAGTCCCACCTTCTGACTGCAGAGTATAGGGACCAGGGTTCCAACTTT

WI-7330	207	C T	---			AGGATGGAAGGAGACACGGGGGAGGAGAACTCTCTTCTGCTAAATCGATAGGAGTCAGTTTTGTCT TAAATGCTGACTACAGCCACTGACATGGTTGGCTGGAAATTTCTCTTTAAATGTGGCATATAGGTTT GTGACACAAGAAAGTCATCTTTGGTGGCTAAGTTTACTAAGGAAATAACTGAAAGATTAAAG TGAGAG[C/T]TGAAAGAGAAATGATAATGCTTCCAAACTGTAGCTGTACAG
WI-9443	211	GA	---			TTAAAAACAGTTCAGGTTGGTGAAGCAGAAAGGGATGTGATTACAAATTTAAATGAATCAGTCACCT GCACAAATTAATCTCTTGGCATACAAACTGGTTTAAATGGCAATGATGACATCATAGCATGA CCAACATCATGGAAGGCAGCTAGAGTCCATCACGCTCACACCTGAGGGGAAGGCACTGCACCCA CTGACGAGAC[G/A]CAGAGACCTTGGACTACAGATGACACCCACATGCCCACTT
WI-7166	59	C T	---			TCTCTCAAAGAGAAAAACCCCTAAGAGACTGAGTTCTGCAAGCATCAGTTCTA[C/T]GGAT CATCAACAAGATTTCTTGTGCAAAATATTGACTATTCTGTATCTTTTCATCTTACTAAATTCGTG ATTTTCAAGCAGCATCTTCTGTTTAACTTGTGCTGTGAACAAATGTGAAAGAGCTCTTCCAAT TAATGCTTTTATATCTAGGCTACCTGTGGTTAGATTCAAGGCCCCGAG
WI-7259b	189	T C	---			GCTTCTCCCCAGGAAGCGGGTCTTGGCCTGGAACCTTCCAGAGAGGAGGGGAGCAATTTTAGCC CCACCTGCTCCCATCTGCCCTTCAACAGCTGCAGGCTGCTTCTCTCTGAGTTCTCTGGGCT GCGAGGCTCCCCCTGGGAATAGAGCAAGACGTGAGTCTTAACCTGGCCACAG[C/T]GGGGGAGCAG AGCCAGCAGGTGGACAGGTGTTTCAGGGGCCCACTTCCCTGGAGCTC
WI-7259	188	G T	---			GCTTCTCCCCAGGAAGCGGGTCTTGGCCTGGAACCTTCCAGAGAGGAGGGGAGCAATTTTAGCC CCACCTGCTCCCATCTGCCCTTCAACAGCTGCAGGCTGCTTCTCTCTGAGTTCTCTGGGCT GCGAGGCTCCCCCTGGGAATAGAGCAAGACGTGAGTCTTAACCTGGCCACAG[C/T]TGGGGGAGCA GAGCCAGCAGGTGGACAGGTGTTTCAGGGGCCCACTTCCCTGGAGC
WI-7322	275	A G	---			GTACTTTAGGCTGTGGAGGTGGGCAATTTAGTGTGACCTTGCACAGGGTTTCTAACAGATGAC CCTGTGAATCATAATTTAAACCTGCATATATTTATAGCCAGTCACATTTGCCCTCTCACCCCTATATG GCCATAAACTGCTAAGCACTCAGGCCCTCCCACTCATCAACCCCTTGAACAGAGAAAGAACCTC TGGTTCTCTATCCCTTGTACATAGAGAGTTTGTGATGGGGCTCTGGCTG
WI-7685	46	T C	---			TCAGTTCTAGTCTCTCTGGGGCCACACAGAACTCTTTTGGGCTGT[C/T]TTTCTCCCTCTGGATCA AAGTAGGACGAGGACCATGGACAGGCTCTGGAGCTGAGCCTCTCACCTGTACTCTTCCGAAAAATCCT CTTCTCTGAGGCTGGATCCCTAGCCTTATCTCTGATCTCCATGGCTTCCCTCCCTCTGCCGACTC CTGGTTGAGCTGTTGCCTCAGTCCCCAACAGATGCTTTCTGTCTC
WI-563	87	GA	---			TGTGACCAATTGTTATTTAGAGGGTTTAAACATGGCCTGACTATACCTGATGGTGGCCAGAATTTT CTGGGGGAGGGCTCCCC[G/A]CCCTGATCATGTCTACCTAACCTGCTACTCTAACAAATACTACTOC TGTGGTATGGGATCCTAAGCCAAAAGCTGAATGAACATGTTCTAGCACTACAGAAATCCATACT GCCCCCTCAGTAAAGGCAATTTTAAATCTCTTTGGATAACCCAGGGGCACAT

WI-931c	191	C A ---	---	GACCAGGGCACCAGAAAGCCACGGAGCCACAGCCACTAGCCCTGAACCTTGACACCCCTGGAGTT TCTCTCCCTCCCTATCCCTCACCAACACCTCCAGTGTCTATCTGCTGTGTCAAAATGATCCTCT GTTGCTGCACTGTCACTACTGTTGTATGGATTATAATTATGTCCAAAAAGCC[C/A]CGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGCAGA
WI-931b	81	A G ---	---	GACCAGGGCACCAGAAAGCCACGGAGCCACAGCCACTAGCCCTGAACCTTGACACCCCTGGAGTT TCTCTCCCTCCCT[A/G]TCCCTCACCAACACCTCCAGTGTCTATCTGCTGTGTCAAAATGATCCT TCTGTTGCTGCACTGTCACTACTGTTGTATGGATTATAATTATGTCCAAAAAGCCCGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGCAGA
WI-931	31	A G ---	---	GACCAGGGCACCAGAAAGCCACGGAGCCAC[A/G]GCCACTAGCCCTGAACCTTGACACCCCTGGAG GTTTCTCTCCCTCCCTATCCCTCACCAACACCTCCAGTGTCTATCTGCTGTGTCAAAATGATCCT TCTGTTGCTGCACTGTCACTACTGTTGTATGGATTATAATTATGTCCAAAAAGCCCGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGCAGA
WI-10870b	91	C T ---	---	GGATGACTTACCAATAGCAGGGTGGGTACATTCATGGGTAAACACCCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAAGTGGG[C/T]ACCTACTTAGAGCAGTGGAGTACCTGAGTACGACCCCC TTAGCAGCAGAAATTACAAGAAATCTTGGACCTGTACTCTGTATACAAAATAAGGACATGGGTCAGC CTGAGCCACTCTTAAACCATGAACCATCACCATTTAAATAACGTTGCCCCCCC
WI-10870	103	G A ---	---	GGATGACTTACCAATAGCAGGGTGGGTACATTCATGGGTAAACACCCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAAGTGGGCACCTACTTAGA[G/A]CAGTGGAGTACCTGAGTACGACCCCC TTAGCAGCAGAAATTACAAGAAATCTTGGACCTGTACTCTGTATACAAAATAAGGACATGGGTCAGC CTGAGCCACTCTTAAACCATGAACCATCACCATTTAAATAACGTTGCCCCCCC
WI-7719b	281	T C ---	---	AGTTTATCTTCCAGATGACCAGCAGTAGACAAATGGATACTGAGCAGAGTCTTAGGTAAAAGTCTT GGGAAATATTGGGCATTGGCTGGCCAAAGTCTACAATGTCCCAATATCAAGGACAACCCACCTAGC TTCTTAGTGAAGACAATGTACAGTTATCCATTAGATCAAGACTACACGGTCTATGAGCAATAATGTG ATTTCTGGACATTGCCCATGTATAATCTCACIGATGATTTCAAGCTAAAGCAA
WI-7719	163	A G ---	---	AGTTTATCTTCCAGATGACCAGCAGTAGACAAATGGATACTGAGCAGAGTCTTAGGTAAAAGTCTT GGGAAATATTGGGCATTGGCTGGCCAAAGTCTACAATGTCCCAATATCAAGGACAACCCACCTAGC TTCTTAGTGAAGACAATGTACAGTTATCC[A/G]TTAGATCAAGACTACACGGTCTATGAGCAATAAT GTGATTTCTGGACATTGCCCATGTATAATCTCACIGATGATTTCAAGCTAAA
WI-10396	72	C A ---	---	GCCTGGAGTATATCTAACTGTGGCCTCCACTTTCATTTTCTTGAACATTCCTATCAACTGGGAA GAGT[C/A]TGAGACTTTATGCCAGTTTCCCTCTCAGATTTTATGACGGTGTCTTTCTTTTGTTA TGCCATTTGAGGGATGATGTTTCTTAACTATGAAGTACTTGGCTGTCTCTCCATGCTGTTTCAGG TTAACAGCCACCATTTGTAAACACTTTGT

WI-10673	94 C G ---	---	---	TCCCTTTATGCACCCAGAGATATTATTAACACCAATTAACGTAGCAGGCCATGGCTCATGGGACC CACCCCGGTGGCACTCATGGAGGGG[C/G]TGCAAGTTGGAACATATGCAGTGTGCTCCGGCCACACA TCCTGCTGGCCCCCTACCTGCCCAATTCATCCTGCCAATAATCCTGTCTTATTTGTTTCATCCTG GAGAAITGAAGGGAGGTCAAGTTGTTTGCAATGATTTGTCAGAGAACCT
WI-7842	57 T C ---	---	---	CACAGCCATGCCCTTGAGGAGCGCGCCACCAGATGCTGAATCCCTATCCCATTTCTGTC/GTATGAG TCCCATTTGCCCTTGCAATTAGCAATCTGTCTCCCCCAAAAAGAAATGTGCTATGAAGCTTTCTTTCTCT ACACACTCTGAGTCTCTGAATGAAGCTGAAGGTCTTAGTACAGAGCTAGTTTTTCAGCTGCTCAGAAT TCATCTGAAGAGAGACTTAAGATGAAGCAAAATGATTCAGCTCCCTTATA
WI-7721	145 A C ---	---	---	CTGCTCATCACGCCACTGGAGTCCACACTTGAATTTGGGCAGCTACCACGGGTCTGCCATGCTCTGG AGGACAAAGGGGGCCACATCCCAACCCAGCTGTACCCAGCCCGGGGAGGTGCCAGCCCTTCCCTCC TGCTCTG[C/A/G]TCTGACTCTCTTTGAGGTCCCTGTATGCTACCTCTGACTTCTGTGGTCCCTCTG TGCTGCTCTCATCCATTCCTCTACTGGGGCTGGGGCTCTAGCCAA
WI-4767b	173 C A ---	---	---	TTCCAGTCTGTTTTATCCTTTTCATTGTCAAAAAGATGCTCTTAGACTGAAATTCATAAAGAGTTCCCT CAGGCTGGGTAATCCTAGATCTTCCTATATCCATTGAGTGTGAGGTGGAGAGAGGGTATGTTT CTTGCCCTTGAGAAATCCTAGAAAGCACAGGGATGACA[C/A]AAATCACTAAGGAATTCACCTAAGA CTCCTCTAACCCAGAGATTTTAACT
WI-4767	50 A G ---	---	---	TTCCAGTCTGTTTTATCCTTTTCATTGTCAAAAAGATGCTCTTAGACTGA/GIATTCATAAAGAGTT CCTCAGGCTGGGTAATCCTAGATCTTCCTATATCCATTGAGTGTGAGGTGGAGAGAGGGTATG TTTCTTGCTTGAGAAATCCTAGAAAGCACAGGGATGACACAAATCACTAAGGAATTCACCTAAGAC TCCTCTAACCCAGAGATTTTAACT
WI-7718f	222 C T ---	---	---	ATTGCACTGAAGTTTTTGAATACCTTTTGATGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAAACTGATGCCAAGGGGCTGAGTGAGTCACTACATGTTCTGGGGCCCGGAGATAGATG ACTTTGCAGATGGAAGAGGTGAAATGAAGAAGGAAGCTGTGTTGAACAGAAATAAGTCAAA AGGAACAAAAATTACAAAGAA[C/T]CATGCAGGAAGGAAAACTATGTATTAAAT
WI-7718e	60 T C ---	---	---	ATTGCACTGAAGTTTTTGAATACCTTTTGATGTTACTCAAGCAGTTACTCCCTACACTGA/T[C/GCAA GGATTACAGAAACTGATGCCAAGGGGCTGAGTGAGTCACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAATGAAGAAGGAAGCTGTGTTGAACAGAAAAATAAGTC AAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGIATTAAT
WI-7718d	31 G A ---	---	---	ATTGCACTGAAGTTTTTGAATACCTTTTGATGTTACTCAAGCAGTTACTCCCTACACTGATGCAA GGATTACAGAAACTGATGCCAAGGGGCTGAGTGAGTCACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAATGAAGAAGGAAGCTGTGTTGAACAGAAAAATAAGTC AAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAAT

WI-7718c	91	C G	---	---	ATTGCACTGAAGTTTTTGAATAACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGG[C/G]TGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAAATGAAGAAGGAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAAT
WI-7718b	248	A G	---	---	ATTGCACTGAAGTTTTTGAATAACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAGATG ACTTTGCAGATGGAAGAGGTGAAAATGAAGAAGGAGCTGTGTTGAAACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATT[A/G]AT
WI-7718a	42	A T	---	---	ATTGCACTGAAGTTTTTGAATAACCTTTGTAGTTACTCAAGC[A/C]TGTTACTCCCTACACTGATGC AAGGATTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGAT AGATGACTTTGCAGATGGAAGAGGTGAAAATGAAGAAGGAGCTGTGTTGAAACAGAAAAATAAG TCAAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAA
WI-7227d	99	G C	---	---	AGGGAATTGTGTTGCTCCTGGAGGAAGCCAGGCATCATTAAACAAGCCAGTAGGTACCTGGCTTC CGTGGACCAATTTCATCTTTAGACAAGCTTTA[G/C]JAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCAAGAGGACTGAGCTAAACA GTGTTATTATGGGAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227c	291	G A	---	---	AGGGAATTGTGTTGCTCCTGGAGGAAGCCAGGCATCATTAAACAAGCCAGTAGGTACCTGGCTTC CGTGGACCAATTTCATCTTTAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCAAGAGGACTGAGCTAAACA GTGTTATTATGGGAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227b	93	G T	---	---	AGGGAATTGTGTTGCTCCTGGAGGAAGCCAGGCATCATTAAACAAGCCAGTAGGTACCTGGCTTC TTCCGTGGACCAATTTCATCTTTAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCAAGAGGACTGAGCTAAACA GTGTTATTATGGGAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227a	24	A G	---	---	CCACAATGCTCTCCACGATGTCAAGGACTCCTGTCTGCTGGAGGTGGGAGACAAGAACCTCCG AAGAGGAAGCAAGAAAGCCGCTACTGTCTATGTTGTGATCCTTCATCGAACAACACTGATCGGAAACT TGAATCTGTTACTGAAATGAGGAGAGAGGACATGTGCTATTGAACAGGCCAACACACTGTAAT ATCCACAGACTCCCTCCCTGCCCCCATCCCA[A/C]ATGATCTTGAGATTTC
WI-7310b	234	A C	---	---	

WI-7310a	64 T A ---	---	---	CCACAATGCCTCTCCACGATGTCAAGGACTCCTGTCTGTCTGGAGGTGGGAGACAAGGAACCTT/A JCGAAGAGGAAGCAAGAAAGCCGTACTGTCTATGTTGTGATCCTTCATCGAACAAACTGATCGGAA AACTTGAATCTGTTACTGAAATGAGGAGAGAGGACATGTGCTATTGAACCTGAGCCAAACACACTGT AAATATCCACAGACTCCCTCCCTGCCCTGCCCATCCAAATGATCTTGAGATTTC
WI-7878b	162 A G ---	---	---	CCAGCAACACCTACACCTTGTACCTGCCCTGGGACTCCTATGATGCCCTGCTGGTTGATAATAATCA GATCATGCCCAAGACGGGCTCTGATAATGCTTGGGCTGATTGCAATGGAGGGCAAAATGCGTCC CTGAGAGAAATCTGGGAGGAGCTGAG/GTGTGATGAAGGTGATGTTGGGAGGAGCACAGTGT CTGTGGGAGGCCAGGAAGCTGCTCACCCTCAAGATTGGTGCAGGAAACTA
WI-7878a	51 C G ---	---	---	CCAGCAACACCTACACCTTGTACCTGCCCTGGGACTCCTATGATGCCCTG/C/GTGGTTGATAATAA TCAGATCATGCCCAAGACGGGCTCTGATAATCGTCTTGGGCTGATTGCAATGGAGGGCAAAATGC GTCCCTGAGGAGAAATCTGGGAGGAGCTGAGTGTGATGAAGGTGATGTTGGGAGGAGCACAGTG TCTGTGGGAGGCCAGGAAGCTGCTACCCAAAGATTGGTGCAGGAAACTA
WI-7381c	213 C T ---	---	---	CTCCACATCCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCCCTTTCTTTCTACCC AGCCCTGCAAGTTTCTCATGGACGCTCGGAGGAGCAGGCTGAGGTTCTGCTATGGTGAGATC AGATGTGGCCAAAGGAAGGAGCTCTGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGACA AAACGGCTC/C/TGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381b	54 C G ---	---	---	CTCCACATCCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCCCTG/C/GCTTTCTTTCT ACGAGCCTGCAAGTTTCTCATGGACGCTCGGAGGAGCAGGCTGAGGTTCTGCTATGGTGAG ATCAGATGTGGCCAAAGGAAGGAGCTCTGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAG ACAAAACGGCTTCCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381a	53 C G ---	---	---	CTCCACATCCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCCCTG/C/GCTTTCTTTCT ACGAGCCTGCAAGTTTCTCATGGACGCTCGGAGGAGCAGGCTGAGGTTCTGCTATGGTGAG ATCAGATGTGGCCAAAGGAAGGAGCTCTGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAG ACAAAACGGCTTCCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-1017b	93 G A ---	---	---	AAATTTGCTCTATTCGGACCCCTCATATTAAATAAGAGCAATGAGAGCGGGAATTTGAACCTCTCTC AGGTACTGACTGTGGGACCAGACAAG/GA/GATGTAGATTGTCACATTCAATCCTGAAACAAACCTG CCAGGCAAGTCTTCTTCCCATTTACAAATAAGGAGACAAAAATTAGGAGATTAAATAACTCATCAC TGTTTTCAAAATAAGGAGTGTGTGAGGTTTTGTCCC
WI-1017a	92 G A ---	---	---	AAATTTGCTCTATTCGGACCCCTCATATTAAATAAGAGCAATGAGAGCGGGAATTTGAACCTCTCTC AGGTACTGACTGTGGGACCAGACAAG/GA/GATGTAGATTGTCACATTCAATCCTGAAACAAACCTG CCAGGCAAGTCTTCTTCCCATTTACAAATAAGGAGACAAAAATTAGGAGATTAAATAACTCATCAC TGTTTTCAAAATAAGGAGTGTGTGAGGTTTTGTCCC

WI-1795b	130 T C ---	---	GAAGCAACCAGAAAGTATCTTTATCCCCATCTAGATTATGCTGGGTTCTCCAGACTCCTACGATTA AATTGTATGCATGTGAACAACACTGATGAGGTACTTAGATCTCAGTGTCTTGAGAGAAAGAAAGT[C]C GTCTACCAATTTACCAAAATTCGTAGTACAAATTAAGTATCTCTGTTATCTCCCCCTAGGAGTCTAA AGTGAGCTGGGGAAGGCAGGATTT
WI-1795a	47 T C ---	---	GAAGCAACCAGAAAGTATCTTTATCCCCATCTAGATTATGCTGGGTT[C]CTCCAGACTCCTACGA TTAAATTGATGCATGTGAACAACACTGATGAGGTACTTAGATCTCAGTGTCTTGAGAGAAAGAAAGTC GTCTACCAATTTACCAAAATTCGTAGTACAAATTAAGTATCTCTGTTATCTCCCCCTAGGAGTCTAA AGTGAGCTGGGGAAGGCAGGATTT
WI-10616d	136 G A ---	---	CACACAATTTGCAAAACACTTCAAAGTGAACGCCCGGACATCATCAGCCCCGTTAACGTCAGGCCATGT CCCACATAGAGAACGCTTTACTCCACGCTCTCCATACGTAGGTCTGGTCTCTCTATCACATTGCCA C[G]ATAGCCCTCCCTTCCCTTCCCTACAGGCCCTCTCAGGGCCCCAGTCCCTCTGAGACTCCC ATGGATCATTCCTGTTTCTGTATCAGGCAGTGATTAACTCCTTTTGT
WI-10616c	136 G A ---	---	CACACAATTTGCAAAACACTTCAAAGTGAACGCCCGGACATCATCAGCCCCGTTAACGTCAGGCCATGT CCCACATAGAGAACGCTTTACTCCACGCTCTCCATACGTAGGTCTGGTCTCTCTATCACATTGCCA C[G]ATAGCCCTCCCTTCCCTTCCCTACAGGCCCTCTCAGGGCCCCAGTCCCTCTGAGACTCCC ATGGATCATTCCTGTTTCTGTATCAGGCAGTGATTAACTCCTTTTGT
WI-10616b	141 C T ---	---	CACACAATTTGCAAAACACTTCAAAGTGAACGCCCGGACATCATCAGCCCCGTTAACGTCAGGCCATGT CCCACATAGAGAACGCTTTACTCCACGCTCTCCATACGTAGGTCTGGTCTCTCTATCACATTGCCA CGTAGC[C]TCTCCCTTCCCTTCCCTACAGGCCCTCTCAGGGCCCCAGTCCCTCTGAGACTCCC ATGGATCATTCCTGTTTCTGTATCAGGCAGTGATTAACTCCTTTTGT
WI-10616a	116 G C ---	---	CACACAATTTGCAAAACACTTCAAAGTGAACGCCCGGACATCATCAGCCCCGTTAACGTCAGGCCATGT CCCACATAGAGAACGCTTTACTCCACGCTCTCTCCATACGTAGGTCTGGTCTCTCTATCACATTG CCACGTAGCCCTCCCTTCCCTTCCCTACAGGCCCTCTCAGGGCCCCAGTCCCTCTGAGACTCCC ATGGATCATTCCTGTTTCTGTATCAGGCAGTGATTAACTCCTTTTGT
WI-1126c	52 G A ---	---	CTCTTATTTCTCTGGGCACCTGCTTTCTTTGGGGCAAACTTCCAGTATCACT[G]ATATAATAATAA AAACCCGTGAAGTCTGCTTGCAATTTCAAGATTCAATATATATCCAGATTGTTTCCCAGCAAGAA AATTTTATTTCTCAAGATATAAAAAATAAATAATTAATTCAGTTTCTCAAAAGGAATATGAAATTT TGTTAAATGCAAAATCCAGCTGAACCTTTTGGGACTTGCTTTTATTTCTT
WI-1126b	230 T C ---	---	CTCTTATTTCTCTGGGCACCTGCTTTCTTTGGGGCAAACTTCCAGTATCACTGATATAATAATAA CCCTGTAAAGTCTGCTTGCAATTTCAAGATTCAATATATATCCAGATTGTTTCCCAGCAAGAAATTT TTATTTCTCAAGATATAAAAAATAAATAATTAATTCAGTTTCTCAAAAGGAATATGAAATTTGTT AAATGCAAAATCCAGCTGAACCTTTT[C]GGGACTTGCTTTTATTTCTT

WI-1126a	97 T C ---	---	CTCTATTCTCTGGGCACTGCTTTCTTTGGGGCAAACTCCAGTATCACTGATACTAATAAAAA CCCTGTAAGTCTGCTTGCAATTTCAAGATTC[CAATATATATCCAGATTGTTTCCAGCAAGAAA ATTTTATTTCTCAAGATATAAAAAATAATATTTAAATTCAGTTCTCCTCAAAAGGAATATGAAATTT GTTAAATGCAATCCAGCTGTAACCTTTTGGACTTGCTTTTATTTCTT
WI-11183c	124 C T ---	---	TAGTGCTAATTTTGGAAAAGTTTGCTGATTTTAAAAATCTTTTAAACTTTGAAAATTTAGAGTAC ATATAAATAAAATAAGACCAGATAGGTATTAATTCAGATGATTTTGGCCCTTGCTCACTAACATTT TTTATGACATACAAATGACCAAAATGATGTTTTTATGAAGGTAGGATAGAGTTTAAATATTGGT ATGGGTGCTAGAGTTAGTAATGGAA
WI-11183b	192 T C ---	---	TAGTGCTAATTTTGGAAAAGTTTGCTGATTTTAAAAATCTTTTAAACTTTGAAAATTTAGAGTAC ATATAAATAAAATAAGACCAGATAGGTATTAATTCAGATGATTTTGGCCCTTGCTCACTAACATTT ATGACATACAAATGACCAAAATGATGTTTTTATGAAGGTAGGATAGAGTTTAAATTCAGTTTGGT ATGGGTGCTAGAGTTAGTAATGGAA
WI-11183a	118 C T ---	---	TAGTGCTAATTTTGGAAAAGTTTGCTGATTTTAAAAATCTTTTAAACTTTGAAAATTTAGAGTAC ATATAAATAAAATAAGACCAGATAGGTATTAATTCAGATGATTTTGGC[CTCTTGCTCACTAAC TTTATGACATACAAATGACCAAAATGATGTTTTTATGAAGGTAGGATAGAGTTTAAATATTGGT ATGGGTGCTAGAGTTAGTAATGGAA
WI-10770b	174 G A ---	---	GCTTGGTTTGGCTTTAGTCTTATTGCTCAGTCTTGAGTCTCCCTTCTGCGCTGGCCCTTTTGATTTCA CCCATACCTCTATGCCCTGCTCAGACCAATTTCCCTATCTGAGCGCTCTTCCCTTGACTTTCTC TTCACCAACCTCTTTTATTCTTCAGGACACTCA[G/A]TTCACATGCCACTCTCGTGACACTGTCTCT TTCACATCTTCTGCTGCTCCCTTTCC
WI-10770a	49 G T ---	---	GCTTGGTTTGGCTTTAGTCTTATTGCTCAGTCTTGAGTCTCCCTTCTGCGCTGGCCCTTTTGATTT TCACCATACCTCTATGCCCTGCTCAGACCAATTTCCCTATCTGAGCGCTCTTCCCTTGACTTTCTC CTGTTCAACCAACCTCTTTTATTCTTCAGGACACTCAGTTCACATGCCACTCTCGTGACACTGTCTCT TTCACATCTTCTGCTGCTCCCTTTCC
WI-9667b	82 C T ---	---	GATGACAACTTCTGCTGTGACCCCTTAGTCCCTGCTCATGACACTTTTCAATCTCTGCCCTGTATCATGG TTATCACTGGACA[CTAGCCACCTCCCGCAGCGCTTAGAACTCCATGAGTAAGGACCCCTGTCTA ATGTCGGCTTCTCTCTTATGGTATTACACACAGTCAATAGGATGGTAGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTCTCTGTACCCAGTACCTAAGTCCAAACTTGCAATCT
WI-9667a	68 G C ---	---	GATGACAACTTCTGCTGTGACCCCTTAGTCCCTGCTCATGACACTTTTCAATCTCTGCCCTGTATCATG G/CTTATCACTGGACACAGCCACCTCCCGCAGCGCTTAGAACTCCATGAGTAAGGACCCCTGTCTA ATGTCGGCTTCTCTCTTATGGTATTACACACAGTCAATAGGATGGTAGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTCTCTGTACCCAGTACCTAAGTCCAAACTTGCAATCT

WI-10400d	189 A G ---	---	ACATTTTATTAGCAAAATCAGCAAAATATAAATAGAAAGTAATTGCAATTCAGACATCTGCTG GTTAACTGTTAAGATGGTTAGCACACATGTAAGCACTTACTAACACAATATTTTATTCTAAATTT TCITTCCTTACCTTACTCTCCCAACCAAAATACGTAAGTACCTATGTCAGJTGCCATGTAG TTTTTGGTTCATTTACTTGCAAAATATTCAAAAGGCGTTAATGCAATTATG
WI-10400c	166 A C ---	---	ACATTTTATTAGCAAAATCAGCAAAATATAAATAGAAAGTAATTGCAATTCAGACATCTGCTG GTTAACTGTTAAGATGGTTAGCACACATGTAAGCACTTACTAACACAATATTTTATTCTAAATTT TCITTCCTTACCTTACTCTCCCAACCAAC/CJAAATAACGTAAGTACCTATGTCATGCCATGTAG TTTTTGGTTCATTTACTTGCAAAATATTCAAAAGGCGTTAATGCAATTATG
WI-10400b	165 A G ---	---	ACATTTTATTAGCAAAATCAGCAAAATATAAATAGAAAGTAATTGCAATTCAGACATCTGCTG GTTAACTGTTAAGATGGTTAGCACACATGTAAGCACTTACTAACACAATATTTTATTCTAAATTT TCITTCCTTACCTTACTCTCCCAACCAAC/CJAAATAACGTAAGTACCTATGTCATGCCATGTAG TTTTTGGTTCATTTACTTGCAAAATATTCAAAAGGCGTTAATGCAATTATG
WI-10400a	46 T C ---	---	ACATTTTATTAGCAAAATCAGCAAAATATAAATAGAAAGTAATTGCAATTCAGACATCT GCTGGTTAACTGTTAAGATGGTTAGCACACATGTAAGCACTTACTAACACAATATTTTATTCTA ATTTTCTTCCCTTACCTTACTCTCCCAACCAAAATACGTAAGTACCTATGTCATGCCATGT AGTTTTTGGTTCATTTACTTGCAAAATATTCAAAAGGCGTTAATGCAATTATG
WI-10809b	78 C T ---	---	AAAGGGCTACAACTAAGGCCAAACCAATGAACGGTATAAGGAGGGTAAATGCAAGGGGAGACCC CAGCTCTACCA/CJTITAGAAAGGGCATTCAAGCACATTCATGAGGCTTCATATACTGGTTAG CAACAAATGGATGTATTAGCCCAAGGCGGGTATGGACCAAAAGTGCCAGTGATGAGGCCACA GTGAATATCCACCTAAGCACCTTCTTGGATGATGTACACATGACATAGGCTTAA
WI-10809a	33 C T ---	---	AAAGGGCTACAACTAAGGCCAAACCAATGAAC/JTGGTATAAGGAGGGTAAATGCAAGGGGAGA CCCAACCTCTCACCCTTAGAAAGGGCATTTCAGGCACATTCATGAGGCTTCATATACTGGTTAGC AAACAAATGGAATGTATTAGCCCAAGGCGGGTATGGACCAAAAGTGCCAGTGATGAGGCCACAG TGAATATCCACCTAAGCACCTTCTTGGATGATGTACACATGACATAGGCTTAA
WI-7038c	266 T C ---	---	CGAGCTTGGGATAAGCAAGGGACCTTGGCGCTCTCAGCTTCCCTGCCACATCCAGCTTGTGTCC CAATGAAATAGTGAATGCTGGGCTGTCTCTCCCTTCCAGGAATGCTGGGCCCCCAGCTGGCCAGAG AAGAAGACTGTCAGGAAGGGTCGGAGTGTGTAACCCAGCATACAGTTTGGCTTTTTCACATTGAT CAATTTTATGAAATAAAAGATCCCTGCAATTTATGGTGTAGTCTGAGTCC
WI-7038b	140 A C ---	---	CGAGCTTGGGATAAGCAAGGGACCTTGGCGCTCTCAGCTTCCCTGCCACATCCAGCTTGTGTCC CAATGAAATAGTGAATGCTGGGCTGTCTCTCCCTTCCAGGAATGCTGGGCCCCCAGCTGGCCAGAG AAGA/CJGACTGTCAGGAAGGGTCGGAGTGTGTAACCCAGCATACAGTTTGGCTTTTTCACATT GATCATTTTATGAAATAAAAGATCCCTGCAATTTATGGTGTAGTCTGAGTCTGA

WI-7038a	31	G A	---			CGAGCTTGGGATAAAGCAAGGGGACCTTGGG(GA)CTCTCAGCTTCCCTGCCACATCCAGCTTGTG TCCCAATGAATACTGAGATGCTGGGCTGTCTCCCTTCCAGGAATGCTGGCCCCCAGCCTGGCCA GACAAGAAGACTGTGAGGAAGGGTCGGAGTCTGTAAACCATACATACAGTTTGGCTTTTTCACATT GATCATTTTATATGAATAAAAGATCCTGCTATTATGGTGTAGTTCIGA
WI-3429b	64	G T	---			ATACGCTTCTGTCTGCCACAGTGAACCAAGCAGCCAGGTGGCCAGGGTCCACACA(G/T) CCCTCAGCCCCCTTCAAGCTTTCATGTGTCATCGGTGACTCAGCACAGAGTTTCCAACCTCATGTGA CAAAATACAGATCCCAAGTCTCCTCCTGGATTGGATCTAGCAAGACCAGAGACGGTCCCTAGAA TCCTGACTGTTAACAAGCACTCCAGGCAATCTTAAGACCAAGCAGCGGAGC
WI-3429a	62	C T	---			ATACGCTTCTGTCTGCCACAGTGAACCAAGCAGCCAGGTGGCCAGGGTCCACACA(G/T)AG CCCTCAGCCCCCTTCAAGCTTTCATGTGTCATCGGTGACTCAGCACAGAGTTTCCAACCTCATGTGA CAAAATACAGATCCCAAGTCTCCTCCTGGATTGGATCTAGCAAGACCAGAGACGGTCCCTAGAA TCCTGACTGTTAACAAGCACTCCAGGCAATCTTAAGACCAAGCAGCGGAGC
WI-6786c	151	G A	---			ATTTAGGACAGTGAAAAAAGGGATTTATAATAAAATCTATGCCATCCAGGAGGTATGTGTCACT GTCCAGAACATCTAGATGAAGTGGCTTCTTTGGCGAAAGGATAAAGAGTGAGTGACGGTGACCT GTAGCCCCATCTTCT(GA)TGGGATAAGGTGTCATTTGTTCTTGGAGGTGAAATGCCACATTC TTTTGGCAGGGGACACTCCTTCTGGGTGCTCTATTGCTCAGTTTCATCAT
WI-6786b	111	A T	---			ATTTAGGACAGTGAAAAAAGGGATTTATAATAAAATCTATGCCATCCAGGAGGTATGTGTCACT GTCCAGAACATCTAGATGAAGTGGCTTCTTTGGCGAAAGGATAAAGAGTGAGTGACGGTGGA CCTGTAGCCCCATCTTCTGTGGGATAAGGTGTCATTTGTTCTTGGAGGTGAAATGCCACATTC TTTTGGCAGGGGACACTCCTTCTGGGTGCTCTATTGCTCAGTTTCATCAT
WI-6786a	106	A T	---			ATTTAGGACAGTGAAAAAAGGGATTTATAATAAAATCTATGCCATCCAGGAGGTATGTGTCACT GTCCAGAACATCTAGATGAAGTGGCTTCTTTGGCGAAAGGATAAAGAGTGAGTGACGGTGGA CCTGTAGCCCCATCTTCTGTGGGATAAGGTGTCATTTGTTCTTGGAGGTGAAATGCCACATTC TTTTGGCAGGGGACACTCCTTCTGGGTGCTCTATTGCTCAGTTTCATCAT
WI-6711b	226	G T	---			GGCTATTTGTAATGCTTGGTATTGACTCCAAAATTGAATAAGTATTGGGAAGAATCCCTCACCT ACTTCCAAATCCCTTACATATCAATTTACACAAAGCCCCCTAAACCTCAGTTCCCAATCACTGAAT TTCATATACCTCCATTATTAAATCAATACATCATTCGAGAGAAAAGACAAACGGTGCCCAACTGGGTT TGGTTGGTGCCTGCACACCCACA(G/T)TGGCAACTAAGTGAATCTCTAAA
WI-6711a	36	T C	---			GGCTATTTGTAATGCTTGGTATTGACTCCAAAATTGAATAAGTATTGGGAAGAATCCCTC ACCTACTTCCAAATCCCTTACATATCAATTTACACAAAGCCCCCTAAACCTCAGTTCCCAATCACTCT GAATTCATATACCTCCATTATTAAATCAATACATCATTCGAGAGAAAAGACAAACGGTGCCCAACTG GGTTTGGTTGGTGCCTGCACACCCACAGTGGCACTAAGTGAATCTCTAAA

WI-10613b	172 A C ---	---	---	ATTGTATGCCAAAATCATAATACCCCTGCATTCTAGAAACATACAGTGTAAATAGAAATTTTGAGCCATA TGGTGAAAAATTTAGAAGTATTATTCTCTATATGTATATACAGTTTAAACATCAATGAATGTGATTT TTTGTCAAGCTTTTGACAAGGCCAGGCAATTTATTG/C/GCCCTAGGAGGGTTACTATAATTTAGA AAGGCTCTTACCTTCCACTCTATAATTTAAGTCTCGGACTAGGATGTAG
WI-10613a	44 G A ---	---	---	ATTGTATGCCAAAATCATAATACCCCTGCATTCTAGAAACATACAGTGTAAATAGAAATTTTGAGCC ATATGGTGAAAAATTTAGAAGTATTATTCTCTATATGTATATACAGTTTAAACATCAATGAATGTG ATTTTGTCAAGCTTTTGACAAGGCCAGGCAATTTATTGAGCCCTAGGAGGGTTACTATAATTTAG AAAGGCTCTTACCTTCCACTCTATAATTTAAGTCTCGGACTAGGATGTAG
WI-7587c	133 A T ---	---	---	GCTCTAGTGGGAAACCTCAGGTAGCTCCCGAAGATCTGTGCTTCCAAAGTGACTACCCCTTGAAGC ACATCCCCCTCTGGATCTGAAAGAGCCCTTGGCTCAGGGGCTCTTTTCCAGCCCTGAGGAAAJA/ TJGGAATGAACCACTCCCTGCCATTCCCTATAAGAAATATCCAAAGACCCAGGCAATTTTGCCOCTCT TTCCACATGCCCCCATATGCTGAGCCAAACTGCACTGGGGGCTGCCCTC
WI-7587b	81 G A ---	---	---	GCTCTAGTGGGAAACCTCAGGTAGCTCCCGAAGATCTGTGCTTCCAAAGTGACTACCCCTTGAAGC ACATCCCCCTCTG/GA/JATCTGAAAGAGCCCTTGGCTCAGGGGCTCTTTTCCAGCCCTGAGGAAA AGGAATGAACCACTCCCTGCCATTCCCTATAAGAAATATCCAAAGACCCAGGCAATTTTGCCOCTCT TCCACATGCCCCCATATGCTGAGCCAAACTGCACTGGGGGCTGCCCTC
WI-7587a	28 C T ---	---	---	GCTCTAGTGGGAAACCTCAGGTAGCTCC/JTGAAGATCTGTGCTTCCAAAGTGACTACCCCTTGA AGCACATCCCCTCTGGATCTGAAAGAGCCCTTGGCTCAGGGGCTCTTTTCCAGCCCTGAGGAAA AGGAATGAACCACTCCCTGCCATTCCCTATAAGAAATATCCAAAGACCCAGGCAATTTTGCCOCTCT TCCACATGCCCCCATATGCTGAGCCAAACTGCACTGGGGGCTGCCCTC
WI-10681b	103 T A ---	---	---	ATGACTCAGGTGACAAAAGAGCATGTCTCCTAGACCCCATTTGACTTACGCAAACTCAATCAGCCAACC ACAGAAAAGCTAAAGACATCCCTTTTAAAAAGCC/T/JAAGACAGCCATTTTAACTCCTAATTCG TAGTTTATGATTTTCTCAAAATTTCCACACACAGAAAGAACTTCAAGGTTAGGTTCTAATGTTA CCATTGCTAACACTATTGCTCTTGGAGAGGAGGAGTGACGCTCTGTAAAG
WI-10681a	41 A T ---	---	---	ATGACTCAGGTGACAAAAGAGCATGTCTCCTAGACCCCATTTG/JTTCAGCAAACTCAATCAGCCA ACCACAGAAAAGCTAAAGACATCCCTTTTAAAAAGCCCTAAAGACAGCCATTTTAACTCCTAATTCG TAGTTTATGATTTTCTCAAAATTTCCACACACAGAAAGAACTTCAAGGTTAGGTTCTAATGTTA CCATTGCTAACACTATTGCTCTTGGAGAGGAGGAGTGACGCTCTGTAAAG
WI-7222c	126 G T ---	---	---	GCCTCTCCTCACTGCTCGAOCCTAGGCTAGGAAAGGGCTGCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTCACCCCTGTTCTCAAGTGGGGATGGG/G/JAATAA AGGAGGGGGAATCCCTTGAACAAGAAGAACTGGGGATAGTTATTTCCACCTGCCCTTGAAGCTT TAAGACAGTGTATTTTGTGTAAGTGTATTTTCAAGACTCGAATTCATTTT

WI-7222b	255	G A ---	---		GCCTCTCCTCAACTGTCTGGAGCCCAAGGCTAGGAAAGGCGCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTCAACCCTGTCTCAAGTTGGGGGATGGGAATAAAGG AGGGGAATCCCTTGAACAAGAAGAACTGGGGATAGTTATATTCACCTGCCCTTGAAGCTTTAA GACAGTGATTTTGTGAAGTTGATTTCAAGACTCGAATTCATTTTCTCA
WI-7222a	126	G T ---	---		GCCTCTCCTCAACTGTCTGGAGCCCAAGGCTAGGAAAGGCGCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTCAACCCTGTCTCAAGTTGGGGGATGGG(GT)AATAA AGAGGGGAATCCCTTGAACAAGAAGAACTGGGGATAGTTATATTCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGAAGTTGATTTCAAGACTCGAATTCATTTT
WI-8054d	41	C A ---	---		AAAGATGACACTTAGAACTGGATCAGTGGCCCTTTCTCTT(C/A)TTATCTCTCCAGTTCAAAATG CTTGCACTTTTAAATAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAACGCACCTCAAGCCTTAGCA CAATCTCTTTGTAGTTTAGCCCTTTTCCGGAAATCGGCTTAGTTGCCACCATAGCCACTCTGCT TCCTGTCAACGCCGCTTTCCCTGGGCGTACAGAGAAATCCTTGCCCTT
WI-8054c	237	G T ---	---		AAAGATGACACTTAGAACTGGATCAGTGGCCCTTTCTCTTATCTCTCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAACGCACCTCAAGCCTTAGCACA TCTCTTTGTAGTTTAGCCCTTTTCCGGAAATCGGCTTAGTTGCCACCATAGCCACTCTGCTTCC TGTCAATAGCCGCTTTCCCTGGGCGTACAGA(GT)AATCCTTGCCCTT
WI-8054b	148	T C ---	---		AAAGATGACACTTAGAACTGGATCAGTGGCCCTTTCTCTTATCTCTCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAACGCACCTCAAGCCTTAGCACA TCTCTTTGTAG(T/C)TTAGCCCTTTTCCGGAAATCGGCTTAGTTGCCACCATAGCCACTCTGCT TCCTGTCAACGCCGCTTTCCCTGGGCGTACAGAGAAATCCTTGCCCTT
WI-8054a	131	C G ---	---		AAAGATGACACTTAGAACTGGATCAGTGGCCCTTTCTCTTATCTCTCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAACGCACCTCAAGCCTTAG(C/G)A CAATCTCTTTGTAGTTTAGCCCTTTTCCGGAAATCGGCTTAGTTGCCACCATAGCCACTCTGCT TCCTGTCAACGCCGCTTTCCCTGGGCGTACAGAGAAATCCTTGCCCTT
WI-10854b	152	G T ---	---		TTCCACAAAACCTTCCCTGGGCGGGGTGACTAAGATGAGAAGTGGGAGAACTGGATAGTTTAAATAA ATGTTTATATTTACTTTAAAGCGAAGTTGAACACGAAAGCAGATAGTTAACGTCCTGGTAAGTTTAT ACGGGTGCGAGGCAACA(G/J)GGAGAGGTACGGGAATAGTTCTACTTCTGTTTTTATTCTGTG TTTTAGACACAGGGTCTGCTGTGTG
WI-10854a	102	C T ---	---		TTCCACAAAACCTTCCCTGGGCGGGGTGACTAAGATGAGAAGTGGGAGAACTGGATAGTTTAAATAA ATGTTTATATTTACTTTAAAGCGAAGTTGAACA(C/T)GAAGACGATAGTTAACGTCCTGGTAAGTT TATACGGGTGCGAGGCAACAGGAGGTACGGGAATAGTTCTACTTCTGTTTTTATTCTGTG TTTTAGACACAGGGTCTGCTGTGTG

WI-9826b	127 G A ---	---	---	AAATTTATATGTGAAGGGTTAGCAAACTATGCCCCACAGGCCCATCTAGCCATGCTATTTTGTG TGCTGATGGCTGTTTGGTGTGTTGACGAGTTGAGCCATTGTGACAGAGGCTGTATGAG/GCCTT CAAAGCCAAAATAAATAATTTACTCTCTGGCCCTGACGGGAAAGTTTGTGATCTAGATATTTAAA GGCAGAGAGATCAGAAGTGTGAA
WI-9826	125 A T ---	---	---	AAATTTATATGTGAAGGGTTAGCAAACTATGCCCCACAGGCCCATCTAGCCATGCTATTTTGTG TGCTGATGGCTGTTTGGTGTGTTGACGAGTTGAGCCATTGTGACAGAGGCTGTATGAG/GCCTT AAAGCCAAAATAAATAATTTACTCTCTGGCCCTGACGGGAAAGTTTGTGATCTAGATATTTAAAAG GCAGAGAAGATCAGAAGTGTGAA
WI-15986	60 T G GTGGGTTTT	TTGTTTGTGT AAACGTAAAA GAAATGT	TGACATTATAT	CGGACACGTGTATATACAAATACAGATCGTATGGGTTTGTGTGGGTTTTTTTTT/GJTTAC ATTTCTTTACGTTTATATAATGTCAGCATTTCAA
WI-8655	29 A G AG	AACTGCAAAAT AGGAAACCAG	CCACCTGGGGC TTOG	TTCAGTAACGTGCAAAATAGGAAACCAGAGAG/GGGAGCCCCAGGTGGGACAAATCATGGCTACCCC TCCCAACAGAACAGGGGGAGGGTGGCCCCCTACACCCTTTAT
WI-8170b	259 G A ---	---	---	GCACCTCTCTCTGAGCAACAGGTACACATTTTCTCTAACATTGATCTATAACACACCAGAACCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAACTACTCTACCAAGATGCTGTGGTAAGGTTAG CATTTGGTGAGAGATTTACAAGGTTAAGATCATGTGCCATCAAGTGCAATCCTATCAATCAGAA ATAAAGGTAAAGGGCCCTCAAATGAAATCTACGGAAAAACATAACACAAGA
WI-8170a	204 T A ---	---	---	GCACCTCTCTCTGAGCAACAGGTACACATTTTCTCTAACATTGATCTATAACACACCAGAACCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAACTACTCTACCAAGATGCTGTGGTAAGGTTAG CATTTGGTGAGAGATTTACAAGGTTAAGATCATGTGCCATCAAGTGCAATCCTATCAATCAGAA A/T/A/AAAGGTAAAGGGCCCTCAAATGAAATCTACGGAAAAACATAACAC
WI-8172	136 C G GACA	CCTTTATTAAA ATTGTTTTCTT	GAAGAGAAAT GTAATACCTGT AAAGGTAC	CAGGATTCCTTAAGTCATCTCCAATCTCCAGGTACATGGTGAAGAGTCACCTGTAAACACGAA ATCTAACCATTAACAAGCTTTTAAATCCTTCGGTAACTCCCTTTATTAAATTTGTTTCTTGACAT A/C/GIAGTACCTTTACAGGTATTACATTTCTCTCACCCTTACA
WI-8183	56 G A TGC	TGAAATAAAA ACAATTTCTGT	TGTGTTGAAAT CAACCTGC	AGCAGGGTTTGAATGATCCCTTATTTACATGAAATAAAAACAATTTCTGTTGC/GA/GCAGGTT TGATTTCAACACAGTTGAATCTGTAAACCAAGCTCGTTTCTGATGCAGGACAAATATCCACAAT ATTTAAACTGCAAGCACCATGC
WI-14149	83 C T ---	---	---	GCCTTATTGGGATTGCAAGCGTTACAGGTTAAAGACAAAACCAAGCATGGGATTTGCCGGAAT ATTAGCGTTAAAGGAGC/TTTGAGTTGAGTCAACACACGGG
WI-8712	44 G A G	CACAGGGAAG AGGTAGTGA	CAGGAAGCCTG ACCATCTC	TCAACAATGACACTGTGTAAACAGCACAGGGAAGAGGTAGTGGAG/GA/GAGATGGTCAGGCTTCTG TTCCCTAACCCAGCAGAGCCCCAGCAACCTAGAAAGGCCCTCACCTAGCCCTTAAT

WI-8827	22 C T	TCCCTGGGAG TCTAGTGTTCAC	GGGATTAGGAT TTTAGTGTTCAC	GGTGTCCCTGGGAGACTATGG[C]/TAGTGAACACTAAAATCCTAATGCCCATGCATTGGAATTATT CCGACTATTACTTCTTTAGTTCCTTCTATCCACCCAGCTCTCT
WI-8833	51 A T	TCTTCATGCC ATTCTCTG	CCTCACACATT ATAGGGGCA	CTCCGGCTCTTAAAGCTCTGTAGACTGTCTTCCATGCCATCTCTG[A]/TTGCCCTATAATGT GTGAGGGTATTACAATAGTCCCTATTCAAACTGCCTTGTCATAAAAGGTCAGCTATGT
WI-8377	63 A G	---	---	ATTTTATGCCATGTTGGTAAAGTTTTCATTTTCAGTACATGGGTAAACCCAGGCCCTTTCCC[A]/GJT TATATCCAGGTATGCTACAAGTTCCTTTAACCTTATCAGAAAGTTATTACTGTTTCTTAGAGAG GCTACCAGGCTAAATTCACCTAGTTGGTTGCTAATGTCTCATTTATTTATCCTGAAGCTCGTG
WI-8850	21 A G	GGGACTTAAC CTTTGGCT	CAACAGCCA GGCAGG	GAGGGACTTAACCTTTGGCT[A]/GJCCTGCCCTGGCTTTGGCTCTGCCCTTGTCTGTTTGGTTTCTT TCTCTTCTACTGGCTTCTTTGCTTTGCCAGCCACTATGCTGCTGT
WI-8853	79 C T	CCCGGGCATTG AGGATA	AGTCTTCTGA GCTTCCAT	ACTTTTCTGAGCTGAGCAACCTCATCTTTAGCTTCTGGTTGATAACGGCTGTTAATCCCCGGG CATTGAGGATA[C]/TATGGAAGGCTCAGGAAGACTTTCATTCICAA
WI-8865b	52 A G	---	---	AGGTGACTGGAATCACAGGCACAGACTGAGGAAGACAGTCA[T]/GGTGAACAACAACATGCT TCGGACTTACCAAGGAGAGTCGAGCTTTCATATAAA
WI-8865a	42 T C	CACAGACTGA GGAAGACAGT CA	GGTAAGTCCGA AGCATGTTG	AGGGTGACTGGAATCACAGGCACAGACTGAGGAAGACAGTCA[T]/GGTGAACAACAACATGCT TCGGACTTACCAAGGAGAGTCGAGCTTTCATATAAA
WI-8895	32 A C	---	---	GTGCCACAAACCTGGACACCAACCAACAGAA[T]/CJCTCCGCTCTTTGAAATTTCCATTAAAGACA CAATGGGGTAATTATACCAGGGATGCTCCAATCGCTCTTTC
WI-8456	93 G C	---	---	CCTTTAAAGTCACAGTCAACTCGACTGTGGACTGATATATTGTGAAATAATAAAACTCTTTTCC AAGGCTCCCATGCTTGGATGTCA[G]/CJTATGTCAAGTTAATAAACAATTTCTAAGTGCTCACTC TCAACTTCTGTATTCTTGCCATGGTCCAGTAAAGTTCAACGGCAGACCAAGTTGTGTAGCAC TGGCATAGACGAGGGCTTCTCAAACCTCCGCTGCTGCTCAGTCAACCCAC
WI-8496b	157 A G	---	---	TTTCATCATCAAAAGTTTCTTTCCATAGAAGAATGGTAATGTTGTATCAGTGCATATTCTATGAAA ATTATATCTCAAGTAAGTCAAGCTAGCAATCAGAGACAGCACTATGTCAAGCTAGTATACAAGGTCA AAGACACAAATGCTGCCAATGCA[A]/GJTATATAGAAATAATACGCGAGCTGTAGAAAAAGTCT GTGGCCAAGTGGGATAAAACAGTAGCAGTGAC
WI-8496	41 G A	---	---	TTTCATCATCAAAAGTTTCTTTCCATAGAAGAATGGTAATGTTGTATCAGTGCATATTCTATG AAAAATCATATCTCAAGTAAGTCAAGCTAGCAATCAGAGACAGCACTATGTCAAGCTAGTATACAAG GTCAAGACACAATGCTGCCAATGCAATAGTATATAGAAATAATACGCGAGCTGTAGAAAAAGTC TGTGGCCAAGTGGGATAAAACAGTAGCAGTGAC
WI-14153	28 A G	GTGCAGGAAG GCCAGC	AACGGCAGGA GGGGA	CTGCAGGTCTATGTGCAGGAAGGCCAG[C]/GJTCCCTCTGCCGTTGTACCCACATCCACAGAGCA GCCCTAGTGCCAGGTGCAGCCACTGCCACCCAGGCACACGGGAACAGGCCATGCTGCTGC

WI-12108	40 C T	TGAAAAGGG TTAAACTCAA ATA	TTGACCTGGTA TAATGAAAGT ATTTC	TCATGTATTACTTCTGAAAAGGGTTAAACTCAAATATC[CT]GAAATACTTTTCATTATACCAGGT CAAGAAAAATGCCACAGCCAGAAAAATTTATTTAA
WI-5989	29 G A	CCACAAAGGT CACAGGCA	GGGTATAACAG AACCGTATGTA GG	CAGGCAACGGTCCACAAAGGTACAGGCA[GA]CGTACATACGGTTCTGTTATACCCCATATATTAC CCCTTCATGTCTCTAAAGAGACATTTCTCTTAGAGATTTCATTTTAGTGATCTTTAAAAAAAAT CTTGITTAACCTGGCTCCATCTTTTCTGGGTGAGGACACC
WI-12201	61 C T	CCCACTGATCA CCTGCATG	CCGACCACATA CCTGGC	ATAGCTTTTAGCCTTTTCTGGAGTGTTATGTCCCAAGCCCACTGATCACCTGCATG[CT]GCCA GGTATGGTGGGGGTGATGGACGTGGGTTGCAGCCCTCCACTGCTCGATAAAAGGC
WI-12018	31 A T	GGCAGCCAGC TCTGACTT	GGAGAGATGAC AGAAACAGAG AG	TTTTATCTGTCAGGCAGCCAGCTCTGACTT[AT]CTCTCTGTTCTGTCATCTCTCCCCACATACCA ACTTCTTACCATGATGATTATACCAATAATACAGTTCTTATATAGGGGCTCTGGAAAAATTAGAC AGTGAAGCATGTTGCAG
WI-14162	57 A G	TGGCTCGCTG CCTC	AGGGATCAA GAGAAAGGC	TTTTTCGTTTGTAAATGATCCGAATGCTTGAGAAAGAAACCCCTGGCTCGCTC[AG]GCCTTTT CTCTTTGATCCCTGAGTTGCTGAGATTAAAGATGAGGTCCCAATGAGAGCTACCAAGATGTAGTCG AGGG
WI-15407	92 A G T T	CATGCCCTTTA AGGATTAAAT	TCTTTTCTCTTT TGGTAGTGG	AGCATGAAGGAGCAGTTTATTGATTGGTATATTCAGGTTTCTAACCAAGCTGAAAAAATTCAAATA CATGCCCTTTAAGGATTAAAGTTTAA[AG]CCACACTACCAAAAGAGAAAAAGATTTATATGATCACAT ATAAGCAATGGAATCAGCA
WI-12319	109 T C	GTTGAGTATT GTTCTGCTCAT AATT	GGGAAGGCTG GTACATATTGG	TCTGATGTCATTTATTGGCACAAAAATATTCTGATACACATGGTGTCTAGACATGGCTACACTTTA TACTTTGTGCATTTAGTTGAGTATTTGTTCTGCTCATAATTT[CT]CCAATATGTACCAGACCTTCCC
WI-12326	25 G A C A	GACAGACTTC AAAAGCAATT CA	AGGTTTGA TATGTATTAA TACTTTGT	CTGACAGACTTCAAAAGCAAATTCAC[GA]CTTCCAGAAATACAAAGTACTTAATACATAATTTTCAAAC CTGTTTGCATTTCAACAAAGTTAGCGTTTGTAAATCAAAATTTGATAACCCGACTAAAAAT TTAAATCCACACTGAAGATCTGGAGTATGGGGGGATAGGAAATTCAGCATATGTATTAT[CT]
WI-12361	63 C T	---	---	TGAACTAAATTTACAAAGTGAACAGTTGGAAGGTACTTATAGGTAGACCTGAGGGTCTGTTACC ATACTGGTTTAAATCCATGTCAAATGTAGTTTACAAAGGAAAGGACAAGTACCTTTGTATAGAATAT ACAGACACAGCATCACACCA[CT]AGGGCCACCGGGAGGGTGGGGAGACGACACTTTTCCCTGGG AAAG
WI-11305	87 C T	CAGACACAGC ATCACACCA	GACCTCCCGT GGC	ATTTTATATGAAGGTTTCTGGTGAATCTTTTAAAGCAGGGAGGAAAAATCCAATAAATTTTAA[A/G]AAGGTTTAGCTATTTCCCAATGCTATTTAATACAAATTGAGGTTAGGACGTTAAGTCTTATCAGA CTGTGACTGGAGCCCCG
WI-11321	67 A G	GGGAGGAAA TCCAATAAAT TTTT	CATTGGGAAT AGCTAAACCTT	AGCATACTGCATCTCCTTTATGGATAAATCATGTGCCCCA[CT]GAGAGCCCCAAAGCTTGATGACAT TCTGTAAGTTACACAAATGATCTGAAGAGTTATCTGTTCTGCC
WI-11324	40 C G	GGATAAATCA TGTCOCCA	ATCAAGCTTTG GGGCTCT	

WI-11352a	69	T C G	AGCAGACGAC ATAGTGGAAA	GACCTCTCGTA GGACACTTAGC	TGACACATGGTTCTGTTTTCCAGAAAGGAGAGAGAAAGTCATCTACATAAGCACAGCACATAGTGGAA AGT/CJ/GCTAAGTGTCCTACGAGAGGTCAGATCATATCCATAGAAAAACAGCTCTCTTTTACTTGCA CACTTA
WI-11371	84	C T G	CAGCTGGAG ATTCTGATTCA	GCCCCGCTGA GCAC	TTAGCCCCATGCTGTCATTTGCAATCACCTGTGAAACCTATGAAACCTATACCTGCCAGGCTCAGCTT GGAGATTCTGATTCAAGT/CJ/GTGTCTCAGCGGGGCTGGACATCCATGTTTGGGAAGAGTTGGCGGGT GATTCGATGCGGTATAT
WI-11385	75	T C G	ACAGAAGACT TTCATATTCTT	GATTCATTCT AGTCATGGTCA	CTTAAAGCATTATAGTTTGGCCTGATGGTGACACAGAAAGACTTTCATATCTTGTCTTTTAAAAAGTC TCTTCAGT/CJ/AGGAAAAAGCTACAGATTTAAAAATATGACCATGACTAGATAAGATCAGC
WI-11388	88	C A AAGTC	TGTTGAAAT ACACGTAAC	TGCCTGTATC CAAGTTAAAT	TCATGTGGCCAGTTAGCTCAGTTGGTTAGAGTGTGGAGCTCATAAAAAATTAAAGAAATGAATGTTTG AAATTACACGTAACCTAAGTTC/CJ/ATATAATTTTAACTTGGATACAGGCATTGTTATGCTAAT
WI-11392	55	T G ATAATAC	GGTTATGTGT CTTGAACCTTA	GTACATTACAG TGTTTGTAAA	TTCTATCATTCCTAATAAATGGCAGGTTATGTGTCTTGAACCTTTAATAAATAC/T/GJC/TTTTACAA AAACACGTGAATGTACTTTCTTGTGCAAGGGGAACACTGAGTCTCCGCTCTAGATCCATTAACTGT CATACTCTTCCCAGA
WI-11396	52	A T T	TTTGTTTTG AAATGGTGT	AGCTTATTTTC ATATTCACCCA	AAAGAAATAAGATGGCATTGTTCAGTTAATTTTGTGTTTGAATGGTGTCTTAT/GA/TGATGGGTGAATA TGAAAAATAGCTTACCTCATCCACTCTAAAGGTAGTGGTGATTTTGAACCGTTGTCAAT
WI-11441	100	C A CAGC	TCCCCACCAAC CAGC	TGCCAGGGCCT TATTTG	CTGTGAGTCTTCCCCAACTAAACCGTGAGTTCOCAGTATGCTGGCAGCAGCTGTCTGTCTTCTTGGTG TATCCCATTAAGTGAATCCCAACCAACAGC/CJ/CAAAATAAGGCCCTGGCACAAAGTAAGCTCTCC ATTTTGTAGAATGAAT
WI-11466	26	C T TTTATTTGCA	TGAGAAGCCA CTTATTTGCA	GTTTATTTGA TAAAAATGAC	ACTTTGAGAAGCCATTTATTTTGCAG/CJ/CTTCAGTCCAAAAAAGTCAACATTTTCAGAAATTTTT TATATAAGTTGTAGGTCAATTTTATAACAATAAACCTTTCTATTATCTATTTATCTCTCACATACATTT CATGTATCCTG
WI-13364	35	A G	TTTTCTTTTGTGCTCTTTTTTTTAGTAGAAGC/CJ/GGGAACAGTTGTCAATACTACCTTCTGTTGG TCCCCTGTTAGACAACATACCTTCTTTTGAATGTAAAATGTCA
WI-11276	41	A G AGCAGAC	GGCAGCAGG AGCAGAC	TGTACTGAGGA GCGGGTG	AGGCAACACTGCTTTATTAGCCGGGAGCCAGGAGCAGAC/CJ/ACCGGCTCCTCAGTACACATT CCCCACCCCTGCTCGGTGCTCCCACTCAGGCTGGGATGGAGGGGCGAGGTAGGTCTGGAA
WI-12210	76	A G A	ACTGGGAAAA CAACTATTGC	TGCTAGTTTGC ATATGTTTTCC	ATTGGAACAACCTTAATAATTTGCATCTCTACATATAGAAAGCTGCTTTGAATAACTGGGAAAAACAA CTATTGCAT/CJ/GGGAAAAACATATGCAAACTAGCATCATTTGTCTCTAGA
WI-14186b	88	A G	AATGGTCTGGTTTTATTGAGAAGCTGTTGTGTCATTTGATGGAAAGACACATACGGTACAAAATTACA GGTGGTTTAGTTCATTACATG/CJ/ATACAAATCATTAGAGTCTTTACAAAGTCATTAGAGTCTTTGGAT TTT

WI-14186a	52 C T A	GGTCATTGAT GGAAAGACAC	AACAAACCA CCTGTAAATTT GTACC	AATGGTCTGGTTTATTGAGAAGCTGTTGGTCATTTGATGGAAGACACATA[C/T]GGTACAAAATT ACAGGTGGTTAGTTTCATTACATGATACAAATCATTAGAGTCTTTACAAGTCATTAGAGTCTTTGGAT TTT
WI-12234	66 A G	GAGAACACTT GTGGGCTT	GGACCTATCAG TCCATGTTGA	ATTTTTTTGGCTATAGTCAAGTGGTTCTAAACTTGAGCTTGAAGAGAACACTTTGTGGGCTT[A/ G]TTCAACATGGACTAGTGGTCCACCCAGATTCTAACTGGGTAGGCTGGGGTG
WI-12345	37 C A	GTGGCAGGAA AAAGAGGAA	TTCAGAGGGG TTCAGG	GGAACAGACCTGATCCAGTGGCAGGAAAGAGGAA[C/A]CCTGAACCCCTCTGCAAGTATTCTCT TTCTGACCAGCTGGGCTTGGCAGCTTTGTGAGATTTGCAAAA
WI-13416	71 C A	AAATTTTGG AAGTTTTTCAG	AGTGTATTAG TTCATGAATA ATTCAA	GAAAAAGGCTGTAATTTTATTTTCAAAATTTTGGAAAGTTTTTTCAGAAAAAAATAAAATGACAAGAAC CATA[C/A]AAATATTGAAATTTATTCATTGAACATAAACACTTAGCAGAGGAAGGACTTTTGTAT
WI-12310	46 G A	TTATCCCAAG TATAATTTTA	TGTTTAAATAT GTTTGGTCTT AAA	TTTGAAAAGATGCTGAATTTATTTCCCAAGTATAATTTTAAAGCT[G/A]TTAGGACCCAAACATA TTTAAACATCTTTACACATACAGAATTTTCAAGTTTACAAATATTTCCAGAAGGCAATTTTCTTAAGCAG T
WI-12086	72 C T	CCGGGAAAC TTGGATT	GGAGTCTTCGG GTCITGG	GAACCGAGCTTTATTGGAGCAAGAGTGTGGACACTGTTTACAAACAAACGTTTCCGGGAAACCTTG GATT[C/T]CCAAAGACCCGAAGACTCCTCCAAAGTCTCACTGTTAGTAAGTCAATTTGGGGGCAGA ACAGGAACATGCCITAGCT
WI-11549	102 T G	GGCATAAAGT TCATAATATTC TTTTATG	GGAAAGTCTGT ACAAATCCCC	ATGTCTTACAGGTTGTAATTTGTTAAGAGTTGTCTATCTAAATTTTTCATAATTTATTTGGCATAAAGT TCATAATATTTCTTTTATGATCTTTTAAATATCTG[T/G]GGGGATTTGTACAGACTTTTCTCTC
WI-11585	79 T C	TGGGTTTGCAA AAACAAAA	CCATGCTTCAC TGATACTCC	TTAGAAGGAAGAAATAAAACACGGTAATGGGAAATCAGTTTCAAGGTAAGGAAGCTGGGTT TGCAAAACAAAA[C/G]GGAAGTATCAGTGAAGCATGGCCTAGAAGTCCAAGAGCGGGGTAGAGT TT
WI-11604	68 G C	---	---	TTAGTTGGTTTCTGAAACTTTATGCTGTTTATTTTAAACCAATAGGATGTTCCAGTTACCAGCATTTT G/CJAGAACTAGGACTTTTCCATGAAATAATTAAGAGCTAAGGAATTTCTGACGCTCACCATTTTTC TTTGTTACTCTGCAGTT
WI-11614c	108 C A	---	---	CAAAATCAAAAAATTGAGGAGGCAAGAACAGAGTAATAATCCAGAAAGACTCAGCTGCTTGAGGCAT GTTCCACCCCTGGACTTGCCAACTTTCAGTGTGAAACTGCA[C/A]ATATTAAGTATTGTCAGCTAC GGACTTCGT
WI-11614a	60 A G	CCAGAAGACT CAGCTGCTTG	AGGTTGGGAAC ATGCC	CAAAATCAAAAAATTGAGGAGGCAAGAACAGAGTAATAATCCAGAAAGACTCAGCTGCTT[G/G]GG CATGTTCCACCCCTGGACTTGCCAACTTTCAGTGTGAAACTGCAACATATTAAGTATTGTCAGCTAC GGACTTCGT
WI-11626b	83 T C	---	---	TTGATTTTACTAAGGCTTCCACTGGAACATGAAGGTAGGGATAAGTGTACAGGATAATATATCTCAG ATATTTTTTAAATAAAAT[C/T]ACTTAATAATAAGAAATTAGCCATACCACATTTGTTCCATTGCTAC AAGAACAAATTGGCAATGA

WI-11626a	39	G A G	TCCACTGGAA CATGAAGGTA	GTGGTATGGCT AATTTCCTATT ATTAAGT	TTGATTTTACTAAGGTCTCCACTGGAACATGAAGGTAG[G/A]GATAAGTGTACAGGATAATATACT CAGATATTTTTAAATAAATTACTTAATAATAAGAAATTAGCCATACCACATGTTCCATTGCTAC AAGAACAATGGCAATGA
WI-11627	23	T C	CCTTCCCTTC ATTGTCTC	CATTGCAACC CATCTCAAG	ACCCCTTCCCTCCATTGCTCTC[T/C]CTTGAGATGGTTCAAATGGGAAGTAAAGCAAAAAGGG AGATGAGAAATACTGATGCCCTTTTGCTGGCTTACTTCCATTGCGATGTCAAGTCCATCCATG
WI-11636	61	A G	GGACTTAAAA AGATCTGCTTA T	AGAACTTGCT AAATATTTTAT GTAACACT	TCAGAAATGTTGCAAGCAAAATACTATTGTAAAGGTGGACTTAAAAAGATCTGCTTATCCTTA[G/TA] TATCCACATAACTCTAGTGTACATAAAATATTAGCAAGTTCTGTGACAGGTGCTCAGTAAACAC TTTGACTCCTTTTTTGGTA
WI-11537	119	C G T	ATTGCTCATCT TACTCTGACCA T	GACCCAGCAA AAAGAATGAT T	GTACCATTTCTTATGGTGGCAAAATAGCAAACTGTGAGTAAACGAGGGCAGCTGAATAAATTTACAG TATACAAATATTAGAGAAATATTAGTTGCAATTGCTCATCTTACTCTGACCATC[G/TA]TAATCATCTT TTTGCTGGGTCCAGGAAC
WI-11654	37	G C	GCCAAAAGAC TATTCAGCAA CTG	GGCTCTCCAG GACAGTTT	AGTAGAACATCAGTGCCAAAAGACTATTTCAGCAACTG[G/C]AAACTGTCTGGGAGAGCCACTCCAG AGCTATTCTAAGACTTCTGTGGTGTTCATACTCTACTCAGAGTTCACACTCATATTTTCATAATTTT ATTTTGGGTGTGGGT
WI-11656	28	G A A	ATTGATTTTAG AAGGAAGTGC A A	CAAGGCTTTGT CCTCAAGTAA	ACCTGATTGATTTTGAAGGAAGTCA[G/A]CTTTACTTGAGGACAAAGCCTTGCCTGSCAGTTGTT AAATGTCTCTGAACAATCAGATTCCAGCGCTGGAT
WI-11680	55	T C	---	---	ACAGATACTTTTCCACGCAACATTTCTGAAATGAAAGCTTTGATTCTCCCCCTTTT[C/TT]GCATAAA GGCTGGGAAGGTGGTTGGCCAGACCGTACATCTTTT
WI-11696	47	T C	TTATCACAGC AGGGGACAG	GGCATTAGAGA AGCCAACCTT	GTCCAAGAACAAAGATACCTTGACATCTTATCACAGCAGGGGACAGT[C/TA]AGGTTGGCTTCTCTA ATGCCACCATCTTGTTTTCAGAACTTTCCACTTCGCC
WI-11702	69	C T	GAATAATACT GAAATAACCA T CAGCAG	AGAACAACTT AAGCAAATTAT ACTGAAA	TTACATGTGGTCAATGTGACATACTTTCAATAATTAATAATGAATAACTGAAATAACCCACAGC AG[C/TT]TTTCAGTAAATTTGCTTAAGTTGTTCTAGAAAACACTGCTAAATTTTGTCTGCAGA
WI-11706	60	C T	TGGCTGGAATT TTCCTCTCTT	ATCACCAAAG AACAAATCCA	TGCTGATTCATCGCTCTACCATCTGGCTGGAAATTTCTCTCTGTACAAATTTATTTGC[C/TT]GGCTG GAATTTGTTCTTTGGTGATTTGCCCCCTTGCTGCT
WI-11709	105	T A	AGAAGCTTGC TTCAGTTTGC	TCATTTCTCT AATTTACGGG A	AATATCATCTCATATCAGGCATGTTTATAAAAATGAGAGATTATGTCTTTTGGCATACTTCATC TCTTCAGGACACAGAGAGAGCTTGCTTCAGTTTGC[T/A]GTCCCGTAAAAATTAGAAGAAATGAAT GGCCAGATGGATGGAATA
WI-11710	103	C A	GCACCTAGCCT CAGTCTTCA	GTGTGGAGGAG GGAGGAG	TTATTACCATCAACCTGTCCCCAGCTTTCCAGCACACAGCCAGCCACACTCTAGACACGCCCTTCAC TCCAGTCCATTCTGGCACCTAGCCTCAGTCTTCAC[C/TA]CTCCTCCTCCTCCACACACTCCTTC

WI-11715b	123	C T	AGCTT	AGGTGGCTGC	TCCCATCCTG TGGCT	AGATGGAGCTGTTGGGGAGGACATGCACACAATGTAAACAGACAAAATGCATTACAACCTGTGG TGTAATGTGGCCACTATGAATCCCTATGTATAAGAGGAAAGAGGCTGGCTGCAGCTTTC/TAAGCCAC AGGATGGGGACTGGGAAGA
WI-11715a	49	A C	AAA	GCACACAATG TAAACACAGAC	CATTACACAC AGTTGTAATGC A	AGATGGAGCTGTTGGGGAGGACATGCACACAATGTAAACAGACAAA/AC/CTGCATTACAACCTG TGGTGAATGTGGCCACTATGAATCCCTATGTATAAGAGGAAAGAGGCTGGCTGCAGCTTCAGCCAC AGGATGGGGACTGGGAAGA
WI-11727	43	G C	TCAACA	AACAATCCTT AAAACAACATA	CCTGTGGTTTG TGTTGCAG	CTGGATTTCTATACCTAACAAATCCTTAAACAACACTATCAACA/G/C/CTGCAACACAAACCACAGGC AAAATGAAAACAGATGCCCCAGACAGACCCCCACCACATGGCACACAC
WI-11728	16	C G	---	ATCTGTGGTTT TCGCTG	---	TTTTATTATCAAACTC/G/CAATTCATTTACAAATGTAAAGTTATCATCAGCTCCCCATCCACTTT CTCCCATCTTCTATCTCTTCCACCCCTACACTTCTCTCCCTACAACCCGGGTTCCAAA
WI-11758	61	A G	TCGCTG	GCCTCACAAA GTATTTTCTAA	TGATGGCCCT GTGGTCTA	TTTTTCCCTCTTTATTAAGTCCGCTATACTAAGAGGAGAACTGTGGTTTTTCGCCTG/A/G/CTAG ACACAGGGCCCAATCACACACAGCTTCTGTAGAGAACATGGAGAGTGCCAAAGATCACCATCA
WI-11295	37	A G	AATATA	GCCTCACAAA GTATTTTCTAA	AAAAGTGCTCA TCTGTGAACCTC T	CCGGCCTCACAAAGTATTTTCTAAATATAATTTGCTT/G/CTAGAGTTACAGATGAGCACTTTTCA CATTAGGTGATATGCAACAACATCACTATTGGCTCAGCAGGAACAGACTTTT
WI-11773	93	T C	---	GGCTCAGAGA GCAAGGAA	---	AGCATGATATCTGCCTGGAGTTTCTGTGAGCTCAGCAACAGCAGAGTCAGAGATTAAAGAAAT ATTATTGCCTCCTTTTTTCCCCCTC/G/CTGATTGTTAATTAGGGAGTCAAGGCCAAGTTATC
WI-11282	42	C G	GCAAGGAA	CCCAACTTACC AAACCTCTG	AAAACCTCAGA CTGTAAATTTT GTGTG	CATGACAACTCTTTATTTAATGGGCTCAGAGAGCAAGGAA/C/G/CACACAAAATTTACAGCTGA GTTTTGCGCGCAGAGACCCCTCTCCACCTTTTTTCATGCCCTGTGTGTACACACACACTGTCCAAAGCCTC AGA
WI-11790	28	A G	AAACCTCTG	TCATCTAATCT GTGAGGTATTT	OGGTAGGCGAG GCTAAGC	TAATTCACCCCAACTTACCAACCTCTGT/G/CTAGCCTCGCCTACCGTACACATGCTCAGAGCAC TTACATTAACTTACAATGGGCAAAATCATCTAACACAAAGC
WI-11879	61	C A	AGTATACA	GGCTCAGAGA GCAAGGAA	GATAGTTGAAC CTCTTCACTTT ATAAAA	TTTTTAATCCCAAAGCTTACAACCATCTTTTCATCTAATCTGTGAGGTATTTAGTATACAG/C/A/AGT GATTTCTCTCTTCTCTTTTTTATAAAGTGAAGGTTCAACTATCCAGACAGTCCCCTATCTA
WI-12469b	91	C T	AAGTTTAA	GTATTTAATGT GGTATTAGAA	CAATTTTCAGA TTGTCTATAGC AAAC	TTTACTAATTTCCATTTCCCTCCCTTTTATAGTTTTTAATGTGGTATTAGAAAAGTTTAAATTACAT ATGTGGCTTATTTCTATTCTATTTCTA/C/TTTGACAGCACAGTTCTTCAAAGTTTGTATAGACAATCTGA AAATGGGTTCTGAACT
WI-11906	52	A G	ATCTGAA	TGTTATAACAT CAAAGAAAGA	TTAATTTCTGC AGTTCCCTCA	ACATTTGAGTAGGAATGACTTTTGTGTTATAACATCAAAAGAAAAGAAATCTGAAT/G/CTGAGGGAACCTG CAGAAAATTAAACTTTTCACTGCTAATTTCTCAGAAATGCCAGAGTAAGATGAACCCCTTTACAG

WI-11909	78 A G	TTTGTTGGG TGGTCAAG	CCTCCTCTGAG ATTTTCTGAAT AG	GCAGTTCTCTGAAAGACAATGGATTGTGGAGCATACTGAAGACTATTCTCTAAATGGCTATTTGTGTG GGTGGTCAAG[AG]CTATTTCAGAAAATCTCAGAGGAGGACAAATGATAGTGCAGCTGCAGCCAGCTCG GACTGGCTTGAAGAGTC
WI-11806	60 T G	CATGAAGAGT GGGCAGTTCA	TCCTGTAAAGC CAATTTTATAT ACTAATAA	AAAAATACCATTTAGCATCAATGCCCAAGTTTGGCAGGCATGAAGAGTGGGCAGTTCA[TT]G[GT TTATTAGTATATAAAATGGCTTTACAGGAAGCATTTATGG
WI-11946	31 C A	CCCTAGTGAATACAACCTTTTGTCTGGAGAC[C]A]CCAGCTAGTCTAAGAAAACCTTCTTAGGCTGAG CTCTCTTGGGAATCTAAGATAAAGAACTGAGATCCTGGGAAGAGGGAA
WI-11965	65 T G	TGAAGATCAG ATCTCTGGTT GATT	CAGCTGTGGTG AATGTTGAT	ACAAAATTCACAAGTACAACACTGCTTATTTCTTGCTTGAAGATCAGATCTCTGGTTTATTTAA[TT G]ATCAACACTTACCACAGCTGAAGGAAATTAACCTGAACCT
WI-11027	90 T A A	TGCCCTACTAC GCTTTTAAAA A	TGAGGAAATGT GTTACAGTATT TTTATT	ACCTATTTGAAACTGCAGAAAGGGCAGGACAAAACAATCAGTTCATAGATTTTCTGGGAAATAT TGCCCTACTACGCTTTTAAAAA[TT]A]AATAAAAACTGTAAACACATTTCTCTCATTTCTCTTACGA ATACTTCTTTTGTATTTGCAAAATCTATGGCATACACAGAGGCACCTCCTCAATGGCCTG
WI-11049	95 C T	TTCTGCTGAAGATCACAAACAATTTCAACCTCTGTGGTTCAAAATAATTTAAGGATCTTGTACCTTT GTGTTATTTTCTGTTTCAACTAAGGAC[TT]AGACITTCAGAAAGCATAGCTTCCCTTGTAAACGTTTTT AAACATCTTTTCAATTTGTAGGAAGGAACATTTCAAAAGCCCCAA
WI-15488	69 C T A C	AAAAGGACAG CCAGATATCA AC	TTTCCATCTTA TTTCATTTCTG TAAC	CAACATTTATCAACATGTTAGGAAAGTTTCTCACTCTGCACATATAAAAGGACAGCCAGATATCA AC[CT]TTGTTACAGAAATGAAATAAGATGGAAAATTTTAAACAATTG
WI-13654	49 A G C G T	AACAGTTAAT GAAACACATC CGT	GGCTGGTGAAG TGATGTCAT	TGCTCAATTTAATGTGATAATCTCCAACAGTTAATGAACACATCCGT[A/G]GTATGACATCATTT CACCAGCCAGCTACTTTCATGTGGCAGAAAAGGTAACTTTTCCCCATTTTACAGACAAAACCCAGT
WI-11070b	135 C T	ATGAGACCCCTGCTTTGAACGTTAAACGTTTGGAAATATGGAAAAGGAGCTAGGACAAATTCCTTGCCT TCAAGTAAAAATGTGACTGAGCAGAAAATCAGCCAGCTATCTTGGTGCAGAGAGGTACTCCAAGTA C[CT]TGTGGGGTCTGATGACTTCCACGGTCACTGGGGATCCAACAGAGGGAA
WI-11070a	110 G T T	CAGAAAATCA GCCAGCTATCT	TTGAGTACCT CTCTGCACC	ATGAGACCCCTGCTTTGAACGTTAAACGTTTGGAAATATGGAAAAGGAGCTAGGACAAATTCCTTGCCT TCAAGTAAAAATGTGACTGAGCAGAAAATCAGCCAGCTATCTTGTGGTGCAGAGAGGTACTCCAA GTACCCGTGGGGTCTGATGACTTCCACGGTCACTGGGGATCCAACAGAGGGAA
WI-12020	121 T C	AATCTTTTATATTTCCAGCTGTTGAGACAGTATTTTGAGGGCTGATGTTACCTCTAGCGGCGAAACC AGAGCCAGCTATTAAGCAGCCAGAAAGCTACAGTAAATGAATACATGACCATTT[CT]CTCTTTTAGC ACGTTCTTTGTTCTCCTC

WI-11076b	142	G A ---	---		CATGGTTCTGCAGCTTACAGGAAGCATGGTGGCTGGCATCGGCTATCTTCTGGGAGGCCTCAGGAA ACTCTGAATTATGGCAGTAGGCAAGGGGAGCAGGATGTACATACCCAGAGCAGGAGAGAG AAAGAGAG[G/A]AAGTGCCACACATTTTAAATGATGATTTCTCTCAAGGAACCTCACTCACTGTCAT G
WI-11076a	106	T C AGGCA	TCCTGCTCTGG GTATGTGAC	GGTTATTCAAA AATTAGTATGG GACA	CATGGTTCTGCAGCTTACAGGAAGCATGGTGGCTGGCATCGGCTATCTTCTGGGAGGCCTCAGGAA ACTCTGAATTATGGCAGTAGGCAAGGGGAGCAGGATGTCTACATACCCAGAGCAGGAGAGA GAGAAAGAGAGGAAGTGCCACACATTTTAAATGATGATTTCTCTCAAGGAACCTCACTCACTGTCAT G
WI-14263	49	T C GGCATATTCA	CGCAGAAAAA GGCATAATTCA	---	ACCTTTAAAGTTTCTCCCACTTACTCCCGCAGAAAAAGGCATATTCAA[T/C]GTGCCATACTAATT TTTGAATAACCTAACTCTCCCTTTTGTCTTCTACTAAGAGAGTTTCTTTTGGCTACAAGTAACA AATTATTGCTGAAATTAGGAAGGGAGCAT[T/C]TGAAATGGGAAGGGGAGGTTAGAGAAAGACAGAG ATTTAAAGAAGCAAGTACCATTTTCCAAGTATAAAACTGTGA
WI-13892	50	G A TAGAAC	CTTTTCATTTT TGCTTTTFAAA	TGATGATGTC A TATACTAAAA ATCAAAG	GATTTGTTTATTCAATCTCGCTTTTCTTTTAAATAGAACA[G/A]CTTTGATTTTGTAGTA TATGACATCATCATGAATTTTCTCTTACTTTGATTTAGGCTCCACCTCAGTAGTTTGACAA AGGTAGATGAGTTCA
WI-13951b	88	G C ---	CATGAGAGGA TCCCTCTCTC	AAAAGCTTCTT TCCCTTGA	ACCTCTTCTGATGACACTGTACCTGTAGGGGTCTAGAGAGAAAGTAGTAGACTCCTACTTTGC TACAATTCAGGATGCAGGGCATGAGAGGATTCCTCTCTC[G]TCCAAAGGAAAGCTTTTGGC AATAATGGAAGAGGAGTGAACAAAGTAATGAACAAACAGACCCAGATCAGAGGAAGAGATG GCTTTCTTGTAAATCTGGAGCA[G/C]ATTCAAGCAGCAATATTTACTGAACACTTGCTATGTGCTG G
WI-13951a	39	C T CAAAA	GGAGTGAACA AAGTAATGAA	TTCTCTGATC TGGGGTCT	AATAATGGAAGAGGTGAACAAAGTAATGAACAAA[G/C]TAGACCCAGATCAGAGGAAGAG ATGGCTTTCTGTTAATTCTGGAGCAGATTCAAGCAGCAAAATTTTACTGAACACTTGCTATGTGCTG G
WI-13264	25	G A TTGCCCAT	AAAAGGCTC TTGCCCAT	GGAGGGAGAG ACGGGAATA	GAGACCAAAAAGGCTCTTGCCCAT[G/A]TATCCCGTCTCTCCCTCCTGACTGACCCCACTGTTCTT ACAATGAACATCCCTCAGCCCATGGCATGGTGATCCCTCTCTCTGGGATCTGTGAATATAACCA ACTGCTTGTCAATGGC
WI-13960	39	A C TGATAGA	AGCAAAAGGA AGTTAAATAC	CATGAAAGGA CAAATTTGCAT C	TTATTTGTCATTAGCAAAAGGAAGTTAAATACTGATAGA[G/C]GATGCAAAATTTTGCCTTTTCATGCA TTTGTGGAGAAAGTACTAATTGTTCACTGTGATTTCCCTCACAAGGAGTTGAGCCCCCTAGATGAC
WI-15843	62	C T CAG	ATCTTATAACC AAGAAGCCTT	CTCTGGCTCAG ACTTGCTCT	AACTCTTTATTTAGCTAGCCCCAGTGACTTTTATGCATCTTAAACCAAGAGCCTTCAG[C/T]AG AGCAAGTCTGAGCCAGAGGTTTATACACATTTGTCTCAGGGTCCACAGGAACCCAGGCTTGGCT

WI-13983	52	G A	TCTCTCCCACT CCCTTAAACCT	CAATACTCTCT TAGCCCACTGG	TTGTGTACTGATTTCCGAAACATAGAAATCTCTCTCCCACTCTTAAACCT[G/A]CCCACTGGGCTAA GAGAGTATTGTACAGAATATGCACATGCTGACTTAACAGAATTAGAACATCCAGGCACCTCACTGAGA
WI-13850	51	A G T T	AATCTCAGGG TCACAGCTTTA	TGTTCCCTGAC AATGTTTGTA	CATGAATCTCAGGGTCACAGCTTTATTTTATAGATTTTAAACACAGCCAT[G/G]TTACAAACATTGT CAGGGAACATTTACAAGAATAAATAAGATGGACTTGCAGGTGTAAAAAGATTACACTTCA
WI-15295	27	G C A	TGTCAGTTTGA ATGTATTCCTG	TGAATAGTTGG CAAAGGAAAA	AGATGTCAGTTTGAATGTATTCTCTGAT[G/C]TTTCCCTTTGCCAACTATTCATTATTGACCATCTTTTC CTCGTCAAGTGACCTGCCATCATCAAGAAAGGCCCCCGAAATATGAGTGAGACTCA
WI-14284	55	C T	---	---	ATTTCAAAACAAATCCAGAACAGGTTCTCACACTTTGAGCCTTTTAGTGCAAAAACA[C/T]TATGCCAT GCGGGAATAAAATGCTTATCCAGTGGAGCGCTCCCTGATGCATTGA
WI-14288	85	G C	CCGCTGCTATT CCCAGAT	GGTCTCTTCC ACCAAATCTT	ATGACCAGACCAGAAAGCCCCCTGTTCTATATGAAGACAAACAGGTGGCCATACCTTGGTGGAGGGATA CCGCTGCTATTCCAGAT[G/C]AAGATTGGTGGAGGAGACCATGACAGATGACAAACGG
WI-13522	33	C T	TGATGTAGTTA CCCCACTAAT ACAAC	CATAATATTG AAGTCAGTGGT TCTC	TTTATTTGATGTAGTTACCCCACTAATACAAC[C/T]GAGAACCACCTGACTTCAATATTATGAGAG AAATTAATCCAGGGAATTTTTCAGAGAGAATAATA
WI-13529	42	T C	CACAAACATT TATTGAACAG TTACCA	TCTATACATT CTCACTCTCTT GCTT	AAATATGATTCCATCCACAACATTTATTGAACAGTTACCAT[C/JAAGCAAGAGAGTGAGAAAGTGT ATAGAGGTGATTAAAGAGTGTCCCTGTCTCGAGGGTTTATAGCTAACAGGGGAACAACCTCTC A
WI-13859	84	G A	---	---	TTATTTGTCAGAAATTTCCAGAAATCAGAGTCTCTACTGGGCAAGTAGAAAAATAGAAAAGTTTACTAC TTTGAAAAGGAAACTAT[G/A]ACAAACAAGTATATATTTCAGGAAAGGACTCTAGAACTTGAGCA ACA
WI-13536	29	T C	---	---	TGAAGGATACAGAAAAAACTCAGCGAAGT[C/J]GAAAAAGGTGGATAGCGTGGAGTAGAGGAGAAAT TAAGCACCAGCTTCCAGTTGTCTCTCCAGTGCCATTACATGGAGTACACTTAATTTTCTCAGCA
WI-13373	52	G A	---	---	TTTATTGTTTGGTAGAAAAACAGGCTCTTTAACACTGAATAAACATCTCAC[G/A]AACTGTGCTC CTAGATTACAAAAAGTCAAAACCATTTCCTTTGACGCGGGCCCTTGAATCTGACATTCAAGTCAC CGTAATAGAAACCAGAGCT
WI-13477b	61	A G	---	---	TTGGTTTTTAATACCTCTTGTGGATAAAAGGACATTGTTTTTTCATTAGCTTGTCTTCAAA[G/G]GAC AGAGAAATAAGATAAATTACCTTAAAGAAATTAATAGAAAAATTAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCTCAGTT
WI-13477a	32	A G AAG	TTAATACCTCT TGTTGGATAA	GAAGACAAGC TAATGAAAAA CAATG	TTGGTTTTTAATACCTCTTGTGGATAAAAGG[G/G]CATTGTTTTTTCATTAGCTTGTCTTCAAAAGAC AGAGAAATAAGATAAATTACCTTAAAGAAATTAATAGAAAAATTAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCTCAGTT

WI-14297	86	A T G	AATGTTGGGT ACTTTTCCAA	TGTGCACATTC AGAAACATTTT	CTGACITTTATTTAGCATGCAATGCAATTTATTTCTGGCAATAAAATTAATATGTGCGAGTTATAAAAAAT GTTGGGTACTTTTTCCAAAG[AT]AAAAATGTTTCTGAATGTGCGACACTAGAAATATATGCGAATCCCTTT AAACAGTCGACT
WI-12229	89	T G AAA	CATGTGCACA AAAAGAGTAA	ACATGTGAATT GTCCCAAAAA	TCCATGTAAATATTTCTCAACAGAGAACACTATCTTTAAATGAAGGATTTACCATTTAAGAAATCAACA TGTGCACAAAAAGAGTAAAAATTT/GJACCAAAAAATTTAAAGATTTTGGGACAATTCACATGTTT AAAT
WI-13582	43	C A	TGCAATCTAG AGACTGGGA	TCTGCGCAGTT AGATTCCA	AAGGCTGCCCTTACTGGACCAATGCAATCTAGAGACTGGGA[CA]TGGGAATCTAACTGCGCAGAG AAATCAAGACCGATGGTGTGAATCTGGGCGAGCTTCAAAATTTCTGCCTCTCTAAACATTTTAC CCAAITTTTTCATTATTGCC
WI-13857	28	A G	---	---	TCTGAGTTGATAAAATGCTTTTCTGAAC[AG]TACATTTTAGGTATCTGGCACAAATTAACCAAAATGT CTGCCCATTTTGTGTAGCTTTTCATACAGTACAGATTTTCATTTGATGTCGCTCCACATCTG
WI-15809	77	T G	TGTTTCTGT TGTAATGCC	TAAGTAGCTA ATTCAATGTTT GTAAA	GTTTTAAGTTCAGAGATGTGAATGGTTTACAAATCTGAAGCTGAAGTTCAATCTTTGGTTTCTGTT GTAAATGCC[TT/GJTTACAAACATTGAATAGCTACCTTAAGTATTTGAAGAGCTTCCATT
WI-15892	123	A T	---	---	TTAATCAGTCTGTGTCAGAAAGAAACAGGACTTGATCAAGCTTCCAGCCCTCACACTCTATCAGCA TAGCAATTTTAAGGATCAGAGCTTTGTTTACATTTGTCTAAACCAAGAGAAAGAA[AT]TGGAAATCA ACTCCACAGATCAACATGT
WI-15801b	81	T G AA	CATACTCCACT CTAGCTGCAGT	AGAAGAGTGG ATGGGATGC	TCITTTATTCAGAAATGGGAAGCGCATTTTCATTTGGCTTGAATGAGAAAGCTTCATACTCCACTCTA GCTGCAGTAAATAC[TT/GJGCATCCCATCCACTCTTCTCTCTTTTGGACTGAAACTCTTCAAAAGAACT GCTGAATGTCCTCTCTC
WI-15801a	24	G A	TTTATTCCAAG AATGGGAAGC	TCATTCAAGCC AATGAAAATG	TCITTTATTCAGAAATGGGAAGC[GG/A]CATTTTCATTTGGCTTGAATGAGAAAGCTTCATACTCCACT CTAGCTGCAGTAAATAC[TTGCATCCCATCCACTCTTCTCTCTTTTGGACTGAAACTCTTCAAAAGAACT GCTGAATGTCCTCTCTC
WI-13763	59	T C	GGCTGGACACT GCAGTGAT	CCACACCTGC CCCT	GCTCGTAAATGAGACAGAACGCTACAATCTGTTCAACACTGGGCTGGACACTGCAGTGA[TT/C]JAGGG GCAGGTGTGGGCGAGGTGGGGCTCTGAGCCGAGGACAAATGTCCATGGCAGAGCTTCCAGAA
WI-13578	48	T A ACC	TCAATAAAGA GCAGAAAGAA	CAGTGTGAAG AACATCTTTT GTC	TTTTTTTTTGGTGAGTGTGTTGCTTCAATAAAGAGCAGAAAGAAAACC[TT/A]JAGACAAAAAGATGTT CTTACACACTGAGCTTTACACAGTCAACCAACATTTGATATTTTGGCTTTTCCCGAGGGCAAAAAGA GAGCTTCCAGAAACCTC
WI-13789	62	G A	TTGGATGGCTG AGGGAG	CAGTGGCTTC CTCTGTTT	TCCAAGGAAAAAGAAAGAAACCAATCAGTGAGAAACCTCAAGAAATGGATGGCTGAGGGAG[GG/A] GAACAGAGGAAGCGCACTGGGCTGGGACTGAATATGGACAGTGGATGGTAGGGTCTCACTCTCTT GAGGTCCCT
WI-13594	66	G A AGC	TTTTTAACACA GATCACAAAA	CCTTTGGGCCA GTACTTTT	AATAACAAGTTTAAAGTTTCGAGCTGCAATGTTGGCAATGCAGGTTTTTAAACAGATCACAAAAAGC[G/ATGCACAAAAAGTACTGGCGCAAGGACAAAAATATGCTAAGAAATTAGGCCAAACAGCTGC

WI-15625	40 C T	---	---	GTTCCTCCACCTACTCCCGCAGAAAAAGGCATATTCA[C/T]GTCCCATCTAATAATTTTGAATAA CCTAACTCTCCCTTTGTTTCTACTAAGAGAGGTTCTTTTGGCTACAAGTAACA
WI-13367	84 C G A	CCACACTGAA GACTCACGAG	TCCCCACCCCA CCCT	GTCTCACTTCTGTCTAGGCTGTAAATTTTCAGTTTAAACAAGTTTCTTATGTGATTTGTGGCCACACT GAAGACTCACGAA[C/G]AGGGTGGGTGGGAATACCTTAATCAATATTTGTGGAAATTTACCCGAT GAAATCCAGTTATTCCT
WI-13600	26 G T	TTAATGAGCC	CATATTGAAAA TTGTTACTAGA TGATGG	CTCACTTTAATGAGCCAGCATCCAT[G/T]CCATCATCTAGTAACAAATTTTCAATATGCACATTATAT TATACTGGAACAAGAAATACGGATTGTGTAGGGAAGAGAGATAGAGACCACCATCAGCAACCCCTCT TGATTCCTTCTCTACCC
WI-13602	89 G T	TCCATTCTGGA GACAACACA	GCATACCTCAT GACAATATTTA ATATTAA T	GATAGGAAGAAGAAATGAAGTCAATAGTCTTTAGCAAGCCAACTAGCTCAAGGAATAGACAGCCC CTTCCATTCTGGAGACAACACA[G/T]AAATCTATTAAATTTAAATATTGTCATGAGGTATGCACT GCCC
WI-13650	76 A T	AAAGATTAC AATATTTCACT TTTAAAAAC	CAGGCTAGGAT ATGAAGAGTA GTTTT	GCATTAAACATTTAAAAATCTGAGGGATATTGATGAGAACTATGATGAAAGATTACAAATATTTTAC TTTTAAAC[A/T]TAAAAACTACTCTTCATATCCTAGCCTGATGACTTAAAGTTACCGG
WI-14319	83 C T A	CAATTCAGG CACAAAGCTA	CCAAATCATCT ATATTGTTGA TG	TGTTTTGATTGAAGAAACATCTCTAAAAATACCATCTGAGTGCAGATAAAAAAGGAAATAGCAATT CAAGGCACAAAGCTAAG[C/T]ACATGCAACAATATAGATGATTTGGGGTGGGACAGTACAGAATT
WI-13528	80 A G AAA	CAATACATTT GCATTTTCTTA	CATGATACCAC AGTTTTCTCTG AA	ATTGGATACATGCTTTTAAAAATGGTAGCTTTTAAACTGTAATCAATACATTTTGCATTTTCTTAAAA AAAGAAAGACATTT[A/G]TTACAGAGAAAACCTGTGGTATCATGCAAGAAAAGCAGAAAAAATTT
WI-13909c	93 A T	---	---	ACTTAACTGGCTTATCTCACGGTAATCTATTCTGTATTTCCAGTGAAGTTTCATCTTCTCCTCAGCT CTCTTCAAACTCGAATATCTTTTTC[A/T]GAGATGTCTAGTAGTACCCACTGCAACATCTCTCAA
WI-13909b	80 G A C	TTCTCACACT CTCTTCAAAC T	GCAGTGGTAC TAGCTAGACAT CTC	ACTTAACTGGCTTATCTCACGGTAATCTATTCTGTATTTCCAGTGAAGTTTCATCTTCTCCTCAGCT CTCTTCAAACTC[G/A]AATATCTTTTTCAGAGATGTCTAGTAGTACCCACTGCAACATCTCTCAA
WI-14323b	86 C A	---	---	TTTTTATTGAATTCCAAATGTAGCAAAATCATTAAAAACAAATTATAAAAGGGACAGAAAAATTAAG AATCAAAACATCAATCTGGAC[C/A]ATGGGAACCTTGAAAAGGCATGGCAGTGGAGACCAGTAACCTA
WI-14323a	78 T C	ACAGAAAAAT TAAGAATCAA ACATCA	GCCTTTTCAAG GTTCCCAT	TTTTTATTGAATTCCAAATGTAGCAAAATCATTAAAAACAAATTATAAAAGGGACAGAAAAATTAAG AATCAAAACATCA[T/C]CTCTGGACCATGGGAACCTTGAAAAGGCATGGCAGTGGAGACCAGTAACCTA
WI-15389b	104 G A AAA	AGATAATGAA ACATCTGCCA	GATGAGGTGAT TCCCACACTT	AAAAATTGACAAATCAACTAGCTTGCTTTTGTGCTGTTTGGAGACTACCATTTTCAAATTTATTATGT AATACACTCATCCAGATAATGAACATCTCGGAAA[A/G/A]AAGTGTGGGAATCACCTCATCTGTGC

WI-15389a	33 G A TC	AATCAACTAG CTTGCTTTTGG	TTTGAATAATG GTAGCTTCCA AA	AAAAATTGACAAATCAACTAGCTTGCTTTTGTGCG/GA/JTTTGAAGACTACCATTTATTCAAATTTATT ATGTAATACACTCATCCAGATAATGAACATCTGCGAAAGAGTGTGGGAATCAOCTCATCTGTGC TGTAATCTGCTTACAGTCCCTTTGCAAGACAGACATATGTTTTGCATAAAGATATAAATTGCTTCAT TTTAAACTAATTTAGTGTTC/JCTTTAAATTATATGAACCTTTGGTGAATTATGAAGTGTACCAAAAC C
WI-15747	88 T C AGTGT	TGCTTCATTT AAACTAATTT	CATAATTCACC AAAAGTTCATA TAATTT	AAGAAAGCACATACATTTCCAGAAATTTGGAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCTCTCGTTAAGTCTGGATATAC/TGGCTTGCA/C/JGGACACCTTTTACG GAGGATTCCGGACAACT
WI-13752b	117 C T ---		---	AAGAAAGCACATACATTTCCAGAAATTTGGAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCTCTCGTTAAGTCTGGATATAC/TGGCTTGCA/C/JGGACACCTTTTACG GAGGATTCCGGACAACT
WI-13752a	106 T C AGTGTGA	CCTTCTCGTTA AGTGTCC	CCCTCCGTAAA AGGTGCC	AAGAAAGCACATACATTTCCAGAAATTTGGAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCTCTCGTTAAGTCTGGATATAC/TGGCTTGCA/C/JGGACACCTTTTACG GAGGATTCCGGACAACT
WI-14339	102 T G TTAC	CCCAATCAAA CAGTACATGA	TCCAGATTCT GGAACCG	AATCATTTAATGAATGTTCCAAACACACCCCTTCACTGGGCTACAGGTAAATTTCACTGGGATGGAAG CAGATGAACCCACCCCAATCAACACAGTACATGATTAC/TG/JCGGTTTCCAGAAATCTGGATAC
WI-13744	115 C T AAACTGAA	TGTTGCTGAAC AAACTGAA	AATCAGGAAA GATAAGCACA GC	TGGATGGATGGATGAGGCCACCTGTGTTCAACAAACACAGTAAATGGAACCTTCATGCAGCTTAGAT TTCTTTGCCAGCTAGGAGCTTGATGTTGGTGTGCTGAACAAACTGA/C/JGCTGTGCTTATCTTTC CTGATTCT
WI-14061	68 C T ---		---	CCTTGACTATATTGTTTTTCCAAATAGGACTATGTGTAGAGAGAGCCCCGGTACATACCTTAT C/JTJAACCATTTTCATCCACCATTGTTGTAATAATCTCATCTCTGGGTCTGGATACCTCAAAACAGAT
WI-15719	69 A C CATTGAGC	ACCTTTTCATC CATTGAGC	TGATACTTGGC AAGAGTTTAA ATT	TTACAGTTGGATTAAACACTACCACACTGAATATACCTGAATTAACCTATTCAACCTTTTCATCCATTGAG C/A/CJAATTTAAACTCTTGCCAAAGTATCATGAACCTTACGAAGAGGAGATAAGAGATCTGATC
WI-13810	106 T C AACT	CTCTAAATCG ATACATCCAA	GAACTGATGCT TGCTGCTAAT	TAATCCATCAATCTAAATCACACATACATAGATCAACAGAAAGTACCACAGTATGCTTTATTTTGCA GGTATTAAATGGTCTCTAAATCGATACATCCAAACTT/C/JAGTTAGCAGCAAGCATCAGTCTCTTC
WI-15736a	27 G T CACA	ATTTTATTCAC ATTAAACTTG	GTTCTTTTGATA TGTTGCTTAGT TTT	GGATTTTATTCACATTAAACTTGACACA/GT/JTAGCAAAAAAATCAAAACATAAAACTAAGCCACA TATCAAGAACAATATACATAGAGATTGAAATTTCTCAATAGCATTTGGAAGGTATTTCCATAAATA
WI-13785d	72 G A ---		---	TCAAACTGCACACTATAAAGTCTTTAAATGCAGCAGCAGGAGATGTGAAGACACAAAATGAAC AAGTGC/GA/JTAGTGACACATAGCTGTACACACAGTG
WI-13785c	56 A C ---		---	TCAAACTGCACACTATAAAGTCTTTAAATGCAGCAGCAGGAGATGTGAAGAC/JA/CJCAAATG AACAAAGTGCAGTGTGACACATAGCTGTACACACAGTG

WI-13785b	40 C G ---	---	---	TGTTGTGACAG CTATGTGTAC T	TCAAAGTGCACACTATAAAAGTGCTTTAAATGCAGCAG[C/G]AGGAGATGTGAAGACACAAATG AACAAAGTGGTAGTGACACATAGCTGTCAACACAGTG
WI-13785a	27 T C TGCCT	AAACTGCAC ACTATAAAG TGCCT	GGATTTTACAT TCAGCCTAGAT ATAGG	GGCAGGAGGA TTTGTACT	TCAAAGTGCACACTATAAAAGTGCTTT[C]AAATGCAGCAGGAGATGTGAAGACACAAATG AACAAAGTGGTAGTGACACATAGCTGTCAACACAGTG
WI-13793	88 C G ATAGG	TTCTCACCCT TTTCTTTCTC	TTTCTTTCTC	AGAAATGGGCTC TTAACCTTGT	AGAAACCAAGTATATCATAGGCAAAATAAAATAGTTTTTACCCCATTTGATACAACATAAGGGATTT TACATTGAGCCTAGATATAGG[C/G]AGTAACAAATCCTCCTGCCATAAATCTATGACTTG
WI-13794	52 A G TTTCTTTCTC	TTCTCACCCT TTTCTTTCTC	TTTCTTTCTC	AGAAATGGGCTC TTAACCTTGT	TAGTCTCCTACAAATTCCTTCAATCCATTTTCTCTCCTCACCCCTTTTCTTCTC[C]AGTACAAGGTTAAGA GCCCATTTCTTCAACAAACAAAAACAACATAGAGCAAT
WI-15729	35 A G GTGTAGACTGC	CTTTGAACCAT GTGTAGACTGC	CTTTGAACCAT GTGTAGACTGC	CTCAGCTTCTT TCTAAAGTGCC	TCATTTAAGTGCACITTTGAACCATGTGTAGACTGC[C]AGGGCACITTTAGAAAGAGCTGAGACTGAA AAGTCTGTCTTGAAGTCCAGGAAGGGTAAGTCCCTGTTTGACGCCCGGGCTGCTCATTTGTTA
WI-13424	66 G A C	TGAGGTTTTTC ACCCTATTCTT	TGAGGTTTTTC ACCCTATTCTT	TTTTTCTCCCC AGGGTCTA	GTCCCTTGACAAAGTCTCCCAACTGGTTGGAGTTTTCCCTCTGAGGTTTTTCAACCTATTCTT[C/G/A] TAGACCCCTGGGAGAAAAACACATGTGTAAAGTGGCTCAGGACATGAGGCAGGCCGTTTCAACAAGAT GCTGGCTAAGCGGCTTC
WI-14065	29 T C AATT	TCTTATAAAA GGTCAGAGGC CAATT	TCTTATAAAA GGTCAGAGGC CAATT	CAAGCTGAATC TGGGATCTC	AACTGTCTTATAAAAGGTGACAGGCAATTT[C]GAGATCCAGATTGAGCTGTCTCATAAAAAGAT TCAACTTCAAGTAGCACAAATTTCTGTCTGCTTTAATCTGAACTTCTTGAAGCACGAA
WI-13446	22 G C TCACTCATCA	GCCATGTTCTT TCACTCATCA	GCCATGTTCTT TCACTCATCA	AAGGGAATCA AAATCAGAAG G	TGCCATGTTCTTTCACATCATCA[C]CCTTCTGATTTTGTATCCCTTTCTGCTCTGTAATTTTTTCTTTC TTCCCTTTTATAGGCGCTAGTCTGTTTGAATACTGTTTGTAGAGTAGTGAGCCCTTTTACITTTTTT CTGACTGCCTAAT
WI-13725	56 A C TGGGTGOC	TGAGCACATA TGGGTGOC	TGAGCACATA TGGGTGOC	CCTGTGTCTC G33C	TCACACAAAGGCATTTGGAAATGTCACCTTACACATGGTGAGCACATATGGGTGCC[C]GCCCCGAG ACAGCAGGATAAGTTTCAACAACTTGACCAGGCAGGTTAGAAAGCAAGGCATGGTTCAAGGATG
WI-15702d	107 T C ---	---	---	---	CAAATGTTTTTATGAAGAGACTCCGAAACAAATAAAGGCTTTCAAAAAGGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAACTGTAAACCCCTGTAAACAA[C]C]ACTAATGGGTTCTTTGAACAAATAGTTT TGA
WI-15702c	101 T C ---	---	---	---	CAAATGTTTTTATGAAGAGACTCCGAAACAAATAAAGGCTTTCAAAAAGGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAACTGTAAAC[C]T]CTGTAAACAACTACTAATGGGTTCTTTGAACAAATAGTTT TGA
WI-15702b	90 C T ---	---	---	---	CAAATGTTTTTATGAAGAGACTCCGAAACAAATAAAGGCTTTCAAAAAGGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAACTGTAAAC[C]T]CTGTAAACAACTACTAATGGGTTCTTTGAACAAATAGTTT TGA

WI-15702a	48 G C A A G	A A C A A A A T A A A G G C T T T C A A	C C T C A C C C C T T T A C C C C	C A A A T G T T T T A T A G A G A C T C C G A A C A A A A T A A A G G C T T T C A A A A A G [G/C] G G G G T A A A G G G T G A G G A A A G C A T G T G A G A G A A A C T G T A C C C T G T A A C A A T A C T A A T G G G T T C T T T G A A C A A A T A G T T T
WI-13831b	113 T C		---	T G A T T T T T T T T A T G G A T G C A C T G T T A C A T G T T A T T A T T A G C G A A G G T G A C T T G G A A A A G G A G A T T C A C A T A C T T C C A C T G T A C C T C C G G G T A A G T T T C C T T C T C T C T G T A G A T [C/G] T C C A T G T T A C A G T C A A C T A T A A A C A T G G C T C A
WI-13831a	56 G C		---	T T T T T T T T A T G G A T G C A C T G T T A C A T G T T A T T A T T A G C G A A G G T G A C T T G G A A A A [G/C] G A G A T T C A C A T A C T T C C A C T G T A C C T C C G G G T A A G T T T C C T T C T C T G T A G A T G T C C A T G T T A C A G T C A A C T A T A A A C A T G G C T C A
WI-13806	62 G A		---	T G A T T G A G C T T A G A A A G G A A G T C A T G T T G A A A T C A G A G A G A G G C C A A A A C T A G G C C T C A G G T [G/A] C C C A T T A A G C A T G C T G T A A T G C A A A G G A A A A G C T T A A A A A A T T T T T A A G G G T G A C T C C A G T A A A C A T
WI-14372	86 A G		---	C A C A T T T C A G C A A A C A A A T C G A G G T G C A A A C A G G G T T A T T T C A C A T T A A T A T A A C T G G A T T T T T T G T C A A A T A A A T A G G G A [A/G] T T C T C T T A A A T A C C A T C T C C T C A C T T C A T G G C C A G T
WI-14373	95 A G		---	A G G C T G T T T T T G A G G C C T G A G G A C C C C A A C A C A T G A C A A C G T A A G A C T G T A A C C A T G T A C A T G T G A G T T A T G A G C T A G G A A C C C T G G A C G A A A C C A [A/G] C A C A T A T A C A A T C A T C T C C A C C T C C C A A C G C C T T T A C T T T C A C A G C C T C T G C A
WI-14078	61 C T G C A A G A	A A A G A A G T A A A T T A G G A A G A	T G T G T C A T G T C T C T T A C T G C	A G A A A C C G A A A C T C A A A A G A A C C A C A C A T G G T G T A T C A A A G A A G T A A A A T T A G G A A G A G C A A G A [C/T] G C A G T A A G A G A C A T G C A C A C A A A T C G A A A C A A G G G C A T G G A G G A A G G A C T T T A G A T G G T C A C G
WI-14083	47 C T A C A C T	A G A C T T G A G A G C T T A A A A C A	G C C T A C T G G A C C T C T A A A C T A C T G A	T T G C T A C A T A A C A C A T T A C T C C A G A C T T G A G A G C T T A A A A C A A C A C A C T [C/T] A T T T G T T A T T T C A C A G C T C A G T A G T T T A G A G G T C C A G T A G G C T T G G C T G A G T T G T T T A G G T C T T A A G G T C T T A C A A G G C C A A
WI-14085	31 A G A A A A A A	C A T T T A T T T T G A T G T G T A A G A	C A G T C A T G T T C A C G T G C T A G T T	T G C A T T T A T T T C A T G T G T A A G A A G A A A A A C [A/G] T A A C T A G C A C G T G A A C A T G A C T G C A T G G A T A C A C G G C T C A G C A C G A G G C T A A A G T C A G A A G T G A G T G A A A A C A A A A T A G C A T G T T G A T T T A A G T G A A A T A A C A G A A C A G G A G G C C C T T T
WI-12169	121 G C T T G C T T	A A T A A A A C T T C C T A T T T C T T	G G G T T C T G A G G T G A A A G A A A A A	G T C A A A G G T T G G C A A A T T T A T T T C C A C T T A T C A A G A A C T T A C A A A A T A T T T T G T T C A T T T C T A A A T T T T C A C C T T T A T T G C T A A G T T A A A A T A A A A C T C C T A T T T C T T T G C T T [G/C] T T T T T C T T T C A C C T C A G A A C C C C C T T A
WI-15705	50 A G A T C	G G A G G G A G A T T T T A G A C T G A	A G C T G T A G T O G T C A A A T A C T C T A G A A	T T G T T T T A T T T G G G A G A A T G A A G G A G G A G G A G A T T T T A G A C T G A A T C [A/G] T T C T A G A G A T T T G A C G A C T A C A G C T C C T C T C T C T T T G T A C T A C G G A G A C C C T G C T T A T A G C C C C A C A G G A A A T C C C T C A T C T G G G T T G C C A G A C A G

WI-14379	102	C T	CAOC	TCTATTAACA GGGTATGTCA	ATCATCTGTT TGAGGTGACA	TTTATGCTGTTGTTTCTACTGGTGGTCTCGCTCACTAATAATCAATCCTAGTATGATTTCTTT TACTTGTGCTATTAAACAGGGTTATGTCACACC[C/T]TGTCACCTCAAAACAGATGATACT TAAATAAAACAAAGCAGAAA[C/A]CCACCATTAAACAAGAGGACACTGCAGAGGCTTATGTACA ACACGTGTCGCCGCGAGGCTGGCGCAGGACTGCCACTCACTCCAAAATTTCTTTGGAGCAGAG
WI-14102	22	C A	---	CGCAGAGCTG CTGTATTTAAA	---	ACCGCAGAGCTGCTGTATTTAAA[A/G]JACAAGCGTCTGGATCTCTGCAGGGGCTGGGACCAGCTGC AGTGGGGGCTCCGGCACTGCTCTCTCCAGGACTCTTCCACCACCC
WI-15937	24	A G A	A	AAACTGAAAC GTATTTCTCC	GCAGAGATCCA GACGCTGT	TGAAACTGAAACGTATTTCTCTCCA[A/C]JACACCGTAGAACTTAAAGGCCGCAAAAGACTCACACCC ACCACCTAGCGGCGAAAAAGGAAGTTTCAGGTGATACAAGATGCTCTGCCATCACACCTGAAGGAT GGTT
WI-15944	24	A C A	A		TTCACGGTG	ATGTTTATGATCAATTCCAAACATACAGTACAGGGAAGGTGAAATGAGTAAGAAAAAATCAT ATTTAAGTCCCGTTAACACTAAGCC[A/G]JATTATTCAAAATGTGTTTCAAAATACTCAGCCAGAT CACCAAAGCTCAGTCACTAC
WI-14124	92	A G	---		---	GACAAAAGGCGAGTTTCTGTAGTCCAGCAGGGCCAGAGCGATTATCAGAACGGTGGTTTGACCT GCATAGATTTTTCACGACTA[C/T]JGTGGCCATGCCATTCTGTAAAGTGAATTAATGAACA
WI-14125	88	C T	CATAGATTTT	GGTTGACCTG CATAGATTTT	GGATGGCATG GCCAC	GTTATTTTCTCACAGTCTGGAGGTAGAACTGTGAGATGAGGATATCACCAGCATGGTTAGGTTCT GGTGAGGACTCTCTGGCTTACAGCTGGCTGTTCTCACCATGCTTCCACAT[G/A]GCCCAAAGAGAC AGAACAAAGCTCTCTGGT
WI-14136	120	G A	ATGCTTTCACA	GCTTCTCACC ATGCTTTCACA	CTTGTCTGTC TCTTGGGC	TTGTTGTTGGCACCAGAAAAGCT[C/T]ATGTTCTATGTTATGTCACTGTACATACTGTAAACAAGACT GCATTAATATTGTTTCTTATGATTGTTTCAATG
WI-14138	23	C T	GAAAAGCT	TGTTGGCACC GAAAAGCT	CAGTATGTACA GTGACATAACA TAGAACA	GGCAGGTTTATTCATAATTTTCAAACCTTGGAAAGCAACCAAGATGCTTTCAGTAGTAGTATATCA GACAAT[C/G/A]AATATTACTTAGCACTAAAGAAATGAGCTATCAAGTATGAAAAGACATGCAGG AACCTTAAATGGATATTACT
WI-13551	74	G A	GACAATC	TCCTCAGTAG TAGTATATTCA	GCATATTCTT TTAGTGCTAAG TAATATT	TTTTTAAGAGTGCTCTCACATCATTTATTTGATTGTCACACAAAACTTTTTAACCT[C/T]GTCAA AAACAACAAGAACAGATGAATAAGGAAGCCAGTGCTTTTGAGATAGAAGCCTTCTTCAGAATCA CCTCC
WI-15953b	59	C T	---		---	TTTTTAAGAGTGCTCTCACATCATTTATTTGATTGTCACACAAAACTTTTTAACCTCCGTCAA AAACAACAAGAACAGATGAATAAGGAAGCCAGTGCTTTTGAGATAGAAGCCTTCTTCAGAATCA CCTCC
WI-15953a	26	T G A T	A	TTTTAAGAGTG TCCTTCACATC	TCATCTGTCT TGTTGTTTTG	TTTTTAAGAGTGCTCTCACATCATTTATTTGATTGTCACACAAAACTTTTTAACCTCCGTCAA AAACAACAAGAACAGATGAATAAGGAAGCCAGTGCTTTTGAGATAGAAGCCTTCTTCAGAATCA CCTCC

WI-14631	82 G A ---	---	---	TGAATTCATGACAGATTTGCTCTGTTTAGTGAAACCCCTCACAAGCACTCTGCATAGTCCGCTTT CTGCTCTTTAAAC[G/A]TGCTGGTCCCTCTGCCAAACTTTTAGGATTGGCCTCCTCAGGGCCTT GTCTGA
WI-6053	24 A G ---	---	---	ATCACCACCGTGTCTAAGAACAAC[A/G]JCTTCATGTCCAACATATCCCGGGACTTTGTCAACTG CAGTACACTCTCTGCAATGAACCTGGCTTCTCGAGGGAAAGCCTCTAGAGCCAGGTAGGGGTGC AGCAGTGGGGTATACTGGGCTGGCCAGTTGGAACCAACGGAG
WI-15964	99 T A CTGGAGGTA	GACTTCTCCAC OCTCTTGC	---	CAGAAACCTCTCTGTGTATTAAAGCTGATGCTAAAGTCAGAGCAGTCCAAAGGCAGGAGCTGCCCTT GGAGGTAGTAAGCTCTCTGCTCCCTGGAGGTAT[A/G]CAAGAGGGTGGAGAGTCTTGGCAAG
WI-12075	103 G A GGCAC	CCCTTCTTTC TCTTCTTC	---	CAGCTAAAGGATCACTGCAGCTAAATACAGATAGAGAAGCAAAAGCCAGGCAAAATACCCATCAG AGACAGTGACAAGAGCAGCTGGGGGCACGGGGAGGC[G/A]GAAGGAAGAGAAAGGGGGAGGAG OCT
WI-12179	96 G A TGGAGGTCA	TCGAATGACCC TGATAGTGC	---	TAATTTAAACACGCCCTTCCACATAGTGGTGGGATCTGCACATTTCTAGAAAGGACATGA ATAGTGATGGAGGTACGGTGGAGGTCA[G/A]GCATCTACAGGGTCATTCGAGGGAACAG
WI-14651	49 C G ATTGT	GGAGATATGA TCTTTTCTGA CTTATT	---	CACAAATAGTGAAATTAATCTGAGCAAGAAATCATTCTCATTTAAATTTG[C/G]AAATAAGTCAGAA AAAGATCAATATCTCCCTGCTTCAAAATGACACTCCCAATTTTACAGGTAAACCCTGTTA
WI-14666	105 T A ---	---	---	AATGTGGACTTTCAACAAGGGTTTAAACTAATCTAATACTTCTACAACACATTCAGAGCAT TATAACAAGAAATTTACAGGAGCTAATGTATTAAAT[A/A]AACCATGAAAAAGAAAAAATCTG ATCTAGATGTACAGAAATGGGCTGAGACTG[C/T]GTCTGGTAGATGCAGTGTGTATGTTCTAC TCTATTACAAAAATTAACAGAAATATGGCTTCGCTTTGTGCAATGTTTATATCACAGTC
WI-13967	103 A C AAATAAAAA	TTGTGTTTCA TCTCCTAAAAG TG	---	AATTTAATAGCAGCTCTGTGTTGTGATTTTAAAGAACAAAGATAAAATATGTCATTCAGCAGTCATTT AAAAATAAAGAGACTACAGATACAAGGAAATAAAAA[A/C]CACITTTAGGAGATGAAAAACACAAA
WI-14408	60 T A G	GCAGACACAC TATTACAGGCT TTACTTT	---	TTAATATTTAGCAAGTTATTGCAACAGGTTGAAATGCAGACACACTATTACAGGCTG[T/A]AAA GTAACAAATGAGTTTACACAATTAATAATTAACACATACITATGGGATTTGTTGAATGA
WI-13683	47 C G ---	---	---	TTTTGTGTTAAGAACAGCATTTTGAAAAATAAACCTATCTGCCCATG[C/G]TTTACAGCCTTTTAAAT TTGTAATATTATATAGTCGTTTATGGTACATATTGATTGTC
WI-13910b	63 C T CGTCT	CATTGAGATAA AGCACACTTAT CAC	---	TTAGAAAACGTATAAAGCAACACAACCTTTTGGGAAAGACCATGGCAGCTCTTTGTGCTA[C/T] GTGATAAGTGTGCTTATCTCAATGAAGCAACCCCA
WI-14635	22 G A ---	---	---	ACATGGCAGATACAGAGCTGTC[G/A]JCTTTGAAGACCACCACTGACCAGGAAATGCCACTTTTACAA AATCATCCCCCTTTTCATGATTGGAACAGTTTCTGACCGTCTGGGAGCGTTGAAGGGTGACCAGC ACATTTGCACATGCAAAA

WI-16002	59	T C	GATAACATAA AATGATCATG AGAAATTC	GCCATCTCTC TTTGACTTTT	CCAACATTTTAAACCTATGACTGGTCATTGATAACATAAAATGATCATGAGAAATTCATTC/GTTA AAAGTCAAAGAGGAGATGGCTAATGCATGCTGGCT
WI-15361b	101	A G A	CCCACITGAAC TCAAGTCATC	AAACTAAAG CTTTGTGCCTA AAA	GTGGAAATTTTAAAGCCATCAAAATTTCCCTCACACTCAATACTGTTGAACAACAAGATAACACAT CTTCTTGCTCATCCCACTTGAAGTCAAGTCAATCA/GJTTTTAGGCACAAAGGTTTTAGTTTTCTCGG GAAATCAAGTTTTAAACCA
WI-14759	73	T C	GCCTTTGACTT GTGGGG	TCCACACTGC OCCC	TGAGTTACAACAAATGAGCAACAAGTTAGAAAAATTTGGTTTTATCAAACTCCTAGCGTTTGACTT GTGCGGTTC/GTACTCAATGGGGGCAGTGTGGACGGGAGGATTGCAACCAAGATTTCATACTG CAA
WI-12535	50	A T	CTAGAGGGTT GAGGTGTAGA TAT	GCTCCACGAGA AGAGAGGA	TCCCTAACATTATTTACGGTGGTGAAGGAGGTTGAGGTGTAGATAT/TJCTTCTCTCTTCTC GTGGAGCCTTACTGAAGACAGGATCGCCGTTCTTGTTTATCAGCTGAGAAAGGCGAGTCTCGGCATC TTAAAGACCTGCGCTCC
WI-13805a	112	G A	AAAGGCACAC GGGGAA	CTCAGCCTGCC TTGACC	TTCCATTCAATTATGCTTGGCTTTACCAATTTTTATAGCTATTGGGAGGCAGGAAAGGGAATTTTGGC CCCAGAAACCATGAGATTTGGGTGAGAAAAAGGCACACGGGGA/GJAGGTCAAGGCAGGCTGAG AGTCACATTTCCAGACCTC
WI-12340	18	T C	---	---	ACACAATATAATTCCTATTC/JCJGAGTGATTAAACCTTATTTGTTTGAACCAACAAAACTAC AAGAAAAACATTTTCAAAACCTTTTTTTTCAGGCTGA
WI-14808	52	T A	ACCCACACA CTACCTGT	GAGGCATCACA ATGTTAAGATT TT	CTTTGAACACCTTTAAGCAACAGTTAAAAAGTACCCACCACACTACCCTGT/TJAAAACTCTTAAC ATTGTGATGCCTCTGCATCAATTTTAGAAAAACAAGAAAAACACACACTGAAGGCCCATGTA AGTTAAAAAAATCGAGTCAGCATTTATT/TJAAAAACTGGACACGCTTCTATATTGCAAGCTCAT TCAAATGCATTTATTTTGATATCCCAAGCCCTGAAACATGAAAAAATATTTACTAAAGGAATGTTG ATTACCAGCTACGACTTC
WI-14816	29	A T	---	---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC ATG/GTJTAGGTGATTGATACAAATACGATCCATAA
WI-12542c	71	G T	---	---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC AT/GTJGTAGGTGATTGATACAAATACGATCCATAA
WI-12542b	70	G T	---	---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC AT/GTJGTAGGTGATTGATACAAATACGATCCATAA
WI-12542a	45	C T	GCTATTAGGC AAACTGAACA TTTAAA	TCTAGAGCCCT CACATGGAT	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAG ATCATGGTAGGTGATTGATACAAATACGATCCATAA
WI-12173	57	C T	GGATACAGCA GTAAAGAATA CAAAAA	CCACCTCTAGA ATGTATGCTCT ATAA	CACCTAAATCATCTAGAAAACTGGGGATACAGCAGTAAAGAATACAAAAATCCCTGC/JTCTTATA GAGCATACATCTAGAGGTGGGAAAGAGGCAATAAATA

WI-14836	28 T C ---		---	TC TTTGGAGGGATAGAGGACAGAGTGTTTCGTTGATTTCGTTTCGGTTTCAGTTGGTTGTGCATT GGTTTTTGTGTTTTCGCTAATTTTGGCCACCCTATAAAAGCAGTGCCACCCAGAGGCAG
WI-14856	60 A T A A	TGGTGACAAG GAAATACTT	TTTGTGCTA CTTTTACAAA CTTT	ACATTTCCTTATGATAGCAACAACATAATATGATGGTGACACGCGGAAAACTAAATATATTTAA AGTTTGTAAAAGTAGCAACAAAATTGAGTATATACTATAAGTGATAGAGGATGATATATGAAAAA GGCTATAAAAAGCTCCAAA
WI-14863	61 G A ---		---	ATGGCAATTTACTTTATAGCAATGAACAAATATTTGTCAAAGGGCAAAATATTTTGTCTG[A/JAG TTAATAAGATTAAATATCTTTTACCACAAAGCTAGAGGTCAACAGTACCACATATTATTGATTGCCACT ACCTGGC
WI-14867	46 T C A	GACATCCAA GGCTCTCTAAC	TGGGGCTGCAG ACACTC	TTTTAATTAAACGTAAAAGGCGAGGACATTCCAAGGCTCTCTAACA[T/CJGAGTGTCTGCAGCCCCA TTCGCTTTGAGATGGAATGTGTTAACCCAGGGTGA
WI-14733	98 G A A	CCAAATTGAC AGATATTCTGC	GATGAGGTCAG GCCATTTATT	ACGGAGTCGTCTCTGATGTTATCTTGTCAAAAATGTTTGGCTGATTCTAATCATGAAAGAACAAATT AGAAAAATCCAAATTGACAGATATTCTGCA[G/AJAATAATGGCCTGACCTCATCAAAAAACATCA ATGTCATGAAAAACACAAA
WI-14898b	79 A C ---		---	TTTTGTACCTATTCCTGTTTCAGTGCATGTACAGGAAGAGTTGTCTCATAGGTGCCACTAAGGAAA ACTTTCTCCAT[A/CJAAGCTGCTGTGTCACGTTGCCCTGGGCTTTGCTAACCCCTGGTGTGCTGCTCT GCCTGTGTTCTGCTT
WI-14898a	50 A C CA	CATGTACAGG AAGAGTTGTCT	AAGTTTCCCTT AGTGGCACCT	TTTTGTACCTATTCCTGTTTCAGTGCATGTACAGGAAGAGTTGTCTCAT[A/CJAGGTGCCACTAAGG AAACCTTCTCCATAAAGCTGCCTGTGTGACAGTTGCCCTGGGCTTTGCTAACCCCTGGTGTGCTGCTC TGCTGTGTTCTGCTT
WI-14907	48 G A GGACTCTGAC	GGCACACATT GGACTCTGAC	TCTGCTGCAAG GGGAAT	TGGTATTTATTCGGACATTACTGTAGAGGCCACACATTGGACTCTGAC[G/AJATCCCTTGCAGCAG ACATTTGTGAAGCTGCTGGTGGCACACCCATCAATCAGTGACTCCTGCAGTGCAGAGGGGCCACATG CAGCATGCTCAGGTGTG
WI-14911	52 G A C	CCAATACATT CAGTTCTCTGGT	CAAACCAGGA AAAGGACCTT	CTAGAATCTGGGAAGTCCAAAGCTCAGTGCACCAATACATTCACTTCTGCTGTC[G/AJAAGTCCCTTTTC CTGGTTTGCAGACAGATACCTTGTGTATCTCATCATGCGCAGAGAAAGAGAGGAAGTAATCT
WI-14913	88 C A ---		---	CTGATGCTTTGACATCTGGGGCATTGCTGTCTCTAGAGAGACTACTTCTCTGGGACCAGCCAAATTC TAGTGATAGTAGAGGACTCA[C/AJCCCTGCACGTGCACCTTTCATATACAGATCAACCAATCCAAAAAC CTACACCTCCAAACCCT
WI-14914	66 G C A	CTGGACACAG TTTTCTCTAGC	CAAGCCCAGGA CAATAAATTC	ATTTCTTGTATGGCTGTCTGAAGCTGTGAAGTCATGCACATCTGGACACAGTTTTTCTCTAGCA[G/ CJGAATTTATTGCTCTGGGCTTGATGGCTTTCACAGC
WI-14926	49 T C ---		---	GTTTATTTCAAAATGACACATCCAGATTGAAATGGGCACCTAGCGAAT[C/JACTTGTGGACCACA AGACTGTCTGAGAACATGTTCAAGACAGTTTTTCAAAATAAAAAATTTTCCCTTAATCAGGTCCA

WI-16083	89 C T	ATGTTTAAACA CAAACATATC AAGGAT	TGAAAAAGATT CCAGGOC	GCATCTTTATTACACAGAAACATCATTTATGTCCTTAATCATTGTTTAAATATAATATAAAGCATGTT TAACACAAACATATCAAGGAT[C/T]GGGCTGGAATCTTTTCCATTCTATAGAAAAGCACTAACCATC CATTAAGCAG
WI-14930	55 C T	GGAGGAGTCC CTCATGGAT	CACAACCAACC AATACCGC	CAGTTCTGTGTTCTGGAACAGCTCTCCCTTTCCACAGGAGGAGTCCCTCATGGAT[C/T]GCGGTATTG GTGGTGTGGTATTGGGAGCACGAGGGAGAGCAA
WI-14946	47 T C	---	---	TCAATACTGAAGGTGTCAAAGTGGTCTATTTGCCCCACAGACATAACAAT[C/T]CTCTAAATCATCTCTA GATCAGGGAGTCATAAGGACCATTAAGGCTCATACACACAGTACTTTATGAAAGGATT
WI-15987b	80 A G	---	---	ACATTAACACAGCACAAATTAAGGGTCCCAAGAGGTGGTAGTGCCTTCCACTATGTGAGGACAC TAAGAAGATGGT[C/A/G]TCTATGAACCAAGCTGCGGTGCCATGCTCTTAAACCTCTCAGC
WI-15987a	32 C T	CACAAATTA GGGTCCAA	GGAAGGCATA CCAACCTC	ACATTAACACAGCACAAATTAAGGGGTCCCA[C/T]GAGGTTGGTAGTGCCTTCCACTATGTGAGGA CACTAAGAAGATGGTCACTATGAACCAAGCTGCCGTGCCATGCTCTTAAACCTCTCAGC
WI-14948	56 T C G	AGGAAACTG CTAATTGTCA T C G	GATGATCTTAC ATCAGTTGTTG GA	GAATAAAGTCTTATTGCCGTCTCTCAGGGAACAGGGAACCTGCTAACTTGTCAAGT[C/T]TCCAACA ACTGATGTAAGATCATCTCTGACCATAGCAACCTGTAAAGGCTTGTCTCCCTCCAGCTGA
WI-16100	52 A G	CAAAAAGCTA TTTTCTACAC T TGA	ACAGGAATGTC AGAAAACAGT ATATTAC	TTGTGTTAAATTCATCAAGGAATTGACAAAAAGCTATTTTCTACACTTGAC[A/G]GTAATATACTG TTTTCTGACATCTCTGTTATCACTCTCTGAAAATC
WI-14958	83 A G	AATAATTTAT CTCTTCTTTT CAAGGG	AATGCAATTCAT TTGGGTTTTT	GTGATTGATCTGTAATTTATGGGATTATTTCAACTCTAAAATTCAGATGAAAATAATTTATCT CTTTCTTTTCAAGGG[A/G]AAAAACCCCAATGAATGCATTTTTCAGTTTCTCCAGGCTTTGAACTGC AGCAGAAAAATTCAGGA
WI-14976	35 C T	GTTGATTGCT TCGTTCAAAG T	TCAAACATAAT CTTCCATTCTA AGC	TATTTTTTAATGGTGAATTTGCTTCGTTCAAAG[C/T]GCTTAGAATGGAAGATTTAGTTTGAGGAG GGGCAGGTTTGGGGTAGGCTCAGCGGCATAGTGGCCACAAAGAGATGCCCATCTCACACCTGGAG ACGTCCATGAGCACCTCG
WI-14981	31 G T	TCAGTGGTGT TATTGGATTT T	CACCTCTGACA TAATACTTAGC ATAAA	TAATTGATTCAGTGGTGTATTGGATTTT[G/T]TTTATGCTAAGTATTATGTCAGAGGTGGAGAAT AAAGAGGAAAAAGAAACAAGTGTGGCTCTCGCATCAACGACCTGATCTTGTACAGGAAGTTTTTGA GAGCTCACAAA
WI-14992	80 C T	TGCATTAAAT GAAGCTGCAG T	GCTATGTGCTC AGCTTTCTC	TGATTACATTTTTTAAATCATGCTACCAGCCCATCTAAGCCAAATTTCAAACACCACCTCTGCATT AATGAAGCTGCAG[C/T]AGGAAAGCTGAGCACATAGCACCCAACTGATCGGAAAGAAACGTA
WI-15002	72 T A	---	---	AAATCTCTCTTTTACACACAGATGAACCTTTAATAAATTACAAATGCACTGAAATGCTTCTTGA TTTCTT[A/T]TTCAGTTTAGGCTCAAATGGGCTCTCTCAAGGCTGGACCTCAAGGCCAGTT
WI-15000	90 G A	GACAGAAAA GACTCAGACT GTCTAA	GTTTCTAGTTC TGCACAACTT CA	TCAAGCCCAATATCTGCAACAATAACATGTATTGAAAGGTATAGAAATAAACAGATGGATAGACAG AAAAAGACTCAGACTGTCTAAGTA[G/A]TGAAGTTTGTGCAGAACTAGAAACAAAAATCCACCT

WI-12323	68	G A	CACAATACTT CATGTACCTAT GAAATAA	CACTGGACATA TTCCCTACCTG	ATTTGTTGATGTTGGTTAAATCTTATCTCTTTTTTATACACAATACCTCATGTACCTATGAATAA G/AJACAGGTAGGGAATATGTCAGTGCAGCAACAGAGGACTCACACCTGTGTCATAGACAGCACC
WI-14683	91	A T	AAGGACGAT TTAGTATCTAA AAACA	GGCATGTCCCA GTGTTTT	CATAAGTTGCATTTATTACGCTCCACGCCATCTAAAGCTACTGTGTACAGTAATCAGGACTGGAGAA GGGACGATTTAGTATCTAAAAACA[A/T]CAAAAAAACACTGGGACATGCCCCCTGAATTGCAAGT TGGAGTTCGTAAGAATCTAC
WI-13470	100	C A T	CCTGCCTTAT ATTGGAATTC	GGGAGACCATG GGTCTCT	ATTTGTTGTTTATTAGCACCTGAAATTTAGGCAAGAGAAACATTTCTACCTGAAGACTCCATGCAGT CAAAATTCCTGCCCTTATATTGGAATTTCTA[C/A]JAGAGACCCCATGGTCTCCCCAAGTGAGGAAGCC AGGGCACTCAGCCCTTC
WI-14712	38	T A CA	TGAATGCTTCC AAGTACAAAT CA	TGAAAGTATGT TGTATATGGTA TTGTGA	TTTGGTGTACTTTGTGAATGCTTCCAAAGTACAAATCA[T/A]JCTCACAATACCATATACAACATACT TTCAATCACAACCTCAAAATATAAAATACCTACAAAATCACATTGC
WI-13712	40	A C T C A T T G	TTTACTTTGTT GTCAATTTTAT TCTATTG	CCATAAGGCTT CACACTTTTCT TAT	TGGGATACCCCTTTTACTTTGTTGTCAATTTTATTCTATTG[A/C]JATTATAAGAAAAAGTGTGAGACCTT ATGGCTTCTGCTTATTGGGCAATATGCAATATAATATTGTGTGTTGTTAAAAATTTATGCAAT
WI-16163	35	C T A	TCTGGTGATGC AATTGAAATA AA	GCTGCCAATTA CATTAACTTAC AA	TCTAAGATTTTACTCTGGTGATGCAATTGAAATAA[C/T]JATTGTAAGTTAATGTAATTGGCAGCATT GCCCAAAAGTTTAAAGAGGACTATTCTTTAAACAAAGACAGTGTCTGACATTTATTTCAGGT
WI-13453	88	T A TC	AATGCACAAA ATCTTGCTCT TC	TCAGATTTTAA CATCTCTTCT AGCA	TTTTTTTATTGCAATTTGAGTGTCTTATTATATTGGGAATTGCAGTGATATTAACATTTGTACAAAT GCACAAAATCTTGCTCTCTCTC[T/A]JTGCTAGAAAGAGATGTAAAAATCTGACCTAGTTGAACAGTCTT AATGAACTCATTGICCAT
WI-16167	58	T C G A T T T T	CGCACTCTAA ATTAGAGATA	TGCTGTGGTG AATAAGATG	CGGATATAATTATGTACCCGCACTCTAAATTAGAGATAGATTTTTTCTGATATACATTT[C/C]ATCTT ATTACACGAGCAGCACACCACGACAGTAGAACAGTCCACACCTGATAAAATTGCACAAGATG
WI-14482	17	G A ---	---	---	GCAGAACCAATTAAATAA[G/A]JAATCTGCAAGTTTCCCAAGAAACTCTGGAACCATAGTGCCTAAT GCCCTTTAAATCGATACTAAAGGAGAGAGAATAAAAGGACTGCTTGATGTGACAGTCACTGGT
WI-15069	81	T C ---	---	---	TGTAGTCTTCAAAAGACATGTTGGCAGATAGCCAGGCCACTACTATGTGTATTTCCAGTATCATGTAC GCACTAAAAAAAT[C/G]GTGTGCTGCTGCTGTGAGTGAACCATTTGCTTAAGATAAA
WI-16156	97	A C C C A G A T C G C	TGAAGATTAA CCAGAGTCGC	AATTGTGTGCA TTTTGAAGAGA	ATCTGGTATTTGTGTATCCCAACAGTATACAGAAATCTCTATAAAACCAACCCCAACCTTCAATA TTACACTAATGAAGATTAAACCCAGAGTCGC[A/C]JCTCTTCAAAATGCACACAAATTAAGACG
WI-15012	59	G T A T G T	GCAGCAAGAT TACATCAGTA TATGT	CTCCAAATAGC CTAGAGTATAG TAAGGT	CATGGCAGCAAGATTACATCAGTAATGTAATAATAATACAGCTTTTTTTCATTGAAGCTTTGTTACCTT TACTATCTAGGCTATTGGAGTGTCCCCCAG

WI-15100	74	G A	TCATTACAGCCAGAAATAACCCAAATATTCCAAATAAAGCAAAATTTGGAACAGACTGGA GTGAGAAC[G/A]GGTTCCACCACCAAGCCCTCAAGACAAGATGGACACGGCAGCTGTTCTGGGGT GCATTTCTAGTGGACTTTAT
WI-14492	92	A T AATTACT		CCTTTATTTTC CCAAATATAA	GTACCATGTT ATATTTTCTTT TAAGAC	TGGTACAGAAATGTTTAATTACAGAGGGCAGTGATTCAGTTAAATAAATAAATAAACCCTTTATTTT CCCAAAATATAAAATTAATAATTAA[A/T]GTCTTAAAGAAATAATAACATGGTGACAGCTTT TCTTTAATTTTATCGGAATCCAGGACACAACAAGAAACACCCAAACCCACATGGAGACAGAAG ACGAGACACAACCTCTCCCCAC[G/C]GCCTCCCTGCTAGAGTGGGACAAAGTGGGGGTGAGAC AG
WI-12002c	89	T C	TCTTTAATTTTATCGGAATCCAGGACACAACAAGAAACACCCAAACCCACATGGAGACAGAAG AC[G/A]AGACACAACCTCTCCCCACTGCCTCCCTGCTAGAGTGGGACAAAGTGGGGGTGAGAC AG
WI-12002b	68	G A	TCTTTAATTTTATCGGAATCCAGGACACAACAAGAAACACCCAAACCCACATGGAGACAGAAG AAGACGAGACACAACCTCTCCCCACTGCCTCCCTGCTAGAGTGGGACAAAGTGGGGGTGAGAC AG
WI-12002a	30	C G GGACACAA		TCGGAATCCA GGAGCCCTA	TGGTTTTGGG TGTTTTCTT	TTTTCAATTTATTTCCAGAAAGAAATCACATTTTCAGTAACAACCTTACATATAGAAATTAACCTTTG TTCTGGAATGGAGCCCTAGTTGCAGTAA[C/T]GTGTATATAATAATAATTGCATATTCAGGATTTTG TGAATAGGTGATTGGGA
WI-15116	96	C T GTTGACGTAA		GGAGCCCTA GTTGCAGTAA	CCTGAATATGC AATTAATTTAT ATGACA	GCAAAAGCAAAAGCTATGGAGGCCCTAAAGGAATGGGA[C/T]GTGTGGTGGCTTGATACCTTGGT GCTTGTGTGATGGAGCAGAAAGTCTTCTGGTCCATGCAGGGGCGTCACATATTTTAACTGCACATAAT TTGGGCAAACTGTCTATTC
WI-12578	37	C T AATGGGAA		GGCCTAAAGG AATGGGAA	TCAAGCGACCA CCAACAC	ATTTACAGTTGGCCAGATCTCCCTTATGTGGCATTGCA[G/A]GAGACACTGCACCTATCTGAGGTTA GAAAAAATGTAGTCTTAATAGCCCTCTTAATGTGTAGCAAGGCAAAATACCATTTCCTAA
WI-15153	40	A G GCATTGCA		CCCTTATGTTG GCATTGCA	AACCTCAGATA AGTGCAGTGTCT T	CCTTTGCTCTGAACTGGGACCAGGATGTGAATAATTTTGAATCTGATGCAGGTGAGGTATGGC TTTAGAATCAATGGG[G/C]TGACITTTTCCCTGTTGGTGGAAACCTCTGTGAGGGTTTGGCA
WI-15215	84	G C TCAATGGG		TGGCTTTAGAA TCAATGGG	CCAACAGGGGA AAAGTCA	AGGAAAGAGTGTGAAGCAAGCGCATCATTTGGATGGAATGATTATGTGTCCAGGACCTTGAGGAC CTAGAAAGCAAAAC[C/T]GGAGTGATTATGCCAATCAAAATTCGAAGTTGGAGATATGCTAAAA
WI-15225	80	C T C		AGAAAGCAAA T C	TTTGATTGGCA TAATCACTCC	AATTTGCTAGTGCAAAATGGACCAGAAATGGAAAGGCTATGTAACATACACA[G/A]TATGCACACAC AGCCATGTCAAGTGTACAGATCCTCTTGTGATTCAGCTTTCTTAAACACATCAAAAGGCTGCA
WI-15152	51	G A	TGACTGTATACCAATGCTGTGCTTAATGTTAGTGACAGACAGATAAATAGGATG[C/T]GTCTGTTT GCCCTAAGCAATTTACAACCTACCTGCGGGAAGAAACAGACATGCAAAACACGAGATAAAACACAAT
WI-15123	55	C T TAGGATG		TGTTAGTGACA GACAGATAAA	TTGCTTAAGGG CAACAGAC	

WI-15182	49 C A	GCACAACCCAG	GCATGGGTTAA	GAGACTGCCCTGTGACACAACCTAGCTAGCTGCACAACACAGGGCAAAATAC/AJTGCTGGATTAAACCC
WI-15198	38 T C	GGGCOCTTGGC	ACCTATCCGTC	ATGCTAATGGGTTACCTTTATTTAGTAATCATGGTCCCTCATAGCATGGTCCAGATCCG
WI-12601	42 T C	TAATCTGCTT	AGGCAGAGTAG	GTGGACCTTACAAGTACCATGGGCCCTTGGCACTATG/CJCTACTCTGCCTGACGGATAAGTTGGC
		TAATCTGCTT	AGGCAGAGTAG	ATATGGTTCAGATTGCTTGTCTACACAGTCCAGTTCCCTAGAGACTAGTCCGACTCTCTT
		TAATCTGCTT	AGGCAGAGTAG	TCAAGTGGTAATAGCCATTATTAGAGTATCTTGCTTTGAT/CJGCTACGTAAGCATGTAAGACT
		TAATCTGCTT	AGGCAGAGTAG	ACAACATTACGACCCCATCTCTTCAAGAGGAAGTCTGGTATTATGGAACAAACATTTTGTCATTCAGAT
		TAATCTGCTT	AGGCAGAGTAG	T
WI-14510	104 A T	TGGCAAAATA	TTGAAAATGGT	ATGTTGAGAGTAATAATATGCCCTACATATTTAGTGAAGTACACCCAGATATTTTGGGGAGAAGAG
		TGGCAAAATA	TTGAAAATGGT	TTGTTTGCTTTTGTGGCAAAATATGCATAACAAAAT/ATJTGGCCAGTTTAAACCATTTTCAAGAGT
		TGGCAAAATA	TTGAAAATGGT	CAGTGTGATGACATTTCAATGGGAAAAGATTGTGCATTTGCAATAAACACCATCAT/CJCCCTGAG
		TGGCAAAATA	TTGAAAATGGT	TCCACAGATAAGTCCGCCGAGAGGGGCTTCCCTCTCTCGCTGGGTGACGTTCCCGAGCGAGT
WI-15239	57 T C	TAATCTGCTT	AGGCAGAGTAG	GAAGCCTTTTCTGGAATG
		TAATCTGCTT	AGGCAGAGTAG	
		TAATCTGCTT	AGGCAGAGTAG	ATGAGTTTATAAACTGGAGACAGCGCATCATATGAAGTGTCTAGCAGTATTAT/CJGCTATTAGCTA
WI-12634	52 T C	TAATCTGCTT	AGGCAGAGTAG	TGTTTACAAATTTGCTCGAAGGGGCTTAGATGTGTACACCCAGAAAGTGGTGTCTCTGA
		TAATCTGCTT	AGGCAGAGTAG	TTTGCTTGAAGGGCTTGACACAAAGTTCTAACTT/CJTTGTTAAATACTCTGGCTTCTCTGGCTGG
WI-15249	34 T C	TAATCTGCTT	AGGCAGAGTAG	TGAGGAGGCACAGGCTGGGGTCTTCAGGTATCCACTGGTGCCCGCATCTGTTCCTCCACTCCCCAG
		TAATCTGCTT	AGGCAGAGTAG	CCACATCTTGGCTCT
WI-12159	28 T C	TAATCTGCTT	AGGCAGAGTAG	CTGTCCGGGGAAGACACCGTGCATAATGC/CJTAAGTGCCTGAGGAGGGGGGCTGTGTGACTC
		TAATCTGCTT	AGGCAGAGTAG	CCAAACCTCGAATATTTTATGAATCTAAGAGTCCAGACGCGAGTTCATCCACGGAGATCTGC
		TAATCTGCTT	AGGCAGAGTAG	
WI-12648	41 A G	TAATCTGCTT	AGGCAGAGTAG	TCCCAGATTGTATGGAATGCCCTAGTGGCATTAGGATGC/AJGAGTGGATGTCCACTTTTAGTAGC
		TAATCTGCTT	AGGCAGAGTAG	AACCGATGTTAATTCACACTCTCCATGTTAGGTGCTTTACTTGGATTATCTCACTTAAACCCACA
WI-12684	64 T C	TAATCTGCTT	AGGCAGAGTAG	ATGAGAGGTAAGTGTCAACAGTAGGCTTAAATATTCAGTAAACCATGTCTGTAACAGCTGTGC/G/
		TAATCTGCTT	AGGCAGAGTAG	TJCCATTAGGCTTTGTTGTTCCATTTAGAGAGCACAGGAGAGGAAATTTAGCATAAATCTT
		TAATCTGCTT	AGGCAGAGTAG	TTTATAAGCTGAATGAAAGAGGTGACACAGCGGACACTGTCTATAAGTGGAAACAAAGGATGAAGCT
WI-15260	75 A G	TAATCTGCTT	AGGCAGAGTAG	AATCATGGA/G/AJGCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGAAATGAGCTGGAGAAATTA
		TAATCTGCTT	AGGCAGAGTAG	TCCTG
WI-15325	39 T C	TAATCTGCTT	AGGCAGAGTAG	AAGGTTTAAATGGACTCACAGTTCCATGTGGCTGGGAGGCT/CJTACAAATCATGTTGGAGGGCAAAA
		TAATCTGCTT	AGGCAGAGTAG	GGCACATCTTACATGGTGGCAGTCAAGAGAGATGAGAGC
		TAATCTGCTT	AGGCAGAGTAG	TATTTGAGTATTTCCATGGGCTTCTCACTCCCTTATACATTTCCAGGGTTGAGGTAGTCTACCC
WI-13936	123 T C	TAATCTGCTT	AGGCAGAGTAG	CCATAGGTTCAGAACCTATGACCTGTATCTTCAGTTGGCATTCAATAGCCTATG/CJTAACTCCATGT
		TAATCTGCTT	AGGCAGAGTAG	GGGAGTTTCAATAAA

WI-14528	62	T G	TTTAACTTTT TCTGGATGGTA TAAAT	CTCGATTAGCA CTTATTATAAA AATTAAAA	TATGCTTTATTGAAGAGAAATAGGCTATTAAATATATTTTAACTTTTCTGGATGGTATAAATTT/GJTT GAATTATAAATTTTAAATTTTATAATAAGTGCTAATCGAGACATCACTGGGTATAATTGA
WI-15347	74	C T	GACTTCAAAG GAAAAGAACA AATTT	TCACTCCCCA AGTCTTTG	TATTTCTTGGGTTTCGGATGCAAAACAAAAATTTTAAAGAAAAATGTGACTTCAAGGAAAAAGA ACAAATTT/C/TCAAAGACTTGGGGAGTGAAGGCAGAGCCTGGTGACAGATGGACGAGGTCTGCAGA CG
WI-14546	95	C A	CCAATTTCTAG TGATAGTAGA GGACTCA	AAGTGCACGT GCAGG	GTATTTCTGATGCTTTGACATCTGGGGCATTGCTGCTCTAGAGAGACTACTTCTCTGGGACCAGC CAATTTCTAGTGATAGTAGAGGACTCA/C/AJCTGCACGTGCACCTTTTCATATACAGATCA
WI-15353	37	G A	---	---	TTTATGGCTGCTCTGTAATACAATGTGGTGAAAAAC/G/AJCTTAATTCAGGACATCTTCCACCTTG TTTTGGCTTCCAGTTGACTGCAAGACCAGTCTCAGGCACATAGGCTGATTAAATCAGTGG
WI-14580	100	G A	CATTCCCATCT GTCITGCA	CCGACCAAGAT CCCTOC	AGAAATTTTCTTTTTTAAAGGACAAGTAACAGATTACATCAAACTTCAGAACTTCTCAATAC CTAGTTATTATACACATTCCTCATCTGTCTTGCA/G/AJGGAGGGATCTTGGTCGGCTTAACA
WI-8540	73	T C	GGCTGCATTT GGCTTA	GCCCTTCTTT TCAGGCAC	CCAGCTGGAGGTGGAATAAATGCGGCAACACAGAAAAAACACAGACTACACACAGGCCCTGCATT TGGCTTAT/CJGTGCTGAAAAAGAGGGCCGACCTCTTGATAAAGAAATGTCT
WI-8039b	97	T C	---	---	AAGTAGAACACAATAGAAATGGCTCAAAAATATCAGAATGCACACTACGCACATCACGAGTAAATACTG TTTGGTAAAACTTTGTTTTCAGTTAAATATGTAT/CJGTGCTCGTGATGTATGATTAAATATCCTTCT TACCACAGTCACTTAAAGAACCAAGCTTAGGACTAGGGACACACCATGCAGAAAAAGACAGGGA GACCAGACACTCTGGTTGAGATGATTTTAAATGCCCGCAGCCGACACCCACA
WI-8039a	87	T C	---	---	AAGTAGAACACAATAGAAATGGCTCAAAAATATCAGAATGCACACTACGCACATCACGAGTAAATACTG TTTGGTAAAACTTTGTTTTCAGTT/CJAAATATGTATGTGCTCGTGATGTATGATTAAATATCCTTCT TACCACAGTCACTTAAAGAACCAAGCTTAGGACTAGGGACACACCATGCAGAAAAAGACAGGGA GACCAGACACTCTGGTTGAGATGATTTTAAATGCCCGCAGCCGACACCCACA
WI-8044	107	C A	---	---	CACAAACATTGAGAAAGTTTCTGCAATTTGCTCTCTCTGATGCTTAAAGATTTTGAGCTTTGACTAT ACGATTTCCACACTGAACGCATTATAGGTTTCTCC/CJAJAGTATGGATTCTCTGATGATTAATA AGCCCGAATCTGGCTAAAGGCTTCCACATTCAAGACATTTGTAAGGTTTTTCTCCAGTGTGGAG TCTCTGGTGTGCAAGAATGGAACCTCGGCTGAATGCTTTTCCACACT
WI-8550	32	G A	GGGAACATCA ATGCAACAAG T	TTTGGGCTTG AGTTTACAAAT	CTTACTACATGGGAACATCAATGCAACAAGTA/G/AJAAATTTGTAACTCAAGCCACAAACTTAGTTA ATAATCATGGTTAAGGGACATTGCCAAAGAGCAACTGATGCCTCAGTGAA
WI-8057	87	T A	---	---	TATTAGATAAAACCCCTTGTCCCGATTTCAGGATGTTTAAATTTGCTCTCTTTAAACTCTGTGACTTTT CCCTGGTTCAAAAGGACAGT/AJGATGGACAGCAGCAGAGAGGTGGGGTCTGAAAAATGTAATCTTT GTGTCAGGACACTCTGTGGCTTCAAACTGCCCCCTGTGACAGGGATGCTGCCCTTCCAGCCCCAAAG ACACTAGGGCTTTTCAATGGACGGGTGTTGAAGCAGCCAGATGGTAAGG

WI-6192	91 A	GAT	GATGCTAAG GATTTAATTTG TTAAAA	TGAAGTGTAG ATGGCTAAGTA TTAAAA	AAGAGGAACAAATTAGCTCAGTCCAACATGATTGGCAGTTGGCATAATTCTAGTGAAGCAAGTGTCT GACTGCTAAGGATTTAATTTGGAT/GATTTTAATACTTAGCCATCTAACACTTCAAGCATAAC
WI-6194	105 T	A	GAAA	CA	AAGTGATGTGCTCCTCACAATACATTTCTCAAACTCAAAACATCATGCTTGAATATCACTGAACCTT GTCACCAAGAAGTCAATGGCAATGATAATAAGAAAT/TAJATGCAGACTACACTCTGAGGATAG AGCTCTAAAGAGTAAAAACAATGGAATTTGGAAAAATAGGAGTAA
WI-6213	164 C	T	---	---	CATATGCTGCTTTATTTCTGTAAGGATACACTGAAACGTTAGATGATAATAGCTAATGACAGAATGT AGAAATGAGGCATCAGCTTCTTAACCACTCTCAAGAAATGTTAGTATGTTATGTCATTACATGTTT ACTTTGATAATTGCTCATTAATACTATGTC/TAATAATAATGTAATACAGTAAGTAGGTGATCC TGCATTTCAAGGTAAAGGTAGGTGGAATCCAGATTCTCTTGAGGAAAA
WI-6217	131 C	T	---	---	CGGGTTAAGAAATACCTTTAAATTTAGGTAATAAAGCTCAAGGAGTGGGCTGTCATCTGTGGTG TCAGTCTTCTGGCCCTGGCTGTGTCAGTGTGCTCCAGGGCTTGACAAGCAGCTCATTCAGG[C/T] GGCCCAACATGGCCCTAGGGTCTGTCACAAGTCCAGCAATCATGGCGTTCTCGTATATCTGATCC AC
WI-6238	175 G	A	---	---	ATAGTCTTTATTTGTCAACGAAGGCTACACGGGATCACTTCTGGTTTGTATGCTTTTTTTTTC TAGAAGGTATCTACATCTGCATTTATTTACAGCCTTGTGGTATTACACAGTCAAGATACAGTGTTA GAAACACAAAAGTGTGAGAAAAAACTTCTCAAAATTTG/AGTTCCAGACTTCAGGAAAATGATT TCCACATGGTAAGGCCAGAGTCTCCAGTGTGGTTCATCCAGAACGACTTG
WI-6272	86 C	T	TAA	AA	CTTGATTTAATCAGGGCTTTGGGTCATAGGGGATTAGTCACTGTCACAGTCATAATAATGCATTTA TTCAGGGAAAACCTTTAAT[C/T]TCTTTGTCTCTCCAAAAACAGCTGCTGGAACACCTCAAAATTA GGGATGTTTCATCTAAAACACCTTTACTGAACTTGATTCCTTGGCCACAGGAAGGTTTACTGTAG CAGAGGACTTAATGCAATGCCATTCGGGCAATAAATGAATACTTGTGATTCATACAGGCAAGAA TCCCAGCATCCAGAGAAGCTCTGTCTG[C/G]CTGCAAGCCATGGCTGCAGACATCAGGGAAGCT GGTGCAGTTCTAGTCTCGCCTCTCGATTTCCTGCCAGCAGTCTCTCTCTCATCTCTGCCCC TCIG
WI-6303	96 G	A	CTCTGTCTGC	TTGCAG	ATGCTTTTGCATGATTTCTAATATTGCCTTTTTCAGAGCTCTGCTGGTAAAAAGTGGGGTGCCATACA AACAGTCCCTTTTCAAGCCAGCGTGTGATGCATCCTGCCAATCAATCACTGTAATGTCCATTGTCCA AACAGGTCAACCGTTGTCTCCATGAAAACTGGATAAAGAGTTGCTGATAGTGT[C/T]CTGGTT CTCCCTTTACATTTCTTTGGGGA
WI-6315b	193 C	T	---	---	ATGCTTTTGCATGATTTCTAATATTGCCTTTTTCAGAGCTCTGCTGGTAAAAAGTGGGGTGCCATACA AACAGTCCCTTTTCAAGCCAGCGTGTGATGCATCCTGCCAATCAATCACTGTAATGTCCATTGTCCA AACAGGTCAACCGTTGTCTCCATGAAAACTGGATAAAGAGTTGCTGATAGT[C/G]AGTGTCTCTGGTT CTCCCTTTACATTTCTTTGGGGA
WI-6315	187 T	C	---	---	ATGCTTTTGCATGATTTCTAATATTGCCTTTTTCAGAGCTCTGCTGGTAAAAAGTGGGGTGCCATACA AACAGTCCCTTTTCAAGCCAGCGTGTGATGCATCCTGCCAATCAATCACTGTAATGTCCATTGTCCA AACAGGTCAACCGTTGTCTCCATGAAAACTGGATAAAGAGTTGCTGATAGT[C/G]AGTGTCTCTGGTT CTCCCTTTACATTTCTTTGGGGA

WI-6375	28 A G A A	GGTTATTGCA TATGGAAATC	AATGTGAGATC TTTATTCTAAC CTTTTT	AAGGTTTATTGCATATGGAATCAATAG/GJ/TATCTTTTACAAAAAAGGTTAGAATAAAGATCTC ACATTTGTAAGGCACATATGAACATTTTATAGCAAGCACAAAGGCGAGTGAGACATCAACAA TTGTGCTCAACAGATGAAATTCATAACCTTGTCTGATAAGACAATTCAAACATACAAATCAAT TACAACATGTGCTTATCAGCTCCCTCCACCCCTATATTTAA/T/A/GCAACTGACAGTTTTGAAG GACACCAAGACAATAGGGCT
WI-6409b	112 T A ---		---	TTGTGCTCAACAGATGAAATTCATAACCTTGTCTGATAAGACAATTCAAACATACAAATCAAT TACAAC/TATGTGCTTATCAGCTCCCTCCACCCCTATATTTAATGCAACTGACAGTTTTGAAG GACACCAAGACAATAGGGCT
WI-6409a	73 A T ---		---	CTAATAATCTCTGGGCACATGGATCCCAAGAGAGATTTGCAGCAGATTTTCAATTATAGTTACTTAA CAGCTAAATAATAAGGGTGTATTTAACTTACTTACAGAGTCACTAAATAATGGAGGGGAAAGGAAA GAGTAGGGCTAATCCAGTAGAGACTGAAGCTG/G/TJ/TATCAACCTCCCTAAGCATCTGTCTGGTCCG CAGC
WI-6523	165 G T C T G	GCTAATCCAGT AGAGACTGAA	AGATGCTTAGG GAAGGTTGATA	TCTCTAGCCCTATTAGGCTACACTGTAGTCACCTTCTATGAGAGCAAGGGAAACAGGAAGATGGGC TCTGGAGTCCAAACAGGATGTGGAGCTCCCTGGTAGTCTCTCTTTTACACAACTTTTCCCTGAGA ACTGTCCAGTCAGGTGGACCTTCAACAACACGCAACAGCTAAAACTCTGAGAGAAAAC/C/G/CTG ACTTTCAGAAAGCATAAAGCTGAGAAAAA
WI-6554	195 C G ---		---	ATTGTAATTAAATTTACATGGGCCCTATTTATTAAGGACATGTGTAATGTTTCCACTTTGTTTTAA IC/TJ/TAATCAAAACATGTGGCTTAAATAATGTACAGATCAATGTAAACAAGTTTGAAAAATGGCG
WI-6558b	68 C T ---		---	ATTGTAATTAAATTTACATGGGCCCTATTTATTAAGGACAT/G/C/JTGTAATGTTTCCACTTTGTTTT AAACAATTACAAACATGTGGCTTAAATAATGTACAGATCAATGTAAACAAGTTTGAAAAATGGCG
WI-6558a	42 G C ---		---	AACCAACAAACTAAGAAATGGGAAAAAAGAAATGGCAGGTGAAGAACTCTTTTCAGAGAAATAAA AGTTGTCAAT/C/JAGCAATGGATGCTGTGTCAGAACATACGCAATAAACTTTAAGAAAAAAGGA ACTCAATGAAGTTACTGTTATATAAAACAGGAGCTCACAGCAGGATGTAAGAGTTAATGGAAGAT ATCGTGAGCCAAAC
WI-6629	75 T C G T C A T A	TCITTTTCAGAG AATAAAAGTT	TGACACAGCAT CCATTGCT	CTGCCCTGAACCAATCAGATTTAGTTAAATCAATCAATCAAACTCCAGCTGTTTCTTCTGCTTT TTACTTAGCAAGGAAACCTTTAGTGAATGCTACTTGACAAGAAAGATCATTTCTCAAGCACA T/C/JACCCAACTTGAAGGTGATTGAACCCCAAAATAATGGGTGGAAACACCAATGAGGTGGAGGA ATGAGAAAGATGTGTGGCCAAAGCTATCTGGTTATATTTGATGTTGCCAAT
WI-6644	134 T C ---		---	TGCTAACACCACCATTTATTAAGGAGAGTACTAGGAAAACTACCAACACAGCATGTGAAACAGT TGGGCACGGTGTAAAGGCACAGACTCTGGAGCCACAGC/C/TJGGCTAATACACTGCAATATTTTA TGTTAGCAAATTATAGCTGGTCTGTGTATAACCAGAAAGCGGTATCTGG
WI-6690b	106 C T A G C C A C A G C	CAGACTCTGG TAGCC	ACATAAAATA TTGCAGTGAT	

WI-6890a	28 T C AGAG	AAACACCACG ATTATTAAGG	GCTGTGTTGG TAGTTTTCT	TGCTAAACACCACCATATTAAAGGAGTTCJACTAGGAAAACTACCAAAACACAGCATGTGAAAC AGTTGGCACGGTGTAAAGGGACACAGACTCTGGAGCCACAGCGGCTAATACACTGCAATATTTTA TGTTAGCAATATTAGCTGGTCTGTGTATACCAAGAGAGGGTATCTGG
WI-6770	53 A G AACATCACA	CAAAACCCAA AACATCACA	GCTTTTGGAGT GTATAATAGTA TGAATAA	GATGTTTAAATGACACAGATCTTCCAAAGTAATCCAAACCCCAAAACATCACAAGJAAATTATTCAT ACTATTATACACTCCAAAGCAAAATACITCAACTGCAATCC
WI-6686	151 A G A	GCAITCTTCCA AAAACAAAGA	CCTTGTAAGTG ACTATTCCAAT GTT	ATTCTGTAGGCAAGGTTGAGCAATCAGTACAGTACACTAATCTTGACCAAAATGGGTGAGTCAGCCTCA TCACAGAGATTTTTTTTAAATTTAGATGAAATTTACATTTAAACATGGTAACCTCAAGCATTTCT TCCAAACAAAGAAATAGJACATTTGGAATAGTCACTTACAAGGAC
WI-6761	32 C A G	GATCTAACAG CTGCAGATG	AAAAGCTGGG AAGGAAGAAG	CCTGAGAGGCAGATCTAACAGCTGCAGATGGCJAJCTCTTCTCCAGCTTTTGTGAACAAAC AATTCTCTAAGGCATCAGAAAGCACTGAGTGCAAAATGGGTGTCAGGTACAAGGCTC
WI-6844	225 T C ---		---	TAAATCTGCCAACTAGCATACGTCCTCTTGCCATCTTGCATCATTAAACAAAGGGTATTTCTCCTTG GTATTTCAAATGATGCATTATACAATAACGAAAGTTAGAAGTTAAATGCAACCTGATTAATATG TAACTGGTAATTTGTTTTAAAGCATAATAATTTGGTCCCTTCTTCATAAAATGGAAATTTAAA TATTTCTCTGATAGTCTGAGGTTJCATCAATTATGATGAGTAGTGCAAAAGTGTG
WI-6824	112 A G ---		---	CGGTTTGTCTACACTTAATGGTTTTTTTTAAGGGATTTTTTCAGGCTTTGTGACGAACATCAA ACAAAAGGTACTGAGTACTCCACAGGGTACAGAGTGTGCCAAJAGJACCTTAGAAAAATTACAT GACACGGAGAAAAATGCCCTCTTGCTCTGAAGAGCTACAGCTAGGGATTGACAACCTCACAGT CTTAGGAACTGGGCAAGTAAGGCAAAATCTTCATCCCTAGAGCTATTGTG
WI-6889	139 T C AATC	GAAAAATGAG ATGCAGTTAA	TCACTTTGGG CTTTTAATTAT TCT	GTACAAAAAAGCTGAGAAGAGGCCAACATGGAAGTGTCAAGAAACATTTCTGATAGGTACGGACAA AAGAGCTCCTTCAATCAAAAGGAGTTACATATTAGTTCTACCATGCTAGAAAAATGAGATGCAGTTA AAATTCTJAJAGAATAATTAAGGCCACAAAGTGAACCTGTTCTGGGGCCCTATGTTGTAGATT CTCT
WI-6911	216 T C ---		---	TCCCCAGCTCATATTTATTTGGGCACAGAGTGGGCACCTCAATAATCTGATGAACCTTGATGAACGAA AAGAGGTCTCTTAAACAAGATATCATCTCCGAAGAGAGAGTCCCAACCATATAAAATGTATGAT CAAGTCCAGAAAACTTTGCCCTTCCCAAGGAATGTTTTCTAATTTGGTTTCAAAGCACACTGGTTCC CACTTTTACCACCTTTJCATGACATTGGACAATAGTACTACTCTTTCTAC
WI-9413	112 G C ---		---	GCCAGTCTCTAGTAAGTCTTAGGGACATGACCAGACCCAGAGCCCTGTTCTATATGAAGACAAAC AGGTGGCCATACTTGGGTGGAGGGATACCGCTGCTATTTCCAGATJGJAGATTTGGTGAAGGAG ACCATGACAGATGACAAACGGGAACAGTTCTCAAAAACAGAGGTATGA
WI-9557	74 C T ---		---	AAAAGCTTTAAAAAAGTGGTGTCTCTTTAGAAACACTTTCAGCAAGATCAAGTAGCCACGCT ACAGCCTJCTJGGTGCATCTTAACCCCTCTCTTT

WI-9617	37	G T	---			TGCTCTTTTATTACGTTTTCACAACACACGCCGTG[G/T]GGCACAGTCTACCAAAGTGCCCGCAG CGCCACGCTTGGCGGGAAGGTCTCTATTCTGCTCTATGGACTGATTGAATTTGGGATGGCCAG CTCCAGAAATGTTCCAGTGGGGGACTCTGTGGCAGAGAGGCTGAGCCCTTGCCACACTGGCAOCCA AAGAGTTGCACGATGCAGCTTGCAGTGGGTCCAAAGCCGGGTGCTGTG
WI-9657	121	T G	---			AATGCTGGAGAAAAACATCAACATTGAGTTGACATTTGTTTGTGAAGTATAGTACCATCCACTAT CATGAATTTTGTTCATTACAAATGATAGAAAAGCCAGATTCTCAAAATAAAGT[G/J]ATAATCTT TGTAATAATAAATGTTTATAAATGTTTATGAAGCTCATTACATTATCTTTTAAAAAAGTAAAAA TTTTAGAACATATGACGCTTTTCATAAATTAATGCTTTTGATATAGATTGAGG
WI-13119b	114	G C	GCTGGGA		AAAAATTAAC CAGGTGTGGTG T	CAGGCTCTGCTCTCTCCAGGCTAGAGTGAGTGACACAATCAAGACTCACAGTAGCCTCAACCT CCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATG[G/C]JACACCACACCTGGTTAA TTTTTTAAATTTTGTAAAGATAGGGTCTCACTATGTTGCCCGCTCJCAAAAAACAACCAACTAAC
WI-13119a	51	C G	---		---	CAGGCTCTGCTCTCTCCAGGCTAGAGTGAGTGACACAATCAAGACT[G/J]ACAGTAGCCTCA ACCTCCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGTGACACCACACCTGGTTA ATTTTTTAATTTTTGTAAAGATAGGGTCTCACTATGTTGCCCGCTCTCAAAAAACAACCAACTAA C
WI-13112	71	C T	AGCTTTT		TTAGAAATTTT GTGTATTATAT GGAAAAAG	ACAGGAATCTGAAAGTTACCAAGGCAATTTTCCCTTTTAGGATCATAAAGACTACAGACTTAAGCTT TTTT[C/J]CTTTTCCATATAATACACAAAATTTCTAAATATCCTTAAAAAAGAAAATATAAATAGT TTCAGTATGTTATGTAGAGTCACATACTATGGCAAAAATATTTTATTAATTGAGGGAATAGGCCAAT TT
WI-12988	36	C A	CTCAGTACAA		CAAAGTGACAA CTACTGATGCT GTTT	TGTTAACATTTTATTGGTACGTGCTCTCAGTACAA[G/J]AAACAGCATCAGTAGTGACACTTTGAT AAAAAGGAAATTTTAGCTTAGTAGTAAAGAAAGCCCAAGGTGAGAAATTAATGAATATGTACAT CTTTATGGAAACTGTTTGTGTGACCACTCTTTATCTTCCCTGTGGATGAGATGTATGCACACACAAGT AAA
WI-13020a	108	G A	CTTT		CTAATAGTGG AACCCTGAGA CTTT	TGCTATTTCATGACAGACACGCTGAGACAAAATATCTTATTTACAGATGGAATAGACCCAGACATTA TTCAGTACTTTAACCACTAATAGTGGAAACCCTGAGACTTT[G/J]ATCTGCAAGGGGTTTAAATAAT GCAAATATCACATATATTTCCATTTTAAACACCATAATTAAGTTTCCATTTTCTTAAATAGAAAATGA TAAAAATGTTTCCCCCAATAT
WI-12837	87	A G	AAAGTCCA		CCATATACAT ATATCAAGGT ATGCTGTTTTT	TGTATAAAAAATCCAACTGTTCCCAAGTACATATGCTCTATGATTTATGCATACATCCATATAC ATATATCAAGGTAAAGTCCA[G/J]TACAAAAAACAGCATTTCCCTATGGCCAGTGTCTACAGAAGT AAGACTGTGCAAACTTTATCGTATAGTCAATGAGATTGCACACTAAGGCAGGATGAGGCAGAAAGCA AGTTGTGTCOA

L42611b	50	G C	---				GTCTCAGGCCCTTCTCTGGCTGCAGAGCCGCTTCTCAGGTTGCTGTGTCGCTCTCTCTGGCCCTCTAG TCTTCCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTGCCCTCACCTTCTCTCTGTCTATACCT GCCCATCTGAGCACCCATTGCTCACCATCAGATCAACCTTTGATTTTACATCATATGTTATTCACCA CTGGAGCTTCACCTTTGTTAC
L42611	34	T C	---				GTCTCAGGCCCTTCTCTGGCTGCAGAGCCGCTTCTCAGGTTGCTGTGCTCTCTGGCCCTCTAG TCTTCCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTGCCCTCACCTTCTCTGTCTATACCT GCCCATCTGAGCACCCATTGCTCACCATCAGATCAACCTTTGATTTTACATCATATGTTATTCACCA CTGGAGCTTCACCTTTGTTAC
WI-1172b	179	C T A		TGAAGAAATG GCTGATACCA	ATGTGCATTTT TCACTGCAG		TGAACGTGTGGTTAAACTAGGCAATTGGTTAAAAATCAATTTAAAAACAGGCCCTAGAAACAGTG ACCAACCTCAAGCAATGATTATCCCTAGCACTCAGATTATGTTCTTGAATACCATTTTCTGCTTTC AAAAAGAAAGACATGAGGGCTTCTTGAAGAAATGGCTGATACCAAGCCCTGCAGTGAAAAATGCA CATGATGAGCCTGGAACATGTTGT
WI-1172a	17	C A	---		---		TGAACGTGTGGTTAAAC/AJTAGGCAATTGGTTAAAAATCAATTTAAAAACAGGCCCTAGAAACA GTGACCAACCTCAAGCAATGATTATCCCTAGCACTCAGATTATGTTCTTGAATACCATTTTCTGCT TTCAAAAGAAAGACATGAGGGCTTCTTGAAGAAATGGCTGATACCAAGCCCTGCAGTGAAAAATGCA CATGATGAGCCTGGAACATGTTGT
WI-1177	35	G C A		GCAGATTGGA AGTGTGAAAA	CACCTACATTT CTGAATATTTA GACTCTTT		AGAGGCAGATTGGAAAGTGTGAAAAAATGAAAGAA/GC/JAAGAAAAAAGAGTCTAAATATTCAG AAATGTAAGTGTGCTGCCCTCAACTGTTCTTTACCCACTTAATCTGCAATTTTGAAAACTAGATTGAAT TCCTTTGCAAAACCCCTTGCAATCATGGATACCCGAGTTAAACCGTTAATTAAGAGACATTAAACATGG CCTGGTG
WI-1231b	141	G A	---		---		TCCATGGTTGGTTGCTACTGACTTTGTTAGCCTTACTGCCCACTATGCATTGGAAACATCCCATATTC CAACTAAGCAGGAGTGTTCACAATAAACAAACATAGGCTCTTTATCTCCTTCTTTCAATTTTCTT TCAC/GAJTTATTCCTCACCCCTGAACGCCCTTCTTCTCGTAGTGACATTTTAAAAATCCACTTTAC ACATCGGACC
WI-1231a	126	T C A		GGCTCTTTATT CTCCTTCTTTTC	CGTTCAGGGTG AGGGAATAA		TCCATGGTTGGTTGCTACTGACTTTGTTAGCCTTACTGCCCACTATGCATTGGAAACATCCCATATTC CAACTAAGCAGGAGTGTTCACAATAAACAAACATAGGCTCTTTATCTCCTTCTTTCAIT/CJTAATTT CTTTCACGTTATTCCTCACCCCTGAACGCCCTTCTTCTCGTAGTGACATTTTAAAAATCCACTTTACA CATTCGGACC
WI-472	114	G C A C A G A A A A G		ACATACATAT CCATTATACA	GACCTTCTTT TCCAGCCC		GAAGGCAGGACTGTGTTTGGAGGACAAAAAGTAAAAATCTTTTATATCTTTATTTTAAATTTTATT TTTTTTCAGGCATATAGACATACATATCCATTATACAAACAGAAAAAG/GC/JGGGCTGAAAAAGAAAG GTCAAGTGAGATTTCAGATATTCCTTAATGCAAGGCTGACAAATTTGGGCTTGATT

WI-478	46 C T	GCATGCTGTG T TACTCTATTT	AAATGCCACAG GTGGCT	AAACCACTGCAACCTTCAAGCATGCTGTGTTACTCTATTTTGTTCCTAGCCACCTGTGGCATTTC CAAAATAGATAATCTCTGCCACCATACTGCTTTAAACACAAATAGAAATCTGGCAGCAAAATATAGC ATAAGCTTACTTCTAAATCAAAAGGCTACCATCAGTACCTTAGCACATTTAAAAAATAAAACCAAC ACTGCCCA
WI-533	29 T C	ATCACAGCAG AGTACCTTTCT	CCTTCCAACCT CTACACAATCT T	AGCCATCACAGCAGAGTACCTTTCTAACTTTC/ATAAGATTGTGTAGAGGTTGGAAGGAGGACAGGA CTGTTCTGTGGTATAATGACCCTGTGTCCAGTTAATCCA
WI-601b	112 T A	TCACTTATCTCTTTTGTGGTGAGAACACTTAAATCTAAGAAATGATCAATTTCAATAAAGATGG TAGTGAGCGAACAGAGAGGTTTCATTGACTCCTAACTGAGTACT/AAACAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
WI-601a	74 C T	TCACTTATCTCTTTTGTGGTGAGAACACTTAAATCTAAGAAATGATCAATTTCAATAAAGATGG TAGTGAGC/TTGAACAGAGAGGTTTCAATTGACTCCTAACTGAGTACTCAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
WI-863	107 A G	CTCCTTCACAA CCTCACCA	CTTCCCGGTAA GCCAAGT	AACAAAACAGACACCCCTGGCTCTTCTCACCAGTCCACATGGGTGCCAAACAATCCACATTCTCT ACATCTCCCCACTGGCTGCCTCTTCAACACCTCACCA/AGTCTGGCTTACCGGGAAGCATAAA GCCAAAGCATTTAGTCTTTTATTGCAACATGGTCTGGCTGCAATAC
WI-919	36 G A C	ACTGCTTGCTT GTTGATTTAAT	TTATTCTAATC CCACATGACAG C	ACTCACTGCTTGCTTGATTATCAACCTAGCC/G/AGCTGTCATGTGGGATTAGAATAAAATA AACACAAAATGAAAACACACAGATTGCTAACAAAGCAGATTCTTTTCAAGGCACACGTAAGAT AATAACTTCAA
WI-991	37 A T	TGCATTATTATGCACCAATAATAACTTCTGTACAT/AT/CTATTGTATTTCATTATCACAAAAT TATGAGTGAGGGATGATTGTATCCCTATTTACAGATGAGAACACTGAGACTTAGAAGAAGTATCT TTCCCAAAGTCACAAAGTTAGTGACAGAGCCGGATTCCGAATCCATCAACTTGAATCCAGAGAAAAT GTTCTGCATCACTGTACAACTGACTCCTTTTCTCCTTTGAAAACAAGGC
WI-1011	70 G C	CAGTATCTGA AGTTTTGTCT OCA	AGGAACACCTA CAAAATGACTT CT	CTTCTGACCTGTTGCAGTGGATAGTGTTTTGAAGGCTCTGCTCAGTATCTGAAGTTTTGTCTCC A/GC/JAGAAGTCAATTTGTAGGTGTTCTGGCGTTTTTGTCTACGTTTCCATTTCTCTAATACACTGC CGTCTTAAGGGAGGGCTTGCAGAGCATTTATCAGATGGCTGTTTGTCTGCAITCTGTGCACTGAAG
WI-5381	178 A T	TTCATGCAGAAAGGTCCATGAGTTACAGAAATCTCAAGGAAGAAAGGCCCTAGAGATGACACCCAGAA ATGAGAGTGGCTTGCTCATGAAAATTGGACAGCATGTCCAAAGCAGAGGGAACAGCATGGAGAAGA AAAATCATACTCTATCCACGTGCAGAAACTGGCAATAGTTTGTG/AT/TTTACTAAAACACAAAATGT TTAATCTGGGGTCCACAAACAGGATATGTTGGCAATGGTATTCTTGTGATG
WI-5791b	76 G A	CTATGTATTCATCTAGCAAAAGCAAGACTATTTGGATAAGTTTCAAAAGATGAGAACAGGTCTTA GAACCTCAG/G/ATCGAAAGGAAGTTCACTAGTCCATAGACCCCTATCTCACTGACCCCAAGGTA AAAAAATAAAATAAAGTAAGAAGACTTACATCAGATTGTGCATTTCTTATTTGCCACCCTGTTGT TAGGAA

WI-5791a	44	C G ---				CTATGTATCCATCTAGCAAAAGCAAGACTATTTGGATAAGTTTC/GJACAAAGATGAGAACAGGTC CTAGAACCTCAGGATCGAAAGGAAGTTTCATCTAGTCCATAGACCCCTATCTCACTGACCCAAAAGGTA AAAAATAAAATAAAGTAAAGAACTTACATCAGATTGTGCAATTTCTTATTTTGCACCCCTGTTTGT TAGGAA
WI-5406c	120	C T ---				CACTCTGCTGTGTCCATGGGTGCCACAGACTCTTCCAGAAAGAGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAAC/CJATATGAGCCCCAC ACTTCTCATTTCCCTTAGAATTTCTTGGACTCTGTGAAGAGGAAAGGAAGAAAAAGAGAGGCAAA GG
WI-5406b	118	C A A	CCAGGATGTC AAGGTGAGAA	AATGAGAAGT GTGGGCTCAT		CACTCTGCTGTGTCCATGGGTGCCACAGACTCTTCCAGAAAGAGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAAC/CJATATGAGCCCCAC ACTTCTCATTTCCCTTAGAATTTCTTGGACTCTGTGAAGAGGAAAGGAAGAAAAAGAGAGGCAAA GG
WI-5406a	42	A G ---				CACTCTGCTGTGTCCATGGGTGCCACAGACTCTTCCAGAAAG/GJGCCACTTCCACAGATGCAACAG GCCCTTTTGAAGGAGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAACCCCTATGAGCCCCAC ACTTCTCATTTCCCTTAGAATTTCTTGGACTCTGTGAAGAGGAAAGGAAGAAAAAGAGAGGCAAA GG
WI-5798	48	G C TG	TTTATCTCCC TTGTTTCTTT	ACTGTTAGAAA ACCAGTATTT TCAAT		CCATTCCTCTCTCCCTCTCCCTTTATCTCCCTGTTTCTTTTG/CJATTGAAAAATACTGGTT TTCTAACAGTGTGCTGGTATGGATACTATGTTATAACATGCATAGTTCTATATGGGTATCA
WI-5415	54	T A TTT	TCTTCATGAAT TCATCTTTTCAG	GGACTAATTCA TGATCCGATCT		CCTGCTAATAATAATTTAAGCACGATTTGTCTTCATGAATTCATCTTTCAGTTT/JATAGATCGGAT CATGAATTAGTCCAGGCTTTAGTTGTAATCGAAATTGGA
WI-5437	41	C T G	TCCAGAGAA AAATCCCAAGA	AGTTTCTAAAC ACAAAATATG GTTTAAG		TGTTTTAACCCAGCAGACCTCCACAGAGAAAAATCCAAGAG/CJCTTAAACCATATTTTGTGTTTA GAAACTCCTGTGCGCAACCACTCTTGATGTGAGTGAC
WI-5481b	131	A G CTGCAGTCG	TGTCATTTATG	TTACTTCCAGG CTCCAAGTATT		AAGCCAAATTCACATTAGTTGATGAATTTGAAATTTTACAGTATCTAATGCATGGGCATCTGTTTCAAC TCTCTGTTTTCAAGAGGAGTAGTATATGCTGAAAAATCTATTTTGTCATTTATGCTGCAGTCG/A/GJA ATACTGGAGCCTGGAAGTAAAGACTTGGCTATTTTCACAATTA
WI-5481a	29	G A AATTT	CCAATTTTAC ATTAGTTGATG	CCCATGCATTA GATACTGTAAA ATT		AAGCCAAATTCACATTAGTTGATGAATTTGAAATTTTACAGTATCTAATGCATGGGCATCTGTTTTC AACTCTCTGTTTTCAAGAGGAGTAGTATATGCTGAAAAATCTATTTTGTCATTTATGCTGCAGTCGAA ATACTGGAGCCTGGAAGTAAAGACTTGGCTATTTTCACAATTA
WI-5492	38	T C ---				TCATGAGTCTTTCTTCAAGAGTCTGTTGTTAAAGTCCCAAT/CJCAAGAAAGGATCCCATGGCCTAAT GAAAGTGTACCTCCACCTTAGGATATTTTGCAGACCAA

WI-5826	134	T C ---				TATTTTTTTTTCTCAATCCTGGAGCACACCATGCTCTTTCTATTCTATTCATGCTTCACATTTATTTTTT TTTCACCTAGTTAAATGCTTTTTCCCTTGATCTAGCAATGGCCAGTTTATACATATTTCTTTAGT[C] TTTCAAAATTAATGCCACCATAGAAATAATTTCTAACCAACAGCCAAACAGCCTCACTCTTCCTT CCTGGTGCATTTACTCTTTACAC
WI-5546	40	C T A	CCCAATACITTT TTCAGGTGAA			CCTTATAACCCCAATACITTTTCAGGTGAAAAAGGGGAAA[C]/TACCCTATGTTTGCTAAAATACAGG AGTATAACAGCATGACATGTTAAGGGAATACAAATGCTTGAGTGTAATCTGATGTGGGAAATAT TAGAAAATTAAGCGAGAGAGGCA
WI-5552	97	C T	GGCACCAGCCT TTTTAGAGT			TGTTTGTTCTGCACCTCCCAACAAGTGGTCAATGAGCCTCAAGGGTTTTGATTGAGCGGGTATGGGT GGGGCTATCGGCACACGCTTTTTTAGAGT[C]/TCTGGGCAATTTGTGCACCTAGTGTGACA
WI-5836b	161	C T ---				TAAAGTGATTTAAACACTCTGTGCTCAATTTTCTCACCTATAAAATAAGATAATAGTATCTAAAA AAAAAGAGAGAGAAATTAAGTGGATAGACATGAATACTCTGATGATACTGTTGTATCCCTGAA TCCTGCAATATACACATGATTCAATGAT[C]/TCCATTTTGAAAAATTAAGCTTTTTGAAATGTTTTTCCA ATG
WI-5573	58	C T	GTTCATAAGG AGGTGGGA		TGAACAGTTGG AGAGTAATGTG TC	TCGGGTATTAGGATGCGTTCAACCTCGATGATGGCGTTCATAAGGAGGTGGGA[C]/TGACAC ATTACTCTCCAACGTTCATCAGAACACTTCAACAGCG
WI-5850b	134	G A ---				CAGGACCTTGGAGCCTTGTGCTTTGTCTCTCCACCTCACTCTTCTCTGCTGCCCCCATGGTGGAGC CTCTCAGGCTTCCCTCTATGCA[C]/TGGCTCTATCTCTATATGGGGCAATATCCAATGTCCCATTCG TTTTGCCATTTCCCTGTATATCAACAGAGAGAGAGGGTGG
WI-5850a	92	C T ---				CAGGACCTTGGAGCCTTGTGCTTTGTCTCTCCACCTCACTCTTCTCTGCTGCCCATGGGTGGAGC CTCTCAGGCTTCCCTCTATGCA[C]/TGGCTCTATCTCTATATGGGGCAATATCCAATGTCCCATTCG TTTTGCCATTTCCCTGTATATCAACAGAGAGAGAGGGTGG
WI-5612b	125	A T TTC	CTATTAATGA GCATCGTGTCA		TTCTCTTGAGA AACCTAAAC ACTG	TGCCTGATTGACACATAGTTATCTGACAGTAAATCATTTAACAATCACAATAATCTTATTTCTGCTG TCACACTAATTTGCAAGCATTCAATTGATTGACTAATTAATGAGCATCGTGTCTATC[A]/TCAAGTGTT TTAGGTTTCTCAAGAGAATTATGCTGTTCTTCTCTGTAACCTCAAGTA
WI-5612a	44	T A ---				TGCCTGATTGACACATAGTTATCTGACAGTAAATCATTTAACAATCACAATAATCTTATTTCTGCTG CTGTACACTAATTTGCAAGCATTCATTTGATTGACTAATTAATGAGCATCGTGTCTATCACAAGTGTT TTAGGTTTCTCAAGAGAATTATGCTGTTCTTCTCTGTAACCTCAAGTA
WI-5636	26	A C	GCCAAATTTAT CCGCAATAA		CATCGAGGACT TTGGGA	TGAGAGCCAAATTTATCCGCAATAAA[C]/TCCCAAGTCTCGATGGAGGCAATTCAGAAATCGGG GCAGGGGAGGAGAGGTGAGACAGATGTGAAGAAC

WI-5865c	103	C G	---			TTAGAAACCTCCATTTATTCTGCCATGGTACATCTTTTAAAGATCTTTTTTTCATTATGCATTC ACTGACTCACTCACTTGTCTCTATCAAAAATTAAAC/G/AAATATTATTTTATTTACAGAGGAA CTCAGAAAGCCAGAAAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAAGGTCACAGTCCCTTCA GAGAAGACAGACAACATAAATTTCCAGG
WI-5865b	99	T A	---			TTAGAAACCTCCATTTATTCTGCCATGGTACATCTTTTAAAGATCTTTTTTTCATTATGCATTC ACTGACTCACTCACTTGTCTCTATCAAAAATTAAACAAATATTATTTTATTTACAGAGGAA CTCAGAAAGCCAGAAAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAAGGTCACAGTCCCTTCA GAGAAGACAGACAACATAAATTTCCAGG
WI-5865	165	T A	---			TTAGAAACCTCCATTTATTCTGCCATGGTACATCTTTTAAAGATCTTTTTTTCATTATGCATTC ACTGACTCACTCACTTGTCTCTATCAAAAATTAAACAAATATTATTTTATTTACAGAGGAACTC AGAAGCCAGAAAAAATGACCAAGACACAGTAAJCCAGTCTCCATCTTCAAAAGGTCACAGTCCCTTC AGAAGACAGACAACATAAATTTCCAGG
WI-5874	76	T G	ACAGAAAAA	ATAATATTAT	CATAGCATGG	CTCAGACATTCATTTTTCATTAGTTGTTAAATTTTGTGATTTTCATAGCATGGATAATATTATACAGAA AAAAAATTT/GTACATATCAAAATGACTGAAACTTACTAGGTAGCAATTTGTTTGCAATTTGCT CATGGAGCCGACGTTTCAGCCTCTCAGTTTTTCCATC/A/TTTTTTCATAATTTACTCTCTTTTCTGTC ACAATGTTCTGCTTCGTTTCAACTCTCATTTGCTGATTGGATGGTAGTCATAAAATATGGGTGATTC AGAAAAATAAGTAAATG
WI-5752	36	A T	TTTTTCCATC	CAGCCTCTCAG	GACAGAAAAAG	TTAGCAGAAACAACAAAAATGTCACAACACTGCAGTAAAGAAAGTGTTTTCCCGATAAAATC/G/C CATTAGGTATTAGATAAGCATCCCATAAACATTTGTGAAACGAAAGCGAGTTTTTCGATTTCACACA GTTGCTGTTTTAACCTCTCTAAATCCCGATAAATAGCCATTAGGTATTAGATAAGCGTCCACGAA CATTGTTGAAACGAAGCCACGTTTTCCGATTACACAGTTAGTTGCTGTT
WI-5760b	61	C G	---			TTAGCAGAAACAACAAAAATGTCACAACACTGCAGTAAAGAAAGTGTTTTCCCGATAAAATACCCAT TAGGTATTAGATAAGCATCCCATAAACATTTGTGAAACGAAAGCGAGTTTTTCGATTTCACAGATT GTCTGTTTTAACCTCTCTAAATCCCGATAAATAGCCATTAGGTATTAGATAAGCGTCCACGAA ACATTGTTGAAACGAAGCCACGTTTTCCGATTACACAGTTAGTTGCTGTT
WI-5760	187	G A	---			AATATCTGGCCTTTTCTTCTTAGGAGAGATTTCACCATGGGAATCTTG/A/GTJGCAAGTTAGAT CCACCCCTCACTATTGAGAAGCTAAAAGTGAAGACTACTCATTTCTCAGTCTTCCCTTGCTG
WI-5944	52	A G	GGAATCTTG	TTCTCACCATG	GGGTGGGATCT	GAGTTTAATGAATCCTGTTCCCTCTTAAAAACCTCTGTTCCCCCACTTCACATTTCAGCAGATATT CTTTCATGGGTATTTTGGCCCAAGTCATGAGGAGATGCATGTAATTTGATCATTTTCAAGAGTGTGAG TAATGCTTGGTA/C/TJTTGCTCTGTGCCGTATCTGCTCCAATCACCCATTCCACGTTTATTTCCTATTAT
WI-5967b	148	C T	---			GCTGAATGAACGGTTATATTACAG

WI-5967	165 C T ...				GAGTTTAATGAATCCTGTTCCCTCCTAAACCTCCTGTTCCCTCCCACTTCCACATTCACAGCATATT CTTTCATGGGTTATTTGCCAAGTCATGAGGAGATGCAATGTAATGTGATCATTTCAAGAGTGTGAG TAATGCTTGGTACTTGTCTGTGCGGTATC/TJTGCTCCAATCACCCATCCACATTTATTCCTATTAT GCTGAATGAACGGTTATATTACAG
WI-6093	53 G C ...				GGTAAGATCCAGAGCCACAGGTGAACCTGCCGGTATTGAAGTCTTTGGGCCA/GCJGTCTGTAATG ATCTGACTTCTCCAGAACCCCTCTTCTCTGGAAGTCCAACCTGTCACCTGAGCCCATTTGAGGGA GCATTTGAACCAAAACCCAGCGACACTGCTGACATTTGACTTTTCAGCAAAACCTTGATTGACGGTGAC ACACCATGCTTCGAGAAGGAATGAGG
WI-6141	80 T C AGGTACTT	CTTCTTAATTA AGCATCTACA			GACTCTGTCTCAAGAAAAAATAATGAATAATTAAGCACTTCTTAATTAAGCAT CTACAAGGTACTTAT/CJCACTGTTCTGGGGTTTCAATCCTCTTCACTTTTAGACTTCAGGAAAT CAGAAAAATGCATGAAACACAGGATTGTTACATGCAGAGAAATAGGGGAGATAAAATTTGTCCTTT CTC
WI-6450	45 T G TGTACA	CCAAAGACTT ATTCTATATCT			ATAGGACAGTTTTCTTCCAATGACTTATCTATATCTTGTACAT/GJAGAAGTACCACACATTTCA AACAAAGGCGAGGCTATGCCAGGGTGGGATTATTTACGGTCAATGTAATATGCATGTAAGACTA TTTTACTGGCCTCTTTATGCTATAAACAAAGGTATTGGTCTATTCAACAAACATGTGTCAATACAG
WI-6461	88 C T ...				CAGTTGTCATGTCCCTCTGGTACTAGATATAGTCTTTATAGAAATATGGTTTGAATAAAGCCACA AATTATCTATAAACACA/CJJAAGGAACGAGGCTCAAAAGTGAACAAAACGGCCTTAGTTTC TAAGTGAAGACTAAGACGATATAGGAATAATAATCCGTGACCTCTTA
WI-7466c	141 G A TTGTCCCTGG	TTTTCACAGTC			GAACTATCCTTTAGTGGTGCCACATTTCTATTCTTGTGATTTTGTGCACACAGGACTTTCTGGGCT ATGAAATAGTCT/CJATTCACTGAAGTATGTAATCAATAAAGACATGCAAAAACCTTTTCACAGTCTT CCTGG/GJAATATCTCACAAAATAATTAATAAATGGCATGCGACTTTCTGATTTAGCCTGACAGG ATTGTTCCCTTT
WI-7466b	80 T C GTC	GACTTCTGGG CTATGAAATA			GAACTATCCTTTAGTGGTGCCACATTTCTATTCTGATTTTGTGCACACAGGACTTTCTGGGCT ATGAAATAGTCT/CJATTCACTGAAGTATGTAATCAATAAAGACATGCAAAAACCTTTTCACAGTCTT TGCTCTGGGAATATCTCACAAAATAATTAATAAATGGCATGCGACTTTCTGATTTAGCCTGACAGGA TTGTTCCCTTT
WI-9814	104 C A ...				TGCTTTTAAAAATAACAATGACCACCCTGACACCATAGTCTGTCTCCATTTGCCACGTCTTCCTC AGTAGAATAAGACAGGGACTTTGCTGGTGTCTATCTC/AJTTCTCCTTCAGAAGAGCACTTTGGCCCT CATAGGCAATCCATAGATATTTGTTGAATGAATGTGCTTTTGCATATTGATTCTCTACATTTGATACA TTCTCAGGAGGGACATTTGGCCTAT
WI-9720b	55 A G ...				CCTCTAACAGAAACTTGACTTCTCAACTCAAAATACCTTCTCTAATAATTTT/GJAGTAACCA AAATATCTTCAAAATAAATAATCTTTTAAATTAGAAGAACCAAGTGTAGAGGTAGTACATTCA CCAOC

WI-9720a	47 A G ---			CCTCTAACAAGAAACTTGACTTCCTCAACTCAAAATACCCCTCTCT[AG]ATAATTTAAGTAACCA AAATATTCCTTCAAATAATTAATCTTTAATTAGAAGAAGCAACAGTGTTAGAGGTAGTACATTCA CCACC
WI-9825	123 A T ---			CACGCTTAAGGCAGGATGTGGCTTATGAGATACCTTTGCATTGCTGCTGCACACCTTGAATCTGCC TGCTGGCTCCCTTACTTTACCTCTCTGTCATGTGCAGATGAAGGCTCAGGGTCT[AG]GAGGATTAG TAAGATCTCTTTCTAAAGACAGGAGAGATTATTTACAAGAAGAACTCACCAGGGTTTAGTTTGCAAT TAAGAATTGCCAGCTTTTGCTGTCATCATCTTGAACATTAAATCCACATG
WI-9748	74 C G ---			CCACTTCAGTAAATCAATTTGTAGCACTTATTTCTAAAGATTCTAATTTTATATGTTTACCCCTTT GTCATT[CG]TCAGACCAAGTACATGTTTTCACACAGCCATCTTTCTTCTCGGAATCTTTCAGAAT TACAGTTATGATGTCCTTTATATCCCCA
WI-9943	91 T C ---			TGAGGCTATGATGCAGATTTGTAGTGACTAATACTATTAAAGCAATTTCAATGTTGTGGCACTGTT CGTTGTGTTTATATCCATCTCT[CG]ATTTTAAATTTCTACTGAGCAGAAAAAATGTATACATT AACCTTGTCTCCCTATTGTACCTTTTAAATATGCAATTCACACCTTCTCTTTTGTCATTTAGGGA
WI-9891	39 T C ---			AGGGCCCTTCAGATCCGTCAAGCTCAACACTGCCTCT[CG]AGTGAGCCTGTGAACCCACCCCAAGAC GGCTGGTCATCAGTGTCATCTCTCTCTTTCCGGACAACACTATCTTTAAAGAAAAAAGAGTGT CTTTGATGATCCATTTTATCCCCAAATAATCTGTTTAAATAATCTCTTATAGGCCAAATCCAAT GTCTGAAATATCTGCCAAGCATGTCTTCTACACAAAAGGGATTGCAAA
WI-9897b	84 C T ---			CTCAGAAATTATCAGATCTTCCCCAAATGTCATGATTCTGTTCTCAACATCTATTTTCTCAAAAC ATTTATCTAGCCTGTA[CG]AAGTCATCCAGTGAGGCTGTTTATTCATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAAATTAGCATCTTATTTTGTACCCACATTA
WI-9897a	83 A T ---			CTCAGAAATTATCAGATCTTCCCCAAATGTCATGATTCTGTTCTCAACATCTATTTTCTCAAAAC ATTTATCTAGCCTGTA[CG]AAGTCATCCAGTGAGGCTGTTTATTCATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAAATTAGCATCTTATTTTGTACCCACATTA
WI-9935b	115 C A ---			AGATAACCCCTGGAAAACTAGAAGAAATTAATAACGTGTTGCACACCTCACCAGAACTGGAAGGAGT CTGACTGTGTTCTTATGGGTGCTTGAGCTGGCAGGGGAGTTCAGACA[CG]AAGCCAAAGAAAAGCC TGATATTAAGAGGCACCTTGCAATA
WI-9935a	42 C T ---			AGATAACCCCTGGAAAACTAGAAGAAATTAATAACGTGTTGCA[CG]TACCTCACCAGAACTGGAAGG AGTCTGACTGTGTTCTTATGGGTGCTTGAGCTGGCAGGGGAGTTCAGACACAGCCAAAGAAAAGCC TGATATTAAGAGGCACCTTGCAATA
WI-9983	146 C T ---			CCTGTTAGGTGCCAGAGTCCATGCTCTTGGCCACAATGTAGGCTGCCTCCCCATTTCTTTGCTTGA TTCCCCAAACCCCAAGGTTCTACCCCAATCTGATCAAAATGCTGACTAGGTCATGGCTGGTCAGGGTAA AGCATTATGA[CG]TAGACACAAAAGACAAAGAGGTAAGTTGCTGTCTCAAGAGAGAGAGACATAA AAACAAATGGATCTGGAACTAAGTAAGGCTTCGAGGAGGAGGTGAGCAAGG

WI-10019	139	A T	TGATGTAATGC TATGTAGCAA ATCT	TGATTACTGT GCTTAGGGGA	ATATCAGTGGGTGAGTATACAGCAATCTATTTGTTTATTTATGTGTGCTATAAATCAATGTTCTTA ACATTCAAAATAGATCTTTTGGCTTCTGCTCAGATGCTTTCAATGATGTAATGCTATGTAGCAAAAT CTAATTTCCCTAAGCACAGTAATCAAGGCCCTTCTACCCCA
WI-10020b	122	T A TTT	GCGAGAAAAG AAATCATGAC TTT	GACTGTTAATT TATTTAATCAT TAGTCTGG	TTTACTTCATTGTGCATCTTGACTCGTATTAAATAAATTATGTTAACTGGCTGAAAAGAAATTTAGGC ATGCATAGAGAAATAGCAGTGTTTTATTGGCGAGAAAAGAAATCATGACTTTT[T/AAAAAATACC AGACTAATGATTAAATAAATTAAACAGTCTAGGGTTCGGGAAGTGGCCTAAAGCACGTTAGTGGCCT CCTTAGA
WI-10020a	39	T C A TAAAT	TGTCATCTTGA CTCGTATTAA ATAAAT	AAATTCCTTTTC AGAGCCAGTTA AC	TTTACTTCATTGTGCATCTTGACTCGTATTAAATAAATTATGTTAACTGGCTGAAAAGAAATTTA GGCATGCATAGAGAAATAGCAGTGTTTTATTGGCGAGAAAAGAAATCATGACTTTTAAAAAATACC AGACTAATGATTAAATAAATTAAACAGTCTAGGGTTCGGGAAGTGGCCTAAAGCACGTTAGTGGCCT CCTTAGA
WI-10064b	170	C T TTTACATG	CCTTTAGATAT ATTGTGATTGT TTTACATG	ACCTTTCTGAA GCCAGATTTC	TCTGAGTCTTTCTGAGACACTTGCCATGGTCAAGGTAGCAGGATCAGGGAAGGCATTATAATAAT ATAATTTGCAGAGCATCTCTCTCTATGCACAGATAATTGGTGGACACTCTGTTTAAATCCAGTATCC CTACTCCTTTAGATATATTGTGATTGTTTACATG[C/TTGAAATCTGGCTTCAGAAAGGTTAGGTGTT T
WI-10064a	54	C A CAGGGAAGG	GTAGCAGGAT CAGGGAAGG	GAGATGCTCTG CAAATTATATT TATTAT	TCTGAGTCTTTCTGAGACACTTGCCATGGTCAAGGTAGCAGGATCAGGGAAGG[C/A]ATTATAATA AATAATAATTGCAGAGCATCTCTCTCTATGCACAGATAATTGGTGGACACTCTGTTTAAATCCAGTA TCCCTACTCCTTTAGATATATTGTGATTGTTTACATGCGAAATCTGGCTTCAGAAAGGTTAGGTGTT T
WI-10289	29	T C CAAACTCTT	TCTCTGTGTCOC CAAACTCTT	ATTCTTGTGT ATTGAATGGAA TTAA	CCAGGGATTCTCCTGTGCCCAAACTCTTAT[C/TTTAAATTCATTCAATACAACAAGAAATTTATAGAA TATGCACCACATGCCACAAAGACACCCCTTATATTAGT
WI-1319	40	A T ATTCTTT	TGGCACTTAG AACATAGTTT ATTCTTT	GCCACACACOC CTATGGT	AAGAAAATCCTTGTGGCACTTAGAACATAGTTTATTCCTTTTATJACCATAGGGGTGTGGCTTATCT TTTACCTGGCATGGCTTTTAGGTCTCTGTTTATAATTTGGTATCTTTTGGCACAAGAGTCTGTTCTGAC AGTCTTATGATCTCTATTTTAACATTAACACTGGTCAGATGTGTTTAAACTTGTGAACCTGCAGC
WI-10316	104	T C CTCTT	CTGTGATTTT CTACCTCTATT CTCTT	GCTTTGGAATG TATCCAAAAGT TT	AGCAACGTTGACAACTTAGTGAGGTGTAATCAGAAAGCATCTATATTATTCACCAGTCACCAACCTG GACTATAGTCTGTTGATTTTCTACCTCTATTCTCTTAT[C/TTAAAGCTTTTGGATACATTCCAAAGCAT CATGGTCACTTCCAGTTATGAAAGGATGTTTAAAGCCAGCC
WI-2572	61	C T ---		...	AGTGAGTTGTGCACAATTTGGAGACATTCGTGACCCCCAACCTTAAACACACTCTCTCCACAC[C/TTAC AAAGTTAACACTTCAGTTACCAAGGTGATGATTGAGCAGA

WI-10368	31 C T	TGAAGCAACC AGGTCTTGTT	CAAGATATTAT ATTTATCTCT AAGAGGGG	GAGGAAGTGCCTGAAGCAACCCAGGCTTGTTC/TCTACCCCTCTTAGAGAAATAAATAATATATCTT GAGATAGGGAGGAGCAGCCTGAGGACAGTCTGGGTTTGTTCACCCACCTGGAAGCAGAAATATOC TTCAAAGCTTTTCCAGTGAGTCATGTTGCTGCTAAACTATATGACCTGATGGATTGCCTTTCAGGG T
WI-10391	32 A G	CTGTCTCAGGT ATGACTCCCA	GGGAGTTAGGA GTCAAGAAGTT GA	CCTCCCGTCTCTGCTCAGGTATGACTCCCA/GTCAACCTCTTGACTCCTAACTCCCATCTCGGTG TCTGCTTCCAGGGGAGCATCTGACACAGCCTTTGCTTGTGTGACAAACAGAACATTGCAGAAG TGATGCTGCGTGACCTCCAGGATA
WI-10567c	146 A C	GTTACCCAGA GTCTTCTAATA	TGCGGCTTCCA GTAGCT	AGCGATGAAATTTATATGTTATGCCTGACTAGCGGGTGCTCAATAAATATTATCTTTTTCATATT TTCCAATTATTAACTAGAAATTTTACCACACAGAAATTTTAAACATTTTAAAGTTACCCAGAGCTTT CTAATAGCAA/A/CJAGCTACTGGAAGCGGCAAGAAATTTAACCCCT
WI-10567b	82 A C	GGGTGCTCAAT AAATATTATT	AAAATTCTGTT GGTGAATAATC TAG	AGCGATGAAATTTATATGTTATGCCTGACTAGCGGGTGCTCAATAAATATTATCTTTTTCATATT TTCCAATTATTAACTAGAAATTTTACCACACAGAAATTTTAAACATTTTAAAGTTACCCAGAG TCTCTAATAGCAAAAGCTACTGGAAGCGGCAAGAAATTTAACCCCT
WI-10567a	60 T C	CTTTT	CTTTT	AGCGATGAAATTTATATGTTATGCCTGACTAGCGGGTGCTCAATAAATATTATCTTTTTCATATT TTCCAATTATTAACTAGAAATTTTACCACACAGAAATTTTAAACATTTTAAAGTTACCCAGAG TCTCTAATAGCAAAAGCTACTGGAAGCGGCAAGAAATTTAACCCCT
WI-11153b	84 C G	TACTTTA	C	CGTTGGGAATATTCTATCTCACCTAAATTAIG/C/AGTGATTAATAATATACATTTTAAACAACTTC TTGCTTTAAGTACTTTA/C/GJGAAGACCTTGACTGTTGGATTTTGGATTTTTCCTTTTCTTTAATA AAACATGCATATTTAAGTTGTGACGAAGATGTACTTATAGTTAATTAATCTGATATCAGCATCCCTT TATGTATT
WI-11153a	33 C A	AATTATG	GTAT	CGTTGGGAATATTCTATCTCACCTAAATTAIG/C/AGTGATTAATAATATACATTTTAAACAACTTC AAATGCTTTAAGTACTTTACGAAGACCTTGACTGTTGGATTTTGGATTTTTCCTTTTCTTTAATA AAACATGCATATTTAAGTTGTGACGAAGATGTACTTATAGTTAATTAATCTGATATCAGCATCCCTT TATGTATT
WI-2616	125 T C	ACAAGAAATTG ATCC	CCATGGCTGTA GTCCAGT	GTTGTGAAACTCCAGTATCATTTCCCTCAACCCAGCTTAAATCACAATCAGCTTTTCTTCCCTGTA GAGCTCAAACTCAGTCTGAATGAATGCTGCACAAATGTAAACAGAAATGATCCTAT/C/ACTGGG ACTACAGCCATGGAGAAAAGCAATGTAGTCAGCAAAATGTTAACAG
WI-11163	58 C T	CAAGTGAATT ATGACCAAAA	TGCTCTTTTCA TTTGAGGTTTT T	TGACTCAAAAGGAAACACACACAAAAAGTTTACCAGTGAATTATGACCAAAATGAGA/C/TJAAAT TTGTTAAAAAAAACCTCAAAATGAAGAGACAAATATAGTTCAAGATTCAGGTTCAATATTGT ACCTACAAAATAGGGATAGTCAATGGTGTGGCAGACTTTTCTTTTCTTTTGT/GTCTCTTA GAATCCATTTTGTCTTTTGGCCAGCATTTCCCTCTCCCATATTTTAAAGGAGAGAAATCACCTTTTCT CTGTGGATGATCAGAGGTTCTGCTCTTCCCAATCCAGAGGAGGTACTATTACCCCATGGGTCAT AGAGAGGATTAAACAGGGTGTGCTGCAATGGGAATATTGAAAACC
WI-10656	59 T G	AGAGAGGATTAAACAGGGTGTGCTGCAATGGGAATATTGAAAACC

WI-11169b	154	T G T T T T	T T A C C A A G A G T T T T C A T T C	C T A C T T T A A A A A T C C T C A T T C A A A T A T A A	C A G C A T A G A G G C T G T T A G T G A C C T T G A G T T A G A T T T C T C T A T C G A G A A A G C A A T A A G T G A A A G T A A C T G A C T T G A A A A A A A A A A A T T A A G C C T A A A G T A G T G C T T T T A A C C A A G A G T T T T C A T T C T T T T T T T T A A A A A A G A G A G C A G A C A T T G T T T A T C A T G T G T T C T G A T A A T T T T T T A T A T T T G A A T G A G G A T T T T T A A G T T A G C A T
WI-11169a	95	A G T T G A A A A	A A T A A G T G A A A G T A A C T G A C	A A A C T C T T G G T T A A A A A G C A C T A C T T	C A G C A T A G A G G C T G T T A G T G A C C T T G A G T T A G A T T T C T C T A T C G A G A A A G C A A T A A G T G A A A G T A A C T G A C T T G A A A A A A A A A A A T T A A G C C T A G A G T A G T G C T T T T A A C C A A G A G T T T T C A T T C T T T T T T T T A A A A A A A G A G A G C A G A C A T T T A T C A T G T G T T C T G A T A A T T T T T T A T A T T T G A A T G A G G A T T T T A A G T T A G C A T
WI-10685	25	A G	C A A G T G C T T G G A C C T T G G A T A G G T C A G A C C G G C T G A A G G T T G G A C A G T T G T T G G T T A G G T T G G A G A C C A A A A T C A G T C A T C C T G T A A T A T A G A T C T T G T C C T T T G G G T T A C C A C T A G G G T C A C T A A A G A G A G A T G G G A G A C A G T C A A T C T T G T C T A A T A A T T C C A A A T A G C C A T G G G T T T G G A C A A A A T A C A A G G T A G T G T C T C T A C T T T A A T G G G C A T A
WI-10686	133	C T A A G G	T G C C C C T G T O C A A G G	C A A T C T C T A A A T T C A T G T G T A G A C A C A	A A T A A C C T G T G G C A C A T A A G G C A A T A C T A G C C C C A T A C A G A G T G T T T A T G T T A A T T A T G A A A A A A G T C A A G A G A A C A A G A T A T A G T T C T G C T A G A A T A C T T G A A A T C T G A T G C C C T G T C C A A G G C T T T G T G T C T A C A C A T G A A T T A G A G A T T G A A T G A A A T G G C A A A T T C A G A A A A G G G
WI-11175	77	T A A	A A A T G A T T C T T T C T G C T C A A A G	C T G T T C T C A C A T T C T T T T T G A A A A	G G T A G G A T G A T T C T A G A A T G C C A C T T A C A G C C C A T G A A A T A T A T T G C C T C C C A A A T G A T T C T T C T G C T C A A A G A G T A T T T T T A A G T T A T C T A C T A T T A T A T T C T G C T T T T T C A A A A A G A A T G T G A G A A C A G T A C A A A A T G T T C A G T A T A G C A A A T T A A A A T T A A A A A G T A A G A A A A A A G A A G C C A A T T T G G G C
WI-10694	144	A G T A T G A G T T T C	T G C A A A T G C T T T A T G A G T T T C	G G C A T T T T G T A A A G G A G G A A A	T A G A G A G G T C T T T C A G T T T C A G G T T G G A G G G T G T G A G G T G A G A T T C A C T T C T T A G A A G C A C T G G C T A T G T A C A G A A A G A T A A A C T C T G A G A A G A A C T C A G T T C T A A A G T G T T C A G T C T T T G C A A A T G C T T T A T G A G T T T C A G T T C C T C T T T A C A A A A T G C C A T C A A T T C C T C A A G G A A A A A A A A A A A A G C T T T C T T
WI-2716	23	T C C	T G A A T T C A T C C A G A A A A A C A G	T C T C T T T T C T C T C T T G T T G T C A T T C	G T G A A T T C A T C C A G A A A A C A G C T T C G A A T G A C A A C A A G A G A G A A A A G A G A A T A A A G G T T T T G T A T A C G A C A A G T G G C T C A A G C A A T T T T C T G T C C C A G T G C A T G G A G C A G T G
WI-10719	115	T C G C C A T T C T A G	T G A C T C T C A A G G C C A T T C T A G	G C A C T G C C A G C A G C C	C A G G C C C A A C T C T G T C A T T A A G T G T T T A G A A C A G A C A C C T C A G T C A C A C A A A G T T C T C T T G T A T G T G C C C A C C A T A A A C A G T A C T G G A G G A T G A C T C T C A A G G C C A T T C T A G T T C G G C T G C T G C C A G T G C T T T T C A G C C T G C T G C C C A T A A C T A A
WI-10721	40	A G C T T G C C A	T G G C T C T G C T A C T T G C C A	G A A A C T C C C A C A T A A A T A A A T C T C A	C A A C C A A T T C A G A T T A A T T T T G G C T C T G C T A C T T G C C A A G A T A A G A T T A T T A T G T G G A G T T T C T G A A G A T T C C C A T G G T A A T A G A T A T C C T C T C C C T G C T T A G G T T T T G A A G A A G T T G A A

WI-11204b	88 T C ...				GCACACGAAATTGATTAAATATTGGCTGACTTTGAGGAGGAGAACAGGGAGTTGAGGTAAGGTTGAGGTAAGGTTG AAAAGAAAAACCTTTACACTTTTCJATTTTAAAGTAACATAAAGGTATTATGTACATTTTAAGTGAT CAAAAAATTTTAATTGGGAAGAGATTTAGTGAATCAGAAAAATAAGTCTGAGGAAATATTATTCAGAAG GCAACATC
WI-11204a	80 T A AACTT	GTAAAAAGGG TGAAAAAGAA	GTATCATTAA AATGTACATAA TACCTTT		GCACACGAAATTGATTAAATATTGGCTGACTTTGAGGAGGAGAACAGGGAGTTGAGGTAAGGTTGAGGTAAGGTTG AAAAGAAAAACCTTTACACTTTTAAAGTAACATAAAGGTATTATGTACATTTTAAGTGAT CAAAAAATTTTAATTGGGAAGAGATTTAGTGAATCAGAAAAATAAGTCTGAGGAAATATTATTCAGAAG GCAACATC
WI-10732	80 C A ATGGTCACT	GCTGTGCTTC CTGTATGTACA	AAGAACAATG CATAACAGAA CTTTAA		ACATGTATTTCCTTTAGTGGTCAGCCTTCCTTACCCCAAGAATATCCCTGGTTTATGCTGTGCTTC ATTGGTTCACCTC/AJTAAAGTTCTGTATGCATTGTTCTTGAGTCCACATAGGTGTTAATCATTTCCA CACCACCTCTGTTTAAACGTG
WI-11206	127 A T ACTC	GGTTGTGTTTT CTGTATGTACA			TAGCTTTTCTTTGACGAGTGTATGAAAGAAATACCACCTCTGTCACATTTTGTAAAAGATAGCACAG AGAGAAGCATTACAGGGGCACAGCACAACATGAGGTGTGTTTCTGTATGTACAACTC/AJTCCAA CCATTAGGATTGTCACCTCATATATAGACAGAATTCAGTGGTGTGATTGAAATCCACACATGGA ATAAGTCTA
WI-11215	68 C T ...				GAAAAAAAAGTTTTAATTGGATTGCTTAGTTGCTTAAATTTGACCTACTTTCAGATTATTTTAGT [C/J]ATTTTTTCTATAATATTTCTTGAAGTGATGGATTTCTATAAATTAAGGAACAGATATTT ACACAGAGAGACAGGATTGCTTGAATTAGTATAACATTCITTTATCCAAAGCCCCATTCACCATGT TTT
WI-11219b	89 G A AGAGAAA	GAGAGAATAT TCCAAAAAGT	GGTCTCTAAT TTTTCTACACT TTCT		ATGAAAAATGCATTAGAAAGAAATGGAGGATATAAATTGAGAGAATATTCACAAAAAGTAGAGAAAA GAGACAAAAGAGATGAAAAATAGGA[G/A]AGAAAGTGTAGAAAAATTAGAGGACCATTCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAAAAGAGGCAAGAAAAATGAAGGGGAGAAAAATCCAC AAACATCTC
WI-11219a	18 G A ...				ATGAAAAATGCATTAGAA[G/A]AATTGGAGGATAAAATTGAGAGAATATTCACAAAAAGTAGAGAA AAAGAGACAAAAGAGATGAAAAATAGGAGAGAAAGTGTAGAAAAATTAGAGGACCATTCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAAAAGAGGCAAGAAAAATGAAGGGGAGAAAAATCCAC AAACATCTC
WI-11222b	136 G A GGCTGG	CATACCACTGC AGTTGTGA	CCTGGTAGCCA AGTTGTGA		AGCCACAGTGGAAATCATTTACACTACCGAAATCAGCAAAATGCTAAAAATTTGGGCTTTGGATTTTGT TTTTGTTTTTCCATAGACCCCGTTGAACCTATTGTTAAACATTTACCAGCATACCACTGCGGCTG G/GA/JTCACAACTGGCTACCGAGGAGAACCTGACACAGACTTCGTAATTGCTTTTCACAGGCTACTGG AAAGCC

WI-1122a	25 C T A	GCCACAGTGG AATCATTTAC	TTTTAGCATTT GCTGATTTGG	AGCCACAGTGAATCATTACACTA[C/T]CGAAATCAGCAAAATGCTAAAAATTTGGGCTTTGGATTTT TGTTTTGTTTTTCCATAGACCCCGTTGAACATTTGTTAAACATTTACCAGCATACCACACTGGCGG CTGGGTCACAACTTGGCTACCAGGAGAACCTGACACAGACTTCGTAAATGCTTTTCACAGGCTACTGGA AAGCC
WI-10775	39 C T CACTC	TTATGCCATA TTAATTCATTA	CTAGATGTATT TGCTAAGAAA ATATGATG	TTGCAAGTTTGTATTATGCCATATTAAATTCATTACACTC[C/T]ACATCATATTTTCTTAGCAATACA TCTAGACACCTGGCACTCAGTAAGGATATTCTGGCACGATAATCATATTGTTATCATAGACATTTGCA GGAACCCACCATATGGATGGATAAATGTGTGTTTAAATGAAGGCAAGCAATTA TTGCATGCATTTATACGAAAGGAATTAATAATATCTTCTTATAGTTGAATTTTAAGTAAAAATAAA GTTATACATATAATACAAAAAGTTGTAAGTATAGTAACAAATGAATTAGAAAATTTGTCAGTGGTTGC TAGTACAGGAATCAAAATTTGGACTATGAACA[A/C]GACATAGTTGCTAAGGATATTCACAAAAATAT TTCATGA
WI-11226	165 A C ---	---	---	CAGTGGCTGGCTACTGACAAAACGTAACATCGTGGCAGGTGGCAAGGGAGGAACATTTACAG[A/G]G TCCATCTCTGATGTACACAGCGGCCAGGAAGGTTGATCTGGAG TGGACACACTGCTCTAGACC[C/T]TCCAGGTCCTCAAGGTGGGTAGAGGCCCTACTGCCCT GCCCTGGGACGACAGAGGCATCAGGGCCTTAGTCTCTCTGGGACAGTGAAGGGCCACCAACC ACAGAAAAATGCGCTAGGCTTTGTAGCAAGAGAGGAAAGCATCTTCATGGCAGGAAT[C/T]CATTT CTGTGTTCTTAGGGTTTGTGGCTGGCCATCAGTTCAACTCAGCCCTGTCCCTGATCCAGCAACATT TCCGTAACCTACCCCTCTAGAAGTCATGCAAGAGAAATGATGA
WI-10778	62 A G G	GCAAGGGAGG AACATTTACA	CTGGTGACATC AGAGATGGAC	GGACCAACACAGAAATTAATTGGGATTCAGGGTTTCTTAAACTATTTCTGCAGAACATTAGTAAAGT TTAAATAAGGATCAGGCTACCAGGAATACAGTTAGGGAACATGTGGATGAATATTTCTTTAGTAGAG GACTTCTAAAAGGTATATAATTTGGATACATTAGGCTCATTTATGAATCTCAAAAGGAGCATGTAGT AGGGCATATCTAA
WI-10789	21 C T GCTCTAGACC	GGGACACACT GCTCTAGACC	TTGAGGGACCC TGGGA	TATGCCCTTCCCAACGAGCCATCCACGCTGCTCTTAGCACAAAAAATAGATACATCATCTGAATG GGCACATTAATCTGCAGGCTCTCC[G/C]TTTCTAAGTCACCTGCAGTTAGGTCTGCAGACACTGTGTA TACCATATAAATCTGATTTCTGAGCAGGAGGGGAGGATGAGAGAAGGGCTGCTCCGTGAAATAC TAGTTCCG
WI-10810	58 C T GCAGGAAT	CATCTTCATGG GCAGGAAT	CAAACCCCTAAG AAACACAGAA ATG	GATTGAGTATTATCAAAATGCCCAAAGACCATTAAACAGATTTAATAGTTAAAGCCAAAACTATA AAGAAATTAAGTGTCAAAAGTGTGTTAAT[C/T]CTTAATACCAATTTTATAGGGCCACCATTAACTT CTGAAGAAAGGTCAGCATATGCAACTAAATTTCTAAAGTCCAGT
WI-10828	23 T C ---	---	---	GGATGATGTTCTGTGGTCCCTTAT[C]AAAGCCCTCTTGATCCCAATGTGTAATATTTTATTCT TGGTATTTCTCGCTTACCCATAGTCACCTGTCAAGTGTCCACCT
WI-10832	91 G C AGGCTCTCC	CATTAATCTGC AGGCTCTCC	CCTAACTGCAG GTGACTTAGAA A	---
WI-10834	96 C T GTGTTAAT	AGAATTAAC GTTCAAAAGT GTGTTAAT	TGGCCCTATAA AATTGGTATTA AG	---
WI-2287	24 T C ---	---	---	---

WI-2296	81 A G	TGTTACTTTGA TTCCTTGCTCT	GCAAAATCACAC AGCTAACTGG	TGGAGGGTTAGAAATGCAGGTGGCATCCTAGAAAAGGTCAGGCTTTAGATAAGTTGTTACTTTGA TTCCTTGCTCTGAC/GGCCAGTTAGCTGTGTGATTGCAGAAAGTTACATTTGTTGTTG
WI-2300	77 G T	GGCACAGAAG CCAGTCATAC	GGTTGGGTCAA TTTTAAAGCA	TTTCATCATGCTGCTTCCCTGGAAATTTCCCTTATTAGCGGGGCGAGGTGGTAGGCACAGAAGC CAGTCATAC/GTJGCTTTAAATTTGACCCCAACCAATTACTAAGAATAGCATTCA
WI-2371	55 G T	GTCCTGTTCTT CCAGCTTCT	CAAAGATTGAC AGCCACCAC	CAATGATCCCAACATTTCCAGGGAAGGCTGGCTTGCTTCTCCAGCTCTT[G/T]GTGGTGGCT GTCAATCTTGACATTCCTTGCTTGACGTGTATAATCCAACTCCCTTGCCCTCCAGCTTTACATGATGT TCTCTCGGTGCTGCTG
WI-2395	122 A C	GAACATAATT GTAGAAAAAT	TCACCTTTCTA TTTATTCTGAA TTCA	GGGGGCACAAATTTAGCTACAGTGCATATTAAAGATAACATAGAAATATCATATAACTGGTTTAC TGAAATCTGAAAACTTAGGATGAGTGAACATATTGTAGAAAAATTTACTATCCAA/ACJCTGAATTC AGAAATAATAGAAAGGTGAATCATCTTATATCATTTAAAGAGCTAAATTTAGTAACAATCTTTA CATTTACACAAACCCA
WI-2437c	192 G A	---	---	CACCAGCCACCACCCCTACAACCTCCTGTGGGGAGTCTGGCTTTGATTATTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCCAATCACAACCTTTCTAAATAATAGACACCAAAAAATTTCCCAATGCTCTAA ATAGATGGACTCAACCCCTTCTCTTCTGCAAGAGGCAATCGACGAACATCACAGTG[G/A]GCTGTG GTGCCAAGGACGCATTATG
WI-2437b	179 G A	---	---	CACCAGCCACCACCCCTACAACCTCCTGTGGGGAGTCTGGCTTTGATTATTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCCAATCACAACCTTTCTAAATAATAGACACCAAAAAATTTCCCAATGCTCTAA ATAGATGGACTCAACCCCTTCTCTTCTGCAAGAGGCAATCGAC[G/A]AACATCACAGTGGGCTGTG GTGCCAAGGACGCATTATG
WI-2437a	128 G A	---	---	CACCAGCCACCACCCCTACAACCTCCTGTGGGGAGTCTGGCTTTGATTATTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCCAATCACAACCTTTCTAAATAATAGACACCAAAAAATTTCCCAAT[G/A]CTC TAAATAGATGGACTCAACCCCTTCTCTTCTGCAAGAGGCAATCGACGAACATCACAGTGGGCTGTG GTGCCAAGGACGCATTATG
WI-2440	71 G A	GCAACCTACT GACAAATTTAA TTTTAGTT	AACAACCTCTGC TATTGGTCTCA C	CAGTAGGAAACGGGTCTCTCCTTAGACCCCTCCAGAAAAATATGCAACCTACTGACAAATTTAATTTTA GTTG[G/A]GTGAGACCAATAGCAGAGTTGTTACCTGCAGAACT
WI-1356	123 T C	TGTTTAGGAA ATAATGACAA GAAAAA	TGGTTACAAC GTACCAACAT G	CTGTAACCTACACACATCCTCCTGTAACTCTAGGTGTTACTTGTAAATACAAACACAAATGTAAATGCT ACATAAATAATTGTCATACTATATTGTTAGGAAATAATGACAAAGAAAAAGCC[T/C]GTACAT GTTTGGTACAGTTGTAACCAAGCCATTTTCCCAATATTTCAATCCACAGTTGGTTTAAATCCACAG AAACCACGAATG
WI-2886	46 C A	CAGAGTCTGG GGGAGAAGA	TTGCCATGCTT TATCTCGTT	ACAGTTAAGAAAAAGGCTGCAGCCGTTGCAGAGTCTGGGGGAGAGA[G/A]AACGAGATAAAGCATG GCAAAGACCACGCTGAAAGTATCCAGGGTGTGTATGTGCACATAGGAAGATCATTACCTCAGCA TAGGAGGAGGGCTAGGCAAGGAAAGGTGTGACAGAAGAACAGAGGCGTT

WI-2906b	77	T A ---			---	CCTGAACACCTGGAGCACTCCCTCCCTTGGACACCTTCATTCTTGCTGGAACTTGCCTGGAATGCTCTTTCCCTCTG/A/GAGCTTTGCTTGGCTTACTTTTCTTTTCTTTTCTTTAGGTTTCAGCTTCAAAGTGACCTCTTAGAGTTGGTTTGTGACCAACAAA
WI-2906a	50	A C TCTTGCTGG	GACACCTTCAT		AGAGCATCCAGGCAAAAGT	CCTGAACACCTGGAGCACTCCCTCCCTTGGACACCTTCATCTTGCTGG/A/CJACTTTGCCTGGAATGCTCTTCCCTCTGAGCTTTGCTTGGCTTACTTTTCTTTTCTTTAGGTTTCAGCTTCAAAGTGACCTCTTAGAGTTGGTTTGTGACCAACAAA
WI-1736	175	C T ---			---	TACTCCTCATCTCCTCATGTCCTTAGACGTACTCAGATTCCATGCCCTGAAACATTTATTTCCCTAAATAGATTCCACCCAGCACTATTTACAGAGAAACAGCATGGAGCAGTTTGGAGCTGGCTCTTAGAGAACTTAAAGGACAGTGGTTTCCATCTGCTTCCA/C/TAAGAGATCTAGGGTGTCTTTGGAACCACTTGG
WI-1851	136	G A GTGTTAAGTA	GCATTGAATT	AACTATAGAT	TTAAACTGAAGTTG	AATACCCACGTCCTAACCCATCACACTGATCATCAATCAGGTTTAAACATATTAAATCTGGGGAGGACACAAACATTTAGACCATAGCATTTGAATTAACATATAGATGTGTTAAGTAATTATTAACATGGTACA/G/AJACAACCTTCAGTTTAAACATTGCTAGTGATCCATGTGGATACCATGTACCTTCTTACATCATGTGA
WI-3000	62	G A AGAGACCCC	CCCAAAACAC		CTCA	CTGATGTTGGGAAGCACTGCTTACATCTCTAAATGTAGCAACCCAAACACAGAGACCCCTG/AJTGAGCTTAGTCAATCCTATAGTGGCAGTACCTGAATCAGTCCCTGGTGCATAGTAGACACT
WI-1754	177	G A TAGTC	AAATTCAACC	CTTAAAGAGA	AAAGTCGAATTGCTCTGG	ATGGATCTGCTCAATTATAGTCCAGATAAACAGCCCTTCTCCCGCCCAACCCCGGATTATTTTACTTAAGGGTTTAGCAAAATTCACCTGACAAAGAGTTAGGTTTCAACATTGACCCCTCATAAAGTGATTTTCTCTTTCTGTTTGTGTTTCTCCCTTCTTAAAGAGATAGTC/G/AJCCAGAGGCAATTCGACTTTCTGTAGCCACAAGATT
WI-3167	37	T A TAGATTC	ACAGATCTAT		TGTGATAGTTT	ACAACACAGCAAAATTC AACCCACAGATCTATTAGATTC/T/AJACCCCATCTCAAAACTATCACATCAAGAGCAAGGAGACATATTACTGGTGAGGAAGCCAAATTCAA
WI-3208	140	G A AGATAAAGA	GTGGAGTGGGC		TGAGATGGGTG	CAAGCACACATTCAGGCAGTGGGCAGGTAGGGAAGGTGGGCACTTGGCAGCAGAGAGGAGGAAGAAAGTTCAGACCGTTGGGTAGGATAAGTGGATCCAAACCCCTTTGTAGGGCAGGTGGTGGAGTGGGCAGATAAAGA/G/AJCCAAAGCCCTAGTTTGGTGGACACTGTGGGGATTCAAG
WI-1775	47	C T TTTTCTCTG	CCTGCATGGTC		AGTTGAGATTT	ACTCCACCAACAGTTTGTGAGCCAAACCCCTGCATGGTCTTTTCTGTC/G/TTTACATCATTTGTCATAAATCTCAACTGACACATCAGTGTCTCTGCCACCCCA
WI-3402	55	G A ACAT	AGCATATTCA	TTGATTTCCTT	GAGGACTTAAAGAGGCATTTTG	CTGCCCTTTACATCCAAAGCCAGTTACTCGAGCATATTCATTGATTTCCCTTACAT/G/AJCAAATGCTCTTTTAAGTCCCTCAACTTTAAAGCGGAAGTTGAGACATGCACAAATAGATTTCCTTAGGA

WI-3416	33 C T GTC	CCAGTTGTA GCATTCAGAA	ACGAGCACAA CTACCTCTAAG AG	TC TGGTTCCTCCAAGTTGTAGCATTCAGAAGTC/C/CTCTTAGAGGTAGTTGCTCGTCGTTAAAA TATGTTTTCAAGATAGTATCTCCCTGTTGTACCTCTCTCCAAACAAGTGTACCAACAGCATTGTTAAG GAAATGTGCAATGCTTGCTACCTCTGACGACACAATAATTAATCCCATTCGCTAAAAAGACCAGG
WI-3453	70 C T ATCAGAGAA	TTCTAGGCC TATCAGAGAA	TCAATTTCCC CATGACTTC	TCCTATTCTACAACAACAGAAATTTAACAAATTTGAAATCAGCTACTCTCTTAGGCCATCAGAG AAT/C/T/GAAGTCATGGGGAAAATGATGCCATGTGAATTTGGAGAAACAGACAGGCATATATGGAG AATTACAGTTTACCAGGGACACAATCCCACTCCAGAGCCATCATCTGTAAAGAC
WI-3474b	109 G A ---	AGTCAGTTCC CTAATTTTAGC	---	CATGCTAGGTAGATCTGATCATGAAGTTTGAACAAACTTAATCATCAAGTGTGTCAACTGGTTTGA GTCAGTTTCCCTAATTTTAGCACAGTATTTAATGAGGTGGT/GA/TGGGAGAAAAATGATGGTTGCG TAGTTGAGTTTCTGTCCACC
WI-3474a	90 A G AC	CCTGGTTTCT GGATGTCT	CAACCATCAAT TTTCTCCGA	CATGCTAGGTAGATCTGATCATGAAGTTTGAACAAACTTAATCATCAAGTGTGTCAACTGGTTTGA GTCAGTTTCCCTAATTTTAGCACAGTATTTAATGAGGTGGTGGGAGAAAAATGATGGTTGCG TAGTTGAGTTTCTGTCCACC
WI-3502	79 C T GGATGTCT	GGTTCTAACC TGGATATAAA	GGGTGAOCCGTG TCCTCA	TTTGACCCCATACATGAGAAATAAACCAATAAGAAATGGTGGAAAAATAAACGGGAGAGACCTGGG TTTCTGGATGTCT/C/T/GAGGACAGGGTCACCCAC
WI-3600b	146 G C CATCT	GGTTCTAACC TGGATATAAA	CCAGTGCAGCC TTCCAT	TCACGGCAAGTTCTGCAGCAGTGTCTTGTACTCCTGCTGTTCCAGAGTCTGATTATCCATGCCCTG ATAGTTCTGT/G/GAGCCACCTAACTCGTTTCTGCTTAAGTTATCCAGAGGTGGTTCTAACCTGGATA TAAACATCT/G/C/ATGGAAGGCTGCAGTGGATGAGGTACAAA
WI-3600a	78 T G ATAGTTCTG	CCATGCCOCTG ATAGTTCTG	GGAAACGAGTT TAGGTGGCTC	TCACGGCAAGTTCTGCAGCAGTGTCTTGTACTCCTGCTGTTCCAGAGTCTGATTATCCATGCCCTG ATAGTTCTGT/G/GAGCCACCTAACTCGTTTCTGCTTAAGTTATCCAGAGGTGGTTCTAACCTGG ATATAACATCTGATGGAAGGCTGCAGTGGATGAGGTACAAA
WI-3678	125 G T ---	---	---	TAAATCATGCTTATTTTACAAGGTAATCCACTCACAATAGGCAATTGATGATCTCTTTCTGTAA GAAAAGCTCTCATGCTCTTCTGAACCTTCTACTTACTGTGCTGTATGATGCACCTG/T/CCTTTTGG ATAGATGGTTGATAGGAGATGGGTTGTTAAAGACACAATTTACCTTGTGTGTTTCAGGGCAGAAATAG ACTCTCTCTGTGTAATCACTGAATGAGTTCCTGAAAGCCTTTATGCTTAC
WI-3687	67 A C ---	---	---	AAAGCGATGTTGAGATACCACATTCATGAAAAAGTAAAAACACACACAAAAATATGACATAAAA T/A/C/JAAAAAATCTATAGTTTATGAAAAATGACTTCCAAAAATTCAGAGAAAAAGTCACTTAAACAGG ATTCTCAATTCAATCCAGAAATCTCTGCTGCTTCTTAACTTTGACTGACACAG
WI-3735	72 T C AAAAC	CCTCAGTTATG TATCAAAATGA	GGCTCACCAT CATGTTTTT	TCTAAATGTGAACCAAGAATCCTGACACGACCTAACTGCCAGTCTCAGTTATGATCAAAATGA AAAAC/T/CJACACCGGTTCAATGAAAAAACAAATGATGGTGAGCCATGTCCCCCTTATTTAATGAAAA GATCTTGGCAATTAATCTC

WI-1819	51	C T	...			GAAAAAGCAGGAAGCCAGGAGGACAAAACCTTTGAAAAAGTCTTTAGCAAC[C/T]TTCGTGGATCCG AATTTAGTGTGATTTGGCAGGAATGCGGGTAACATGTTCCAGTGTTTTAACTTGCACAGAAATTGC CAGATTAGCGATTGTTGACTTGTCCAAATTAATGAATGTGGAAGAAAAAAGGGTGGTAACCTGTT AAGCCTGCTGCAATGTTTAGACACGAGGGTGGGGTGGGAGGTGGAATACC
WI-3746	116	G A	...			GGCCTATTACATGACACTGGGCCAAGATCTTGCTTCCCTTTCTTCAATAGATAGACTAACTAGAAA ACTGCCCTGGCCAGGAAGATGGTTGCTTCATCATCTCTGTCTCTGC[G/A]GCCCCAGGATAAAGCA GGCA
WI-3867	49	T C C A A		ACAGTCATTT AGTCTTCTCTGA	TAAGATAACC ATACTAGGTAC ATCCG	AGCAATGAGTTAACTCCTTACATGAACAGTCATTTAGTCTTCTGACAA[T/C]CGGATGTACCTAGT ATGGTTATCTTATCTGACAGACAAAGACACTGTGACACAGAGATTGTTACTTGAACAAAAGACACAGT CATTAAAGTGAGAGAGCCAGCATCTTAATCAGGCTCAGTGATCTGCCAAACCAACCCCTTCTGCTATAG CATC
WI-3898	25	A C G		TGACCAATGTC TTTAGAAGCA	TCGTCGGTGTG CTCTCC	CAATGACCAATGTCTTTAGAAAGCAG[A/C]GGAGAGGACACCGACGAGACACACAGGAAGGAGTGAG GTGAAGATGAAGCAGTGTGACGACGCAAGGTGAGGAGCAAGGGTTGCTGGCCACT
WI-3901	114	A G	...			GGACCAATGTCCTCAGAAAGTACATCAAGCCCTGGACGGTGTCTCTAACACTGTGACCTCAGGCA AGTCATGTCTGCTTCTGAAACCTCGGCTTCTCACCTGACAAAGTGG[A/G]TATCATGTGCTACACTGC AGTGTATAATGCTGCAT
WI-3914	99	C T G C		TGATTCTTCTC AAGACTCACA	TCTAGAAGCAA TGAAGGATGG	CTGAGGAGATTGATGCTACTTTACTGAGGAACTTTTATTACCTCCCTGAGTTTGTGCCCTTGCAA GACATTGCTGATTCTCTCAAGACTCAGACG[C/T]ACCATCCTTCACTTCTGCTTAGACCTATAACTAG ACTCAAGTCCCAGCAGGCCCCTTAAAGGTAAGGTACAAAGTGTGACCCCATGGGAGGTATGTTACGCTA CAAAAGAG
WI-4019	33	G A A		CCAAGAGCGT CCTATGAATC	AACAGCAATA ACAGGAACAA ATG	CCACTCCCAGGCCAAGAGCGTCTCTATGAATCAT[G/A]CATTGTCTCTGTTATTGCTGTTCAACAGAT GGCAACTCTTGCAAGGGAGGGGTACAAAGTGAATTTTATAGATGCTGCAGGAGACGAAGGGTC
WI-4091	84	A T G T C A T G C A T G		TTGAGGTCTTA GTCATTGCATG	TGAGTTCCTAT TAAGTGACAAT ATTGTT	TAATTCACATTGCTCTGTTTGTGCAATTTATTGCTTCTTATGTAAACACAATCACCAACATTGAGG TCTTAGTCATTGCAATG[A/T]GTATAACAATATTGTCACCTTAATAGGAACTCAAGCATAGTTAIGTGT ACATTTATTGCTAACAGCAG
WI-4160	117	A G C A C A G A A		CCTATAATTTA GCAACAATAT	TGCAGGTAGAA TTTTCTAATAT AGCC	TCCTCTCTCTGTAAAGGAAGTCTGATTAGATGCCCTTTGAGGTTAGGTGGCTTCTAAGATGGTAATT ATCTGTCCCAAGTTTGTTCCTATAATTTAGCAACAATATCAACAGAA[A/G]GGCTATATTAGAAA ATTCTACCTGCATCCCTCCCTGGATCTGAACGTTCTTCATGATAC
WI-4168	32	A G A A C A		GGTGAGAGTC AAATTGATAC	ATTGCCAAACA GATTTTCAGA	CGTTGCTGGTGAGAGTCAAAATTGATACAAACA[A/G]TCTGAAAATCTGTTTGGCAATCTATTAAAGG CAAAATATACCAGCAGTGGTCTAGCAATTTCACTGCTGGGCATTACCTAACATAAATGAT

WI-4177	68	T C	TACCTA	TGAATAAGCA CGTATTAATTT	AAGGCAGCAA ATCATGATG	ATGCCCTAACCCAAATAG ATCCCATTAACCCAAATAG ATGCCCTGCGATATACCTTCCAAATGACTAGTATGAATAAGCAGCGTATTAAATTTACCTATTATATTT AT/CJCATCATGATTTGCTGCGCTCTTCCAAATTTACTACAAATTTGATTGTCACATGAGGCCACATG
WI-4199	51	A C	AAAA	CTCCCCAAGTT AGTCAATATA	ATATGTGTG AAAGGAACAC AGGAACAGAC	GCCATGAGCAGAGGGTGAAACCACCTCCCCAAGTTAGTCAATATAAAAAA[A/C]CACACATATTG TTATACCTAATCAACATATAATGTTATAGATTAAACAGTCCACAGCAAAACA TTCTGCTGCTACTGGTCTGCCCTG[C/T]GGTCTGTTCTCTGTTCTCTTCAATGTTCAACTGCTTGAT CTGTGCCCACTAAGGTATCAGGTTTATATGGCACAGGATGAGGGGCTTTGTAGACCAGAGTTTCTT GGAAATTGCAACATTTGGGCAT
WI-5163	24	C T	CTGCCGT	CTGCTACTGGT	C	TAAGTGCATTAACTGTACAAGTCCACAAATACCTCTCCACCAAGTGCTAAAGCAGTTTAAATAACA GGTTCAATATGAGTCTTGTGAAACAGGGGTGGGAAGGATCCTGTAAAGG[A/G]TAAATATTGTTT CCATAATATTGAAGATGTG
WI-4250b	117	A G	---	TCAATATGAG TC TTGTGAAAC	---	TAAGTGCATTAACTGTACAAGTCCACAAATACCTCTCCACCAAGTGCTAAAGCAGTTTAAATAACA GGTTCAATATGAGTCTTGTGAAACAGG[G/T]GTGGGAAGGATCCTGTAAAGGATAAATATTGTTT CCATAATATTGAAGATGTG
WI-4250a	94	G T	AGG	---	TCCTTCCCAC	TAATGTCTGCGGAGATAATAGGAAGGTCCCATCCCTCTGATACCTTGGTGGTCCCCCATCACCT [G/C]CCTTACACAACCTTGAAGTAGGCCCATCCAAACACTGGTCAGAGAGTAACTGTCGAC
WI-4255	68	G C	CACCT	TGCTCCCCCAT	G	ACAGCCTCTTCAAATGGCACAATCAAAGCACCAGTAAAGCAGAGGCAAAATCTGG[C/T]CTCAC CATTTGGAAAAGTCTTCTGAAGATAAGGGAGTGAATGACTGCTAGAAGAGAAATGATTGGCCTT
WI-4256	57	C T	---	---	---	AGTTCACCTGCCTAGATGAGTAGACCATGTGCTTTGTTAAATGTACATGGCAGGACCGGAAATGG GATG[C/T]TACTATAGATAATCTTTTTAAATGACTCTCTTGGTCTCTTCAAGATATCACCAGCCAC CCAGGACACTGCCATACT
WI-4325b	71	C T	---	---	---	AGTTCACCTGCCTAGATGAGTAGACCATGTGCTTTGTTAAATGTACATGGCAGGAC[C/T]GGAAA TGGGATGCTACTATAGATAATCTTTTTAAATGACTCTCTTGGTCTCTTCAAGATATCACCAGCCAC CCAGGACACTGCCATATCT
WI-4325a	58	C T	---	---	---	TGGGCAGAAAGTCGGGTATGGCAAGTCAGGGTGGGTTAACTTGGATGCCACTCTGCTGCTGCACTTCT CTAGACTCTTGACCCCTGCAGGAGGATCCCTGGCCTCTGAGTTTATCATCTCCCACTCCAGCCAG GGCCCTGTATCTGTTTCAGGCC[C/A/G]GAATCGTCACGGCTCACAACTGTGGAGGTAGGAATGACGA G
WI-4347	158	A G	---	---	---	CCAGTCTAGGCTGCAAGGACTTCAATTCTGGGGCAGTCTGGTGTGCTAGGGTCAGAGGACGG ACCTGAGGGGACACACAAACAGTGGGACACCAGGGGTACTTGTATCACCT[C/C]CTCCCGCAACCCCA AGCAGCACAGCTTGCAGCTCCAGGAAAGACTCCTTACTTCCACTTGAGAAAAGGAGAGGGAAGAGA AAAGAGGACTTTGACACACAACCTTGG
WI-1936	117	T C	---	---	---	

WI-5204	54	CT	---	---	TAGATTTTGATTGATGACAAATAGGGAAGCCCTTTGTTAAATTGGGTTTTGAAGAA[C/T]GAAGAAAA TGGAAAGGGAAGAAATTGACAGAAACCAAGAGAGTGTGAGGGGAGCAAAATCCAGTTTGACTGGA ATATAGAGTGATGTCAGGGTTG
WI-5215	70	AG	CTCAAAA	TTGGC	TTTCCCTTATTTATTTAGGAAGCAAAATGTTTCATACAGGACCCTTAATATTTAACAGACTCAAAAA TAT[AG]GCGGAAACTATCTTTACAAAATTATCTCCATAGCAAGTAGACATTTTAGCACATTTTCCT GTAGTCAAGGTTTTAAAGGCCAAATGAAGTTGACTAAAGACAAAT
WI-4448	112	TG	ATATAA	GTCTTT	CCCTGAAATGTGCTTTGCTTCTCCTCCAACCTCTAGGGAACCTTTTCCATGTCAGGTGAAGGTTTTGA AGAGTACTTTAATTAACTTGTATCAAGAGATGGGTATATAA[T/G]AAAGAACCATGTAAAGATTT CTTTAATTAGTGAATTTTCATCAGGGCTCTTCCACTGCTATCAGTAAA
WI-4456	49	CT	TATAGTCC	GCATGAACCTTG	ACACATTTCAATTTGCTTTAAGTTGAATTTATTCAGAAAAATTATAGTTCC[C/T]CAAGTTTCATGCATAA CAGGAAACACCAGGTGGGCAATTGATTGAATTGT
WI-4461	49	AG	CTTCC	ACCAATTTCA	CTGAAACTAATGAGGTGCTAAATCACTGTTATTTTAAATATCCTTCC[AG/G]TGAAATTTGGTGAAA GGTCAAGAAATGAAATTTCCACTTTTAGATTTCTGGAAATTTTATTTGGATGATAATGCAATGGGC CTACTGGATTTTACTTTGCTCAAGCCAGACACACGAAAGTATATAAAGAAAAACAGTTAGTAATCTT TCACCTTT[G/A]TATTTCTCTTCTACCTCAGGGAATC
WI-4465b	75	GA	---	---	CTACTGGATTTTACITTTGCTCAAGCCAGACAAACGAAAGT[AG/G]TATAAGAAAAACAGTTAGTAAT CTTTCACCTTTGTATTTCTTCTTCTACCTCAGGGAATC
WI-4465a	41	AG	ACACGAAAGT	TCITTT	GGGTTAGGACCTCGAGATCTTTTTCAGAAAGCACAATTCAAACCATAATGGCAGTGCACAGGTAACCA GTGGTGAGATGCTCTGAGTTCAAGGCTGCTGACATGGCTGAATATATGTTGAAGAAATAAA GGAGTGAATAAATGAATGCCATAATC[T/C]CTGTGTTTTTGTCGCCACCTCTCACACCTTTCCCTGG CACA
WI-1949b	160	TC	TAATC	GACAAAAA	GGGTTAGGACCTCGAGATCTTTTTCAGAAAGCACAATTCAAACCATAATGGCAGTGCACAGGTAACCA GTGGTGAGATGCTCTGAGTT[G/C]AAGGCTGCTGACATGGCTGAATATATGTTGAAGAAAT AAAGGAGTGAATAAATGAATGCCATAATCTCTGTGTTTTTGTCGCCACCTCTCACACCTTTCCCTGG CACA
WI-1949a	86	TG	ATGCTCTGAGT	GCCTTG	GGGTTAGGACCTCGAGATCTTTTTCAGAAAGCACAATTCAAACCATAATGGCAGTGCACAGGTAACCA GTGGTGAGATGCTCTGAGTT[G/C]AAGGCTGCTGACATGGCTGAATATATGTTGAAGAAAT AAAGGAGTGAATAAATGAATGCCATAATCTCTGTGTTTTTGTCGCCACCTCTCACACCTTTCCCTGG CACA
WI-4529	64	TC	AAGATG	AAAA	TGAGAGAGTTTTGGATTATTCATCTCTGCAACACTCCAAAGTAAGTCTATCATTTCTGAAGATG[T/C] GAGTCTCTTTTATATCCTATGATTATTTTTCAGGAAGTGTATTTTAGAATATAAACTCCTGGGT CCCATCCAGGCTAGGGTCAATGGCATCCATGGGTGCTGGACAAGATGGGCCCTAGGATCATTTT

WI-4540	110 A G	GCACATGTGG CATCC	GACAATGCAGC CATGCA	AGCTTTCCTTTCTTAAAAATGGTGCCATAGTACTGGCTTCTGTGTGCATCAGGAAGCAAGCCTAT TGCTCGGTAAACAGTACTTTGCAATAAGCACCATGTGGCATCCGAGTGATGGCTGCATTGTCCAGTC AAATGAGACAACTTCTCTAT
WI-4582	226 T C	---	---	AGCAAGCATCTGGCAAGCCTCGGTGACCAGAACATTAAATTCACCAAAACACCCACCTGCTCCAAATGT CCATGTTAATGCAATTATAGAGACTCCAGTAGCATTCAAGGCCAGTTTAACTTATTCCTGTACACA AATAACTTTATGGGAGACAGCATTGTAATCAAAATCAATAAATGACTCGGTTTGGCTGTACAAGCAT AAACAGAACGCTTGCAAAATATGGTTTCCTCTTGTAGAAACCATTTGAT
WI-1965	105 G C	AG	GAATGGATGGG TCATCTCTCT	CAAAGTTAGTTTAACTTGGGGGCAACACAAAAGTTATGAGTACTCAATAACCTATGTTCAAGGG TAACCAACACCTTTTGGCATTGAGGAAGTGTAAAGG/CJAGAGAGATGACCCATCCATTCCTGG GCTTCTTATATGACACCATACTATTCACACAGATGTGGAGTCATTTATTTGGTTGGTGATGACAGT CATGG
WI-5248b	99 C T	TTG	AGAAAAAGAG AAGAAAGGAA AAA	TGTTAAAAACCATACAGTTTGTGCTGCTACGTTGTAGAGCAACCCAGAAAAATTAACACGCCTAC CATTTTCACTGTTTCTATTGACCGTACTTG/CJTTCTTTGCTTTTTTTTCCCTTCCTCTTTTCTG CCCTCTTTAACTAT
WI-5248a	38 G C	CTACGTTGT	TTTTAATTTT TGGGTTGCT	TGTTAAAAACCATACAGTTTGTGCTGCTACGTTGTAG/CJAGCAACCCAGAAAAATTAACACGCC TACCAATTTTCACTGTTTCTATTGACCGTACTTGTCTTTTCTTTTCCCTCTCTCTTTTCTG CCCTCTTTAACTAT
WI-4596	69 T A	TGAAGCAGAA AGCACTGTGA	CAGGAGATGGG CCTAATAATG	CATTGGTGGTGCCAACTTCGGTGACATTACTCTGTGACTTTGCTCTGAAGCAGAAAGCACTGTGA C/T/AJATTATTAGGCCCATCTCCTGCTGAGCCCTGCCTACAGCAATTTGTACATATGGCATTGGG ACATATCTCTGAGCCCATCACTATTTGACAAGATTCTCTTTTAAACA
WI-5252	119 A C	---	---	GAAATAGGGCAAAATTAAGACTTCAATAATTAAGAAAGTCTTGGGAAAGGATTGTGATGATCATTG AATCTGTTTAAATACAGAAATTAATACCTGAATACCTGTGTGAATCATTTGCTTTT/CJTTACCATGTACA TATTATATGAATTAACAATGTAAAAATAGTATGACTAAGAAATATTGGGCCCT
WI-4606	61 A G	CT	TTAGGTGCTTA AGTTGTCTACT TGG	TGCAAAAAGGAAATGATAACCCAGGACTGTTGTTCAAGCAATGCTAGAAAATTTATGCCCTA/A/G/C CAAGTAGACAACTTAAGCACCTAAGGCAGAAATGAAGTTTCTCTTGTCAATTAAGTCTCTATTC ATTACCATTTATCGGGTAAATTAACACTGGAAGTAATGCCAGGCTAATGTTAGATTATGATAAT TACAGTCTTTGCTATGCT
WI-5257	77 C A	GAGGCATGAA GCAAGAGG	CCAGGGGCAGA TGAAAG	CAATGAGAAGTTACCAGATCGGGGCAAAATTAAGCATATGAAATACCAAGTTGGCAGAGGCATG AAGCAAGAGG/CJ/CTTTCATCTGCCCTCGGTGGGTTTTCAGTAACCTGCAACATGCTTTGCTCC CGGATGAAAAGATACCTTCTATGACTCAGCAATTCACCTCTAGGTATGCACCCCTAAACATGGGTG GCAAAAT
WI-4649	50 C T	TTCCGAATG	TGACTAGGTG TACTTACAGA AATCATC	TCACTGTTTAGAAAATTTCTTCTCTCAGTGAGACCATTCTTCCGAATG/CJTGATGATTTCTTGTA AGTACACCTAGTACATCTATGAGCACACAATTAACAAGTACTTGTACCTGAATTTGTATTTTAA AAAATCTCCCAATATTG

WI-4650	148	A G	GCACAAAGAA AGTATAAGTT GTCCTT	CTGAAGTGTTA AACTGGATTG G	AACTGTGTGGTATGATTGTTGTGTTATTTCTGGAGAGTCAGTTACTCTCAGTAGATCATAAAGGG GACTTGGGAACCAAGATATCTCAAGACATTTAATCCTAGAGACACAAAGAAAGTATAAGTTGTCTC TTATATTGCTTTT[A/G]CCAAATCCAGTTAACACITTCAGTAACGTT
WI-4677	82	T C	TCCAAAAGTG ATTAGGTGAA AAA	TTTCAACAGTG TCATTATTCAA CTT	AAATCAGATTTTGAACATACGTGACATTTTGGAAAAATTTGCCAAAAGTATTAGGTGAAAAAAT GAGTTGAATAAATGTT[C/A]AGTTGAATAATGACACTGTTGAAAATGATGAATCTGCTTTCAATTCA CATGGAAGGAGACTAGAACACAGCAGGTTTATAGGGGAATACTCAT
WI-4698	135	C G	---	---	ATGATGCTATCATGAGGAATCTGTAGAAAAATTTTCACCTGGCAATTTGACCTGGAATTTCAAAATAAGTTTGCC TCACCTGGGAAACTGCTTATCTTGATGTCAGTGACATTTCTTTTGTGACGGAAGAAAACTTCAA C[G]TTCGAGAAGGCTTAGATTATATCGCTGAAGCCCATCTG
WI-4722	88	G A	TGCACTATGG AACACCAC G	AATATGGAATC TGCAATTCAGTT G	CTTCCCATTTGCCAGTTAGATGACTGCCTCTCCACCAGCCTAGAAAAAGATGGGAGATTTATTTTC TGCATATGGAACACCACAC[G/A]CAACTGAATGCAGATTCATATTGAATACTGGGAAATCAGTGA AAG
WI-2020	145	C A	---	---	GCCACAGTAAAGAGGAAAAATGGAGCCATGTAAACAGAGGAGAGCTTTCTGAAGATCAGTGTATTGTCA TAAAGGTCAGTAAATCACTTTGATGGTTGAGATTTTCAAAAAACGTGAAATTTATTGAGTAACCATGGG TCAACTATGAT[C/A]CCAAAAACAGCAGTGTGTCTAAAAAATATGATAGTTTCTTCTCCTGTGCCACC GCAATGAAAAAGGAGTT
WI-2028	176	T C	TGTTTACGTT CCTGCTCATC GAA	GGTTGGAACT CAAAATACCTA GAA	GACTACAGGCACAGACAGGCAATGTGTGGCTTGCACAGGTTTGGTTTGTGTTTAAAGTTAGATT TGAATCCTTTAAAGAAAGAAAGTGGCTCTTCAAGTTTACTACAGACCTCATCTCCTGGTTCTCTTG CACCCAGTCCACTTCACCTGTTTACGTTCCCTGTCTCATC[T/C]TTCTAGGTAATTTGAGTTTCCAACC TGTGG
WI-2033	183	T C	GGGTGCTAGA ACTAATCCCTC A	CAGTGGTTCCA CGTTCTOC	ATGTGTATGAGCTCCACATTCGCAGATTCACCAACTATGGATAGAAAAATATAGTATCCCAGATGG GCAGCCCAAGGATCAGAGGGCTAAATTTTAAATTTTCCAAGGTTATACAGGACAGTGTGGAAATTT AGCATTCTGGGTTTTGGCATCCATCAGGGTGCTAGAACTAATCCCTCAT[C/G]GGGAGAACGTGGAAACC ACTGATATACCAAT
WI-4745	131	T C	---	---	TTATGGATACATGTTTCTGGTGAAGGACAAAGATTGAAGCAAAAGGACAAAGGAGATCAACTGGG TAGAATAACTCATCGATCCACAGGCCCTCTCCACCATTTCTCCATCTACTTTCTACTCTGAT[C/G] AGGCAGACTTATATGAAAAAAGGGA
WI-2034	150	T C	CCACAGTGCA CCAAGGAC CC	GGGTAAAGAT AGAGTGCAGGT CC	CCACGACTATGCTTCAGAGTCCCTGGTACTGACAGAGAAGGCTTTGAGGACCATGTGGCGCCCAAGA CCTCCTTCTCGGGTTTCACTGAAAGACGATGAATCTCTTCTACAGCAGCTGGACTTCAACCA CAGTGCAACCAAGGAC[T/C]GGAACTGCACCTATCTTTTACCCCTCCGACACCCAGATGCTGAGATGCC ACACTCTGAGTG

WI-2038	155	C T	TGTCCTTTAA GTGTGAAGT ATTAATTAG	CA	ATTCCTCTTG AAAGAAACAT CA	TCAGGTGACAAGAAAAAGTCACATTTCTCAATCACTCAACCATGCTGTTATTGCTCTCTGCAGTGT ATCCAAGGATGTCACCTTTTGGAACTCTGTAGATCAGAAAAACTGCTTTAAAGTGTGTAAGTATTA ATTAGATTCTATTTTGATA[C/T]TGATGTTCTTTCAAGAGGAAATTTGTGTAAGAGGATTCCCAATT TGCAATTCATTGGC
WI-4782	113	C T	GATGCAGAAG ATAACTAGAA AATGC	GA	GAATCTCTTG GTTATTTTCT GTTC	TCATTGACTTTTAGAGTTCCTTCAGTCTTTATGCTCTTATTTCTTTAGGAAAAAAGTGGCTAGGAGAA CACAAATTCAGGTTCTCTCCAGATGCAGAGATAACTAGAAAAATGC[C/T]GAACAGAAAAATAACCA GAAGAGTTCATTATGGTTTTTTTCCAGAACGATTAC
WI-4788	65	A G	GCATAGAATC ATCTTGCTAAG TTCC	GGATAAAAT AAAATTTTGGC ATAA	AGGAGAGTTTGGCTCTTTCCGGACTCTTGGAAATTCAGTGCATAGAATCATCTTGCTAAGTTCC[A/G] TTGAAAAAATAATATGCCAAAATTTTAAATTTATCCAAAATTTAAGTCGAGATTATAATTGATATTT AAAAACTATATTGAGTCTTTCTAAAAAGATGGCGTATCACTCTA	
WI-5300	38	T C	TCCAGAGAC CACCTTCATC	CTACTCTTTCT ATTCATAATC CAAAAA	CTTACTTCCAAAGTGTTTCCAGAGACCCTTCATCT[C/T]TTTGGATTATGAAATAGAAAGAGT AGGTGTTATTATCTCTCTTTTACCAAGGTGAAATTGAGGCTCAGAGACAAGGTAGATGATGAGCCCA AGGTCAGTGACAGAGCCA	
WI-4818b	121	G T	TGATAATGGG GCCCTGT	CCTTCCCTTTA TATGTATGCCA GA	TATAATGTTTGTTCATAGTTGCCATAGACTAGGTATGTCCACACATGAATAACAATCTTATATA ATAATTTATTCAAGAAAGGAAAAATATACATATGGGTGATAATGGGCCCTGT[G/T]CTCTGGCATA CATATAAAGGAAGGCTAA	
WI-4818a	43	A G	TTGCCATAGAC TAGGTATGTC C	CATATGATAT TTTCTCTCTG AATAAAT	TATAATGTTTGTTCATAGTTGCCATAGACTAGGTATGTCC[A/G]CACATGAATAACAATCTTAT ATAATAATTTATTCAAGAAAGGAAAAATATACATATGGGTGATAATGGGCCCTGTGCTCTGGCATA CATATAAAGGAAGGCTAA	
WI-5317	139	T C	TTCCATTCTG GTAGCAGGT	GATGCAAGA AGAAATGAGTC C	TTTTCCATTTGTTGATTCCTTTTGTCTGAGCCCTTAGATCTCCTTTAAATTAATAGCAAGGTTAAT AATATAATAATATGATGTTATATATACAAATTCACACTCAACAGGAATTCATTTCTGGTAGCAGGT ATA[T/C]GGACTCATTTCTCTTTGCACTATTTCTAGGTTATTTGCAGCCCCGAGATCTACCCAGG	
WI-4888	56	G A	GCAAGATATA AAGATTAAAG AAGATAACA	CAATTCOACTA CCTCATTTATT CA	AAATGAGTAACCCCAAGTTACTCGGCAAGATATAAAGATTAAAGAAAAAGATAACAAGA[G/A]ATGAAT AAATGAGGTAGTGGAAATTCCTTGATAACTGGAGTAGTGCCCTT	
WI-5328	44	A G	---	---	AACATTTTAAACCATGCTACATTTACAACACTGAAAAGACAG[A/G]AAAAAAGAAATATTTTG CCTCAAAAAGCTCTTAAGAGATTATGTAATAAAGAAAAAATATGAATCAGAAAAAGGAAAGAAAT AGAAACACGTGATCTGGAAGGAG	
WI-4897	93	A G	---	---	GCCTTTTGTAGTTAAGTCTTTTGTAGTGTGCTTTTTTTTCCCCCACTAGGTACTCTCGGCCCAAT CCCCAAAAGAAAAAAGCGCTTGG[A/G]GATAAACACATCTTC	
WI-5345	29	G A	---	---	CCCTGCTATAGGTGAGTTTAAAAATCCT[G/A]CCTGCTATGTTTGTGTTGAAGCCACATCCACT GAGGTATATTCTGTCTGCATTTTCTATATCACTCAGCTTTCAGATCCACTCCACTCAACTTGACAG	

[illegible]

WI-7593	46 G A ...	---	TTTGTGTTGCTCTGGACACCCCACTGCTCCAGGATGAAAGGAGAG[G]AATGAGATCAGTTTGGG CACTTCTCTTGAATATAAAGAAATCAAGATTACAGTCATGTTGGGACTTCTTCTCTCTCCAA
WI-6962	78 A G ...	---	AGTGCATCTTGGGGAAAGGGCTCCAGTGTATCTGGACCAGTTCCTTCACTTTTTCAGGTGGGACTCTT GATCCAGAGA[G]GACAAAGCTCCTCAGTGAGCTGGTGATAATCCAAAGACAGAAACCCAAAGTCTCC TGACTCTGGCTTCTATGCCCTCTATCCTATCATAGATAACATCTCCACAGCCTCACTTCACTTCCAC CTATTCTCTGAAATATCTCTGAGAGAGAACAGAGATTAGATAAGA
WI-7059	43 C G	AAGCACCCA GCCATC	GCAGAGAAGAACCATGCCAGGGGAGAGGCCACCCAGCCATC[G]TGACCCAGCGAGGAGGCCAA CTATCCCAATATACCTGGGTGAATATACCAATTTCTGCATCTCCAGAGGAAATTAAGAAATAAA GATGAATTGTGCAACTCTTAAAAAA
WI-9063	53 A C TT	CACTTCACTGA AAGACACCAT	AGCAGCCATCAGATGATCTGTTTTTACCACCTTCACTGAAAGACACCATTTAT[G]TACCCAAAGGG CAGAAAGTAGAACTTACTATTCAATAATGTTTGACACAATTGGAATTGTC
WI-7079	293 T G ...	---	AAGGGCATTGAGACTATAAGCAGTAGACAAATCCACATACCATCTGTAGAGTTGGAAGTGCATT CTTTAAAGTTTATATGCATATATTTAGGGCTGCTAGACTTACTTCCATTTTCTTTCATTGCT TATCTTGAGCACAAATGATAATCAATATTATACATTTATACATCACCCTTTTGACTTTTCCAAAGCCC TTTACAGCTTGGCATTTCTCGCTAGGCCCTGTGAGGTAAGTGGAT
WI-9074	38 A G AAAAG	GACAGATTTT GACCTAGTTCC TT	TGGATGCCGAGGTAAGTTCTTTTGTCTAAAAGAA[G]AAGGAACACTAGGTCAAAAATCTGTCC GTGACCTATCAGTTAATAATTTTAAAGATGTTGCCACTGGCAATGTAACTGT
WI-7104b	249 C T ...	---	GGAGTTTGGCCCTTCTAAGGGAAGGAGATCTTTATCTTCTGGTTGGCTTACCAGTCACGTTGGGA GAAGAGAGAGAGTCCCAGGAGACCCCTGAGGGCAGCCGGTCTACTTTGGACTGAGAGAGGAGGCC CCAGGCTGGAGCAGCATGAGGCCAGCAAGAGAGGGCTTGGTTCTGAGGAAGCAGATGTTTCATGCT GTAGGCCCTTGACCCAGGTGGGGCCACAGCACAGCATCTTTG[C]TJ
WI-7104	157 C A ...	---	GGAGTTTGGCCCTTCTAAGGGAAGGAGATCTTTATCTTCTGGTTGGCTTACCAGTCACGTTGGGA GAAGAGAGAGAGTCCCAGGAGACCCCTGAGGGCAGCCGGTCTACTTTGGACTGAGAGAGGAGGCC CCAGGCTGGAGCAGCATGAGGC[C]A/CAGCAAGAAGGGCTTGGTTCTGAGGAAGCAGATGTTTCAT GCTGTAGGCCCTTGCAOCAGGTGGGGCCACAGCACAGCATCTTTGCT
WI-8974	34 C T AAGAACTCA	TGTAGGGCTGA GCTGGC	CATACATGAGAGCCCTGAGCCCTCAAGAACTCA[C]TGCCAGCTCAGCCCTACACCAGTTTCCACC TGGAGTTTCATGCAAGGGCAAAAGGCAGTGCCATGCAAGCTGTTAA
WI-9161	61 C T CTTGGC	GCTTACAGGAG AGACTAGACA GGAA	CTGTGAGGGTGACGTTAGCATTACCCCAACCTCATTTTAGTTGCCTAAGCATTGCCTGGC[C]TJTC CTGTCTAGTCTCTCTGTAGCCCAAGAAATGAACATTCCA
WI-9014c	93 T C ...	---	CCCTGTCCCATGCTGACCTGTGTTTCTCCCCAGTCATCTTCTCTGTTCCAGAGAGGTGGGGCTGGAT GTCTCCATCTCTGTCTCACTTTAT[C]GTGACACTGAGCIGCAACTCT

WI-9014b	44 C T	---	---	CCCTGTTCCCATGCTGACCTGTGTTTCTCCTCCAGTCATCTTTC/TGTTCCAGAGAGGTTGGGGCTG GATGTCCTCATCTGCTCAACTTTATGTGCACTGAGCTGCAACTTCT
WI-7023b	206 C A	---	---	TCTGAGAGAAATGACTTGTGGGAGACACCCCTGCAGATCCTCATGGTTTGTGACAGACCCCTGCGTGTCT CAGTGCCTTTAAGTGATCCCGCTGTGCTGACTTTGAGTGGGATCAACATCTGTCTCTACGGGTCCCC TCTTTTGGCCCAAGTATTCATGGCAGGTTTGTGGACACCTACTAGCTTCCCTTCCCATTCACAC A/C/A/CACACATCTTGCTACCCAAAGCTCTGGCTGGCAGCACTAA
WI-7023a	56 A C	---	---	TCTGAGAGAAATGACTTGTGGGAGACACCCCTGCAGATCCTCATGGTTTGTGACAG/A/CJCCCTGGGT GCTCAGTGCCTTTAAGTGATCCCGCTGTGCTGACTTTGAGTGGGATCAACATCTGTCTCTACGGGTCT CCCTCTTTTGGCCCAAGTATTCATGGCAGGTTTGTGGACACCTACTAGCTTCCCTTCCCATTCAA CACACACACATCTTGCTTACCCAAAGCTCTGGCTGGCAGCACTAA
WI-7093	54 C T	---	---	CTGAAATCCCTCTCTGCTGGCTGGATCGGGGACCCCTTGGCCTTCCCTTC/TGGCTCCAGCC CTACAGACTTGTGCTGAGCTCAGGCCAGTGTCCGACCTCTCTGGGCTCAGTTTTCOCAGCTATG AAACAGCTATCTCACAAGTTGTGAGCAGAGAGAAAGCTGGAGGAGCCGTGGGCCAAT GGGAGAGCTCTTGTTATTAATATTGTTGCCGCTGTGTTGTTGTTA
WI-9171	62 G A	---	---	ACATATCTGAAAAATGTTGAAAGCCTAAGCCAGGATAAAGAAAGTAGAGATAATAATCA/G/A TCTTTACAACCGATGGTAATTAAGCTTGATTCACAAGACTTCATGC
WI-9174	47 T C T	CTAGACCCC ATTCTCCTATT	TCTAGAGGGTA TATAGGACAGG ACTG	GTGTGAGACCATCATGGTGCCAGTCTAGGACCCCATCTCCTATTAT/C/CJAGTCTCTGCTCTATATA CCCTCTAGAAACAGAAAGCAATTTTAGGCAGCTATGGTCAAAATTGAG
WI-7753	52 A G	CCATGTTCCGA GAAGAACAGA	CAGAGGCTTG AAATACAGGG A	AAGCCAGATGCACATCCCTGGAAGGACATCCATGTCCGAGAGAAACAGAT/A/GJATCCCTGTATT TCAAGACCTCTGTGCACTTATTTATGAACCTGCCCTGCTCCACAGAACACAGCAATTCCTCAGGCTA AGCTGCCGGTCTTAATCCATCCTGCTAAGTTAATGTTGGGTAGAA
WI-9186	76 G A	CCACTTCTCCC CGCA	AAAGGGAAAG TCTGACCTAGG T	AAAGAACTACAGAGGACGATGTCCAAACAAAAATGGCATCACCTGTCAAAAATGGAGTTCCACT TCTCCCGGCA/G/AJACCTAGGTGACACTTCCCTTTCATCTT
WI-9193	94 G A	AGAATATTGT CTGCCTTAAAG CA	GGTGTGTGTGG TAGGGG	TTGGACAAACCTAGAAATTTCTCCCTTTATGTATCTCTATCGATTGTGTAGCAATTGACAGAGATAA CTCAGAAATATTGTGCTGCCCTTAAAGCA/G/AJATCCCCCTACCACACACACCCCTGTCTC
WI-9015	48 C T	---	---	TTTGGATTGATATCGTGAATCCTCAGCCGAGAAATGGGCTGGATTG/C/TGCTTTGGTTAATACAT CTTCCCTAAAGAAGATAAACACAAAAATCCATTCAGGTAGCTCGGCAACCACTAAGAA
WI-7254	37 A G	GGTCTGAGAG AGGAGCCAC	GGAGTGGGTGT CATTAGGGA	GGAGCCAGGAGACAGCGGTCTGAGAGAGGAGCCAC/A/GJGTCCTAATGACACCCACTCTAGCC CTGAGGCTCGTGGCCCTCAGACTGGGAGAGTCCAAGGAAGGAGGAGGAGCCACTCTCTCAATGC TCAATGGCTCCCTGAAATCAAGACAGG

WI-9231	32 G C	CAGGTC	CACCTGCCAC	GTGACCCTGTGAGGTGAGTCCGCCAGATTGAGCTGTGAGTGGGCAAGTGTGTCAAAGGGGC
		GATTGA	ACTCAGAC	TGCCCCCAAGAGATGAGGCTGAGAGCAGGAGTTGAGGCCGGAAGATCA
WI-7836	120 T C	CAAATAACA	GCTCAGAAC	TTGTTGGGAAATAGAGAGTTGAGATAAAGCTCTCATTCAGTAGTACTGAAAGAAAAGTCTGCTA
		ATGCAACGTT	CAAGATTAGA	GAATGATAAATGTGATGGTGTCTATAACTCCAAATAAACAATGCAACGTTCTTCGATTCTTAAT
		C	AATC	CTTGGTTCTGAGAGCCATTGGTTTCAGTTGTAGCAATCCCATACAGCT
WI-7286	65 T C A	CAGCTCAGCT	AAACAATCTA	TCCATTCTTTGGCCCTGCAGCATGTGATGCTCCAGAAATTCAGCTTCAGCTTAAGTACAGATTC
		TAACTGACAG	ACCAGAAAGCT	GTAAAGCTTTCTGGTTAGATTGTTTTCAGTTGGTGATGATGCTTTTCCATGTGACCTGTATAT
		C A	TTAA	TTCCATCATATCTCAAAGTAAAGTCA
WI-7858	91 T G TAAAT	CTAAGCATGT	CCCAATTTTA	CAAAATCTTGGAAATATCTCAAATGTTAATAACAATAATGAATTTTCTCATGCATATCTACTACT
		ACGTGAATTT	TTAAAGTTTA	AAGCATGTACGTGAATTTTAAATTTGATATAGATGTAAACTTTTATAAAAAATGGGGTGTGG
WI-7860	50 C G	A	CATCTAT	GAAGATTAGGGAGGGTGTCTGTGGTCTCTCCCTGCCCTCCCTCCCAACCA/GTGGGGAGAGACC
				TGTGATTTGCCAAGTCCCTGGACCTGGACCACTGAGCTGAGCTTATGGTTGGGGTGTGAGGACGG
				TGAGCGTAAGTGGGGAGGAAATGGGTAAGAAGTCTACTCCAAACCTAGGCTCTATGTCAGACCCAG
				ACCTAGGTCTCTCTAGGAGGGAACAGGGAGACCTGGGGTCTGTGGAT
WI-9064	29 A G TTC	CGTACCTCCAA	GCCTGAGTGA	CAAGCGTACCTCCAAACATAATTGATTC/GTATCTGCGAGACTTACACTCAAGCAATCCTGAGG
		ACATAATTGA	AGTCTGCAGA	AATACTGAGGAGGGCTGGCTACTGCTCTGCACTCTGCTGCTTTG
WI-7307	128 G T			CACACTGTCTGCTTCAGTGTGAGGTCTGGAGGTCTGGCAGGTGAGGTGGGTAAGCCGGGTTCCACA
				GGCCCCAGCCCTGGCAGGGGTCTGGCCCCCAGGTAGCGGAGAGCAGTCCCTCCCTCAG/GTAACT
				GGAGGAGGGGACTCCAGGAATGGGGAATGTGACACCACTCCTGAAGCCAGCTTGACCTCCAGT
				TTGCACAGGGATTGTCTGCGGGGTGAGGGCCCTGTCCCAACCCGCC
WI-9274	25 C T G	GAAATGTGAC	CAGGTAGAATT	GAGGAAATGTGACTTCACCTTTGGTG/C/CAATGGACAGAAAATCTACCTGTGTACATAGGAGAA
		TTCAGTTTGGT	TTCTGTCCATT	GTTTGGAAATGCACCTAATAGCTGGTTTACACCTTGATTTCGAGGTGGAAA
WI-7313e	266 T C		G	AATTCCTTTCTGGTAATCAGGCACATGATGAACCTTTGATTAGTAGGTCTGTGATTAGTCTTAAT
				TGTTTTCAGTCTTTTATGTTTATATCATAGGTATAGGTGGACCTAAATCCCTTATCATATCTTTAT
				AATTCAGCCAGTGTATCCACAGTTTTTGTATGTTTTTAAGTAACCTATTATCTCTGGATTTCATG
				AAGGTGAATATCGTTTTTGTAACTGAATAGATTGTATAGCGATGA
				AATTCCTTTCTGGTAATCAGGCACATGATGAACCTTTGATTAGTAGGTCTGTGATTAGTCTTAAT
				TGTTTTCAGTCTTTTATGTTTATATCATAGGTATAGGTGGACCTAAATCCCTTATCATATCTTTAT
				AATTCAGCCAGTGTATCCACAGTTTTTGTATGTTTTTAAGTAACCTATTATCTCTGGATTTCATG
WI-7313c	256 C T			AAGGTGAATATCGTTTTTGTAACTGAATAGATTGTATAGCGATGA

WI-9281	68	G A ---	GCTAACACITTT TTAAACCGT	---	CATTTATTTTG AAAGCTATTCA GACA	ACTGGTGGGAGACTGTGAGGATCCAGGATTCCAGTATTCCTGGCCACAGGGCCTTGCTGGCTACTGG [G]A[T]GTAGTTTGCAGTCTGTGTGCTTCCCTCTCTTATGACTGTGTCCC
WI-7848	142	A G CTC	GTATATTACA ATGATCACCG ACTGA	---	CCOCACAGAAC TATTGTAAAC AA	TTCTGAAAATATAACCAGCCATTGAGCTATTTAAAACTTGTAATTTTAAATTTACAAAAATATAA AATATGAAGACATAAACCCAGTTGCCATCTGCGTGACAAATAAACATTAAATGCTAACACTTTTAAAA ACCGTCTC[A/G]TGTCTGAATAGCTTTCAAAAATAAATGTGAAATGGT
WI-9304	70	G A ACTGA				TCAGTTTGGTCTTCAGATTCTGAGGAAATGCTTTGTATTGTATATTACAATGATCACCGACT GA[G/A]AATATGTTTACAATAGTTCTGTGGGCTGTTTTTTTGT
WI-7933b	314	C A ---		---		TTACAGAAACTTGCCCTGTGCCCTGTGTCCCATGCTAGGGGGAGGGGTCTTTTCCTTCTTCTTCTTC TACCTACCCCTTTCTCTTGGCAGGGCCTCGTATCTTACCTTCTGTCCTGCTGGCTGGCTGCAC AGAGGATTGCCCTTCTCTTTTCAGAGCTGGCCCTCGATGCCAAATTAGCATTTAGTATTTGCACAA AGTCTAAGGGACCATGGCTGCCTGCCTTGGGAGGAACCATAGCTCCCT
WI-7933	96	G C ---		---		TTACAGAAACTTGCCCTGTGCCCTGTGTCCCATGCTAGGGGGAGGGGTCTTTTCCTTCTTCTTCTTC TACCTACCCCTTTCTCTTGGCAGGG[G/C]CTGTATCTTACCTTCTGTCCTGCTGGCTGGCTGCTG CACAGAGGATTGCCCTTCTCTTTTCAGAGCTGGCCCTCGATGCCAAATTAGCATTTAGTATTTGCA CAAAGTCTAAGGGACCATGGCTGCCTGCCTTGGGAGGAACCATAGCT
WI-7374	182	T A ---		---		CCCAGATGTGCCCATCACGTTTTTCTGAGGCTTTTGTACTTTAGTAAATGCTTCCACTAAACTGAAA CCATGGTGAGAAAGTTTGACTTTGTTAAATATTTGAAATGTAAATGAAAGAGTACTGTATATTA AAAGTTGGTTTGAACCAACTTCTAGCTGCTGTTGAAGAATATATTG[T/A]CAGAAACACACAAGGCTT GAT
WI-9343	78	C T CCTCTGCCA	CCAACAACAT CCTCTGCCA	TG	AAATGAAACTT ACGTTTGTG	GGTCTGCTCTGTACCTTGACCCCTTCCCTTCTCTGCTTCTCTCTCATCATCATCCCAACAACAT CCTCTGCCA[C/T]ACACAACAAAACGTAAGTTTCATTTGGGCAAA
WI-7386b	104	T A ---		---		CTATATGTGAGAGCGTGATATCTGGATGGAAGTTGGCTGGATGATCTCCAAAGTCGTTTCAACTCT TAAAGACATCTTAAATCCTGAATGTAACAAATTGTTA[T/A]GTGTTTAGAATCAGAAATTTGATTTTGA ACTTGAGTAAATTCATCCTT
WI-9357	75	A G ---		---		AAGAAGGAGCTCAGTTACGGGGTTTTTAAACCTTCATGAAAACCTGAAGAGTTCACTTTGTATTAT GCTCTT[A/G]TGATTTACAGACTGATGCCAGACAACCTTGGGAAGA
WI-9360	79	T C TTGG	CTTTAGAAAA TCTGCTTTAAC	A	CCTAGGGAACA CAATTAGAGGA	TGAAGGGGTGTGGCATCTGTGTTTCTGATGCTTACTACAATATGTGAACCACTACTTTAGAAAACTGTG CTTTAACTTGG[T/C]ATTCTCTAATTGTTCCTTAGGAATGACTGTCCCAAG
WI-7423	107	T C GTTC	TGCTGGGCTGT	GGTCCAGAAGA GGOOG		TGCTCCCTGTCCCATCTGCAGTGGACCCAGGCCACCCCCCTTTGAGAGGTGGGGTGAAGTGTCTCTT GGCAGGGGATTTGTGACACTGCATTGCTGGGCTGTGTTCT[C/G]CGGGCTCTTCTGGAACCTTGCAACCGTG GATACCAGGCCATGTGCCATGGTATTGGGTCTCTGGAGGGTGGTGAATAAAGGCATAGTGTCT

WI-7424	131 T A	CAAGAGAGAG AGAGGAAAGA AAAA	TGCAAAAGAAA GAATGAAAGTT G	CCAGGAGCACTAGAGAGGGGAGGGAAGCAGAGATTAGAGAAAAAGCCACCGGAGGAAAGG AAAAAACATCGCCAACCTAGAAACGTTTCATTCTGTCATTCCAAGAGAGAGGAAAGAAAAA T/AJACAACTTCATTCTTCTTTGCACGTTTCATAAAGCAATCTACATA TCCTGCAAGAAGTCTCAAGCCTTTTGTATTTTGTGCAATAAAGTACAGCTTTGTCATAAGAGTGAAA TTGGCTAGCTTAAATGGATCCATAAACTTCTCTTAATTTAAGTGAGAJC/TCTTTTAAACACCT GTTAAATTTAATGTAGCAGCTGAGAATCTAAATAATATGTACCACCTCGTTTATTTGTTCATTCATCCA TCCCTTTCCCATGAATATTCA GTGGCCACTACATGTTATAGAAACCATCATCTTTGTCACACAGCAGCATGTATGAATAAAAGGCTGAG TTATCACTAAGCAGGAGAAAGCAITAAAGGTGCCATTTAAAGGACTTTTAAATCAACCTAA TAAACTCTAATTCGTGACTTTTTAAAGATCTAAGGTCAATTTAATACATGCTGAAAGGGTCACA ATTAATCTTTGATCTTTTTACTCACTGTTAACTTATATAAT/AJITCAGAAC TACAAATGAATGTCTTTTATTTCGGTATGCATCCACATTTTCAGCATTTAGTGTCTCTGAACAGCAAG TGGAAGACGCAGCAATTTGCCAGGAGGTCAAGCCACCAATTTTCGGGATCTGCTGTGCACACCGG GTTCCTCTTAATCCCTGCTGAGGATCTTG/AJGAAGCAGCAGCAGCACCAAAACCAAGGCATGCA CCGGATTCAAGGTCITTTTGTCCAGTTGTCAGATTCCAAACTAGACCCCA AACAGTACCACCAACACATGACAACTGCCAGGCAAGGCTTGCTTCCTCCCTCTTTCGCTCCG ATGTGCTAGTCAGCAAGGTGGGGAGGCACCGATGTTAGCTTCGCCAAAGGGAGTATTACAGAGA GAGGCTTGGGAA/GC/GGAAGGAAACCTGGACAGGCTTTTCAGCACTGAGAAATCACTTAAAACTG ATTTGCTTTCAGTAACTGGTATGCTGAA ACCAAGAGATCAGCTGTCTAAACAGAGCTTTTGTGATTG/TGGGCTTCTGAAAGAAACCTTG TGACAGCTTCTCACTGACCTGCAGGACCGAACCTGACCTGAGAGGGGATGGGGCTCTCTCAGAAAA GAATATTTGGGCGAGAACCTGGAACCTGGCCACCGGACATCCCAATATCCCTCCTCCTCAGGG CTACCCCGACATCTCAGCCAAATGAAGGCTCGAA GGGTGAGACGGTTTATTGTGCACATTTACACAGCGTCACAGCTCTGGGCTGGCAGGGCCATGCTC CTGTGGTCGGGCTGCTCACAAGGGCGTTTCACTTTTTCACCACTATGTACAGTCAAGTCTCCAA GGTGATGGGCTACAGTCTGCTGATGAGTGTGTACACACATTTTACATAAATTACACAGACTC ATACATGAAAAAT/AJAGAGCCTAAGGGCCTGTAITTTAATGAGAAAAA AACTTGTTTACAAAATAGGCTTTCAAACTTCATTACTGAATGTAAAGTCAATGACTGTGTTT TAAATATGTACCAAGGAAATACAAATGGATAATGATCATTTTTCATGCTCAGGAGAGAACAGCAC AGAAATAAGGATACTGCAGAGGTGCAAGGAAACCGGAACCCATTGTGTACACTGTCTTCACACAG TG/AJGCATCTTCTCACCTTAAGTGCAGCTGTGCAAGATGCCTCAGTGIG
X86400	118 A C	---	---	
WI-8053	242 T A	---	---	
WI-6190	165 G A	---	---	
WI-6275	148 G C	---	---	
WI-6421	41 G T	---	---	
WI-6905	215 T A	---	---	
WI-9420	202 G A	---	---	

WI-9448	184 G A ---	---	TGGGGCTGCTTTTAGACTTCATTTCTAGAGCAGACACCTAGTAGAGGAATACCTGGGAGAGAGAC TGCCTTGCCCATGGTGGTTAACTACATGAGGGGACTGAATCTCTTTGGATGCCAGTCCAGATCCC TTTTAAGAAAAATGGGCTTGTTCCAAAGGCTGAGAGCTGGCACCAC[G/A]CACTGGTTTCTAAA TCTCTGGCTGGATTTTATCCAAGCGCATGTTCTTAACGTGCCCGTGAGCAG
WI-9470	204 G A ---	---	ATGTCAGAAGAGACACAGACAGAGGTTTTCCTTTTAAATGCTAAACAAGTCCACTAATCCACA GATCTGAAAAAGTACAGCTCTCCAGGTTGATAATCAGATCCAGGCTTTTCTTGTCAGTCCGCTTA TGAGATCACGAATATGATCTCCCTAAAGCCCCAGATTCTACTAGAGCCGCTGGGGACACTGATGAC AA[G/A]GCAATCAACTCATCTCCTCAAGCTCACAGGGCTCACCTTCCCAAG
WI-1245b	201 G T ---	---	GATGATTTCTGAAGTCTCAGCAGCCCTGATTCTAAGCCTCATAAGGAAGAGTAGGTGTTAATGGCA TCTAGGGCAATGGTAGGTCCTGATGCAGATCTGCTGAGCCATGTGCTGGCATCACAGGGTGGT TTATTAATTTCAATTCATCTGGACAGCCCTTCTTATAACGTACATCCTTGCCCTCTTCTGAGGC[G/ T]CTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1245a	85 T C ---	---	GATGATTTCTGAAGTCTCAGCAGCCCTGATTCTAAGCCTCATAAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGGTT[G/C]GCTGATGCAGATCTGCTGAGCCATGTGCTGGCATCACAGGGGT GGTTATTAATTTCAATTCATCTGACAGCCCTTCTTATAACGTACATCCTTGCCCTCTTCTGAGGC GCTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1031	149 G A ---	---	TCAGTGATAAGGACAGGTCTAGAACAGCGTTCCCAACCCCTGGCACCAATGACAGTTTGGACCAAA TAACCTTTGTTTCAGGGGACTGTCTACACATTGTGGGATGTTAGCAGCCTCCGTGGCTTCTACCCA CTAGATGCCAGCA[G/A]CACAAACACCCCTCCCAACAATCATGACAAATGAAAATGTCTTTAGACATT GCCAAATATACCTTTGTGGGACAAAATGGCCCTGATTGAGAACCACTGGTT
WI-5385	110 G A ---	---	AATGAGTCATTGTGGAGTTAGAGGAGGTTACTGAAAATGGTGACTCCAATGGTGGGATTTGAAGAGG GAAGTCTCGATAATTTTAAACATATGGTTCTTGCCAGGAATCG[G/A]CAATGCTAATCTATTGCTTAA TTCCTTATCAACAGACTCTTTGAATCAATTTAGAGATACTCAGTGACCCCATGGCTAGAGTTCCCTGAC CCCTGCTACGGGAACATTGAATGCA
WI-5403	199 T G ---	---	ACCAAAACCGTTGGCAAGGCTCCCCAAGACTCACCAACCCCAACTTTGGTGCTTACCCATGCCGGGTG GGATTGAAGAAAATAACCATAAATAATGCTACAAATTTTCCAGTAGTTACCAGGCACCCAGCCTAT TGGAAGAAATCATAAATGTAACCCCTACAATGTATTGCTCTGCGCTTGGTCCAGGCATAGAGTT/G]GGCTACAACCCATTTTATCATTTGAACCCCTCAGAAGCATCCAGTTGGGGCT
WI-5801b	157 G A ---	---	TGGTATTTTTCCTTTTCTTAAATGTTATGATTAAATGATGCTTTGTAGAAATTTGAAAAAATGTAAA TCAGAGAACAGAAAGAAAATAAAGTATAGTTGAACCTCTAACAAATTTTAGATTTTAAAGGCCTAG GGAAAGAAAGAGAGCCCTGGGA[G/A]AGGGAATGAGAAAAAGCACACCAAGAAAAAAGTGTGT GGCTTAAGGGGAAGCCCAAGGAAGTTAAGT

WI-5801a	48 A G ---	---	TGGTATTTTCCCTTTTCCCTAAATGTTATGATTAAATAGTGTCTTTGTGAG/AAATTTGAAAAATGT AAATCAGAGAACAGAAAGAAATAAGATATAGTTGAAACCTCTAACAAATTTTAGATTTTAAAGGCC TAGGGAAAGAAAGAGAGCCTGGGAGAGGGAATGAGAAAGCACAACCCAGAAAAAAGTGTGT GGCTTAAGGGAGCCAGGAAAGTTAAGT
WI-5896	61 C A ---	---	TTCTATTTAAATCCTGTGCCCATTTGCAAGACTGCATTCAGTCTGCATGAGCCTTAGTTTC[C]/ATAA AAGCCCTCACACCGAGGACAATGTTCAGAACTAAATGACTGCAGGTGAGCAATTTCTGTATTA TACAACTGGGACCAAGATGACTTTATATAGTGGCAAGAGACAATCAGGCAGACTGGGAGGACC TTATAATAGATTATAAGGCTGTGGTGAGTTATTTTAACCT
WI-7461	153 C T ---	---	TATTACTAGGTTTCATAGAGCCCGTTGTAATGATAAATAGCCAAATAGTTAAAGAGGCTGCAGGCC AATTCTAAGGCTCCTCACTTCCCTTCGAACCCAGCCTCAGAGATGACACTTAGCTGCACATTTCCCTG TGGCAGGGGACTGTGCT[C]/TGTTCCTGTTGGTCCCGGAACCCAGTGTGGTGGCTGGCACAGAG GAGGCCCTGAGTAGCATGTGTGCA
WI-9716	221 G A ---	---	AGAAGACAGGAGCACTGGGATCAAGGACTGATAAATCTGAGGCTTTAATGGTCCCTTGTCTCTAAC GCTTTTGGTATACCTTCTCTCTGAAGACCAACCTTTCAAACCTCTCAGAACACAGGCAAGATGCAT ATTCTGATGTTTCAGATGTGACTTCTACATTCGGAACCTAGATGAGTAGGCTCTCTTCATCT CAATTGAAATTCAGAA[G]/AAACACCTAATTGGCTCATCTTTGGATCA
WI-9760	49 C T ---	---	TTTTCGTTAAGTCTTGTGAAGCCACACAGAGTACTCTCTTAC[C]/AAGTGTACTTTTGA TATATTTATGGGATGATCTATCCCTACTTAAGATTTCTCTCTCAGGTAAATATCCATTTCCCT TTGTCAGGAGTTCTTATTTGGCTTCTTTCTAAACCTTAACCATCTGCTTATCTCTGCTTGACA CATGCTATTTAATCAAGGTGACATT
WI-9855	31 A C ---	---	GAAACCTCGTTGGCTCAAAGGAACTGTAG[C]/AAATTTCTTTTATTTTATTTTGTGTTTTAACTC AAAGAGTGGAGTTTGCAATTGACCTTGATGGCAGCTGCTCTTTGTTTGGTGTAAATCCTCTAGT GGGCACCTTTCGCAAGCAATTTAGAGCAAGGTGGTGGCATGGAGTTGTGTGAGGTGCTGAAAG TAGCAAATGGAAGAAAGGTTAATGGA
WI-10312	41 A G ---	---	AAGCCAGTGGGAAAGCAGACAAAACACTCCAGAATAC[C]/GAGATATAAACATCATCATCA GTAGAGATGGATGACCTAGGAGGTGATGCTGATGAGGGCATGTGAGCCAAAGACATTTGGGTCT TGAGGGTTGAATAGGAGTTTGTCTGGTGAGTCTGCCAGTCCCATAGTAGGTGTTCCATAAATAAG AGTGACTAACTGAGGTAGAGTCACAGAGAAATTTCA
WI-11152	179 C T ---	---	GATTTCTTGGCATGCAGAGCAGATACGGCAAGGCATCTTGGGCAATTTGGAAGGAACGAGCCCTA ATTATAGAAACAGACTCTACAAAGGACCAAGTTAAAGGTCTCGACCCAGGGGACTGGTGGCCAAAG TCAGTCAAGGCATAAAGGGGACAAAGTGGGACAAAGGCTTGTCA[C]/TCTGTACAGAAACATTGAA AACAGCCAGTACATGCCACTGATAGA

WI-1968	167 A G ---	---	TGGTGAGGAGCTGTAGGCTGAAGAATAGTCTGCTCTGGCTTCGTTGGAAATGGATGAGTCTCT TTTACAAAATTTTCCCTCCATGGGTGTTAAGTTAGAAATCATGGAGTTGGAAGACTTAGATTCA ATTTGGGGCTGTACAGTTTACTGGAAGTTGTAG/GJGAACTTGAGCAAGTGCTCTTAATGTCTCTCA GCCTCAATGCCCTTCCCTGTAA
WI-4701	198 G A ---	---	GGGTTCAATTAACAGCCTTCCACTGGGTCTCAGATTGCACGGAGATGTAAATAGGAAGATAG AAAAATGGTGCCCACTATTGACTTGTAAACACCTACAAAACAACACATTAACTCTCCCCACTCTA CCCGCCAAAGTCTACCTTTTGGTCTTTATTTCTGTCTAATGACCATACTATTCCCAATTAGA[G/A] CCATGTCAATTTTCAGAAAAGCAGTATA
WI-4823	164 C A ---	---	TTTATCTTCCAAACCATTGTGTCTTTCACATACCTTTACGTAATTTAAATCATGTCTTTAAATTA TGCATTACTTGTGGCTACAGACATTGCTTCCATTTGTAATTCCTAACACAGCAAGCATAACT GATGTCCATCTTGTATTCCTAAAC/C/AJAAAGAAAAGTGCTTTTGTGCATCTGCCCTCTCTGT CTTCTCTGTTTCCACTCTGTATTTCCCTATTCCAGCATTCATGATTA
WI-4860	72 A G ---	---	AAAAAACAACCTTCATTTGACATTTCTAAGAAGATAAAGAAAACAACGATCCACTGTGTGTTGCTT GATTT[G/G]GGAGATAAAACCTGATCTCTAAGAAAATTAACCAAGCAGTACACTAAATAGCCT TTGTGTGTGGTTTTCAGGAAAGAAAGCCATCCAACTAAGTTGCTAAGAAAATAATGTTTCATATCA CTCAACTCCACATAGAGCATTATATATAGCA
WI-9705	111 C A ---	---	TGAAGGACCAGTTTGAATGCCTACCAAGGTAAGTAATCGGAGGGGCGAGGAGTAGGAGTTGCTT CCGGATGTTGCATAAAATCAGGTTCTTTAAGGAGTTCCGGTGCC[C/A]AAAATTTTAACACTGATGC TGCTACAAACGCACATAGAAATCGGTGTAGATTGCGGTTCCCTAGTAAGTAGCTAATGTTTAGATA TGATTGTTGAATTAATGTTGCTGTGTTCTTGGTG
TIGR- A004248	177 A G ---	---	CAAATAATCTCTGCTTAGAAGTTGCTCTAGGGCCCATGGATTCATGTAAGGGTGGGCGAGGTTGGACTG AAGATCTGTGGCAGGGCTCAGAGACGGGGTGAGGGGAGAGATCGTGGGTTTCATGAGATCCCAT CTTGGCAATACGGTTATCCCGTGGTCTTCATACGCCACAG/A/GTCTCCAAATTTTCAGGGGCTCC GTGGGATGGTGGAGCCCAATGAAGACCAGGTAGATGCCACCTAGAGATG
U17579	34 T G ---	---	GGGATTCAATGTGTCTGCTCATCCAATAAGCAGT/GJCATGACCTCAGCCCCATCTTTCTTCCC TATGTTCCAGAGACAGAATAGACCTGGCCCCCTTCTTCTAGGGGATCACAATATTGGAAGGATGAG GACTCCAAACAGCCAGCTCCCATGCCAATAAGAACGATGAGTGTGGGATCAATTTCTATGGAGCC TGGGAGAGGGGATCCTTCTAGTTGA
WI-7747b	88 T G ---	---	GTGAGAGCGAGGCTGAGCCTACAGATGAACCTTTCTGGCCTGCTTTCGTTAACTGTGTATGACATA TATATATTTTAAATTTGATT/GJAAAGCTGATTACTGTCAATAACAGCTTCATGCCCTTTGTAAAGTT ATTTCTGTTGTTGTTTGGGTATCCTGCCAGTGTGTTTGTAAATAAGAGATTGGAGCACTCTGA GTTTACCATTGTATAAAGTATATAATTTTTTATGTTTGTCTGA

WI-7747a	44	T C ---	---	---	GTGAGCGAGGCTGAGCCTACAGATGAACCTCTTTCTGGCCTGC/T/CJTTCGTTAACTGTGTATGAC ATATATATATTTTAAATTTGATTAAAGCTGATTACTGTCAATAAACAGCTTTCATGCTTTTGTAAGTT ATTTCTGTTGTTGTTGGGTATCCCTGCCAGTGTGTTTGTAAATAAGAGATTGGAGCACTCTGA GTTTACCAATTTGTAATAAGTATATAATTTTTTATGTTTGTCTGA
WI-7189	197	T C ---	---	---	TCAGAAATTTCTCTTCAGCTCATTTTGTCTCTCACAATTAAGGGAGTAGTTAAGTGAAGGT CACATACCAATTAATTTCCCTTCAAACAATAATATTTACAGAGAGGAGCAAAATATGGCCTTT CTTCTAAGAGATATAATGTTCACTAAATGTGTTATTTTATATTAAGCCTACAACATTTTTC/CJAG TTTGCAATAGAACTAATACTGGTGAAAAATTTACCTAAACCTTGGTTATT
WI-7850	57	G A ---	---	---	AGCCCCAGCTGGACTCATGGATGTCACCCCTTGTCCCTGCTCTTCTGCCTGG/GA/CTCATGTA TCTGGCAGCTCTGGTACCTCTGTGGGTGCCATCTCTACCTCTGACACAGACTGCCCTTGAAGCT GAGAAGGCACAGGGCAAGGAGCCAAAGACCACAGAGCCTCAGCCAGCCAGGATCCGTCCCTCATTT ATTGGTGAATGATGAATGGGAATGAATCAGGGGCTGTCTACTAGAGCC
WI-7907	69	G C ---	---	---	CTCTCTCTTATCCCATCACCCCTAAATAGTCAAGTGAGGAGGCTGGGAAGAGGTGGGAGGAGG G/GC/JAGAAGTGAAGGAAGATAGGAAGATATACCTCTCTGTTATTTTTTAAAGAACATTTGTT GGTGGCAGCAATCTCCCTGTCCCTATCACTGTAGAGGCCAATTTTATATCTATAAATATATAAA AGCAAGTCAAACTTGGATGTATCAAGGTAAATTAATGTCAAAAGTTTAAAT
WI-7919	242	T C ---	---	---	GAAGGCAGCTGGATCACTTCCCGCAGTCCCTGGGCAGCGCTTGTGTGGAACACAGAGCTCCTCCT CAGGGGCCCTGGCAGCTCAGCTCCTATTTCTGTATGATGATTTGGTTAAACACTGTCAAATAAGAGAT GTGCCAGATTTAGATTTTCTTACCCTAATCTGTGTTAATATTGTAACCTTTATCCATTTGAAAGTGCA AGCCCATTTCAGATAAGCTATAATCTGGTCTTTAAGGAA/T/C/JACAACCTT
WI-7928	101	T G ---	---	---	CTCCCTCCTATGTCTCTCAGCAGCAGTGGGGCACACTTGTTCATCTCTGACCGTTTGTGGGCTA TTCCCTGCAGTGCAGACATCGTCAAAATTCAT/GJACAAGAGGAAATTTTCATGCAGAAAGCTGTA TGCAGGATGCTCACTGATGTTTGCACCTTAAACCTGAAATTCAACTCTTTATATAGGATTTCTTTT CTATCTCCATCTCCTCATTAAAAATACGTACATTTTCGAGGTAATGGTA
WI-7936	131	T A ---	---	---	TTTTGAGTCAAAGACTTAAAGGGGCCAATGAATTAATATACATACTGCATCTTGGTTATTTCTGAA GGTAGCATTTCTTTGGAGTTAAATGCACATATAGACACATACACCCAAACACTTACACCAAAC(T/A) ACTGAATGAAGAAGTATTTGGTAACCCAGGCCATTTTGGTGGGAATCCAAAGATTGGTCTCCCATATG CAGAAATAGACAAAAAGTATATTAACAAAAGTTTCAGAGTATATTGTTGAA
WI-7944	99	T C ---	---	---	TACACGTTCCAGCCGTTGCCCACTCATCTGCGCGCTTGTCTTGGTGGGGGCGAGATTGGGTGG AATGCTTCCATCTCCAGGAGACTTTCATG/T/JAGCCCCAAAGTACAGCCTGGACCAACCCCTGGTGTG TGTAGCTAGTAAGATTACCTGAGCTGCAGCTGAGCCCTGAGCCATGGGACAGTTACACTTGACAGA CAAAGATGGTGGAGATTGGCATGCCATTGAACTAAGAGCTCTCAAGTCA

WI-7805	101 A G ---	---	TTTCTAGGCTGACAGTCTGATGCATGATTTTTTATAAATATTTTATCACTCTGTGAATTTGGATCTT TTTACTTTGAGCATATATTTAGAAATATGTGTA/GTGTAAAGGATCTCCACAATGTCTGCAGTGTG AAGGCAGGTTTCATTTGGTAATAGTTTAAACAGTCAGGAAGGCTAAACTGGTCAGTATTAATGTGTAGC CCTACCAAAAATAGCCAGTAGTATCTGAAAATGAAAAATAAATGAAGTAT
WI-7416	137 G T ---	---	GGCCAGGAGATTAGCAACAGGATCTTCTGTTACTTACTTGCCTTTTATCTTCCCTCTTGGCC CAGTCCCTTCTCCAGCTTCTGAGCTCTGCACAGACAGACACTCAGTGTCTTGGCAGTGCT [G/T]TACTCTCAGGTGCAGCATACATAACCCAGTAAGAGACTAAATCTGCAATATATAAAGAGCTC CTACAAATCAGTAACATGAAGAACACTCAAAAATTGGCAAAATGTCATCAG
WI-140	252 C T ---	---	ATTTGAAGATTGGAGGGCTTTCAGAGGAAAATAGATTTCATTTGGATCCCCAACTATAATGACA AGTTTTTAATTAGGTGATCAAGGCTTCTAAAGTGAAATGCAAGTTGTACCAGTAAAGTTTATA TCTCCATTGAGCCAGCTCATTTGCCAGAAAATTCAGGTGAGTGGATTGGCCAGACTATCTGGCAAG GATGAAAATTTTAGTTTAAAAATGTGTCATTTGCTGTATTGGCAATTCCT[C/
WI-198	218 C T ---	---	GAGGTCTTTCAGCAACATGGAAGCCCTACTGCTTCAACCCCGAGTCCCGGATCAAGTGTGGCAAC CATGATGGAACCTTGGCATGGTTTAGTACCCTGGACCAAGTAGTCATTCCTGACTTTTAAAA TCTAAACAGCCTTTGATGGGACAATCTCTGCTAAAGACTAACCACTTCTTATCTTATCTTACGCTA CCTGCTCCCTTTC[C/T]GTTTAAACAAGCATAGAATATCTGAACAAC
WI-205c	146 T C ---	---	TTTCATGGTCCCAAGACAGATTTTAAAGAAAGAAAATAGCCCTCATCTCCTAACTATGACTTGGTCGG AAGCCAAGAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGCTGACTTTTCAAT GCATGAGTTTGT[C/C]CAAGGCTTGATGGGAAAATCTCAACATTTGTTACCTAAGAAAGAGGATGT ATCTTACTTTGTTTAAAAAACTGCATATGCCCTTATTTTGTAGTTCCC
WI-205b	146 T C ---	---	TTTCATGGTCCCAAGACAGATTTTAAAGAAAGAAAATAGCCCTCATCTCCTAACTATGACTTGGTCGG AAGCCAAGAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGCTGACTTTTCAAT GCATGAGTTTGT[C/C]CAAGGCTTGATGGGAAAATCTCAACATTTGTTACCTAAGAAAGAGGATGT ATCTTACTTTGTTTAAAAAACTGCATATGCCCTTATTTTGTAGTTCCC
WI-234	165 G C ---	---	GAAGACTGAGTTTCCAGGAGTTGCAGCCGTTTCTCTCGGGCCATATGGCTAATAAGGAGCTTGAGCA GGGATTTCAACCTGTTTGCACCCCAAGTNCCTTCCAAGAGGTCTCAGACTACCTCTCCATCTCCCCCT CTCCCCACACACACAAAATACAGAGATTG/CJAATTCAGGAGCCAGTTTCTAGGTGGCTTTGAGC AATCATACACAGTAATCTCTTGGTGTCTTAGTTTCTCAAAATGGGAAATGG
WI-276b	25 A G ---	---	AGCTTTTGAATCCAAAACCCACATTA/GTCTTGACTCTCTTATCTCCTCTTGTGTAACTATCTCC CTGAGGCAGAAAATACAGAACACCTGTGGCTGCTGAACGGAGGAGGATGGGGCGGGGAGACAT CGGTCAATGTATCAAGCATCTCTCTGCTGAAAGACCTCTCTCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTGTCTTATCTCTCTGCTATCTCTGATGACTGGGCAAA

WI-276	25 A G ---	---	AGCTTTTGAATCCAAACCACATG/GJCTTGACTCTCTTATCCTCCTCTGTTGTAACTATCTATCC CTGAGGCAGAAATACAGAACCCCTGTGGCTGCCTGAACGGAGGAGGATGGGGCGGGGAGACAT CGGTCAATGTATCAAGCATCTCTCTGCCTGAAAGACCCTCTCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTTGCTTATCCTCTCTGCTATCCCTGATGACTGGGCAAA
WI-427	59 G A ---	---	TTTTCCCAATCCACAGTAAACTAATAATGGATATAGAAATTTAGAACTACTTCC[G/A]GTTT TTTCCCTGGGAAATATTCACAAACATTTGGTCTGCAATCAGGTTAAAGACATAGTGTGCCA TTTGTCATCAGACAGGTAGAGCCCTGACTCTGGCAGGATTAGTACCAGTGTGAGACTTTATGT ATTCATTATTAGAGCCAGGTCTTGCTCTGTCAACCCAGCTTTCAGTGCAGT
WI-562c	106 T C ---	---	CTCTTCACTCCCAACACTATATTGCTTACTTAATGGTTACAGATTAAAGCCAGAAAGGAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTTAAAT/CJAAATGGTCCTTTATTTAAAAAAA AAAGNTATCTAAAGAGAAACCATAATAATCTCTCAGGTAATTTATGGCCACAGCCAAACCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-562b	106 T C ---	---	CTCTTCACTCCCAACACTATATTGCTTACTTAATGGTTACAGATTAAAGCCAGAAAGGAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTTAAAT/CJAAATGGTCCTTTATTTAAAAAAA AAAGNTATCTAAAGAGAAACCATAATAATCTCTCAGGTAATTTATGGCCACAGCCAAACCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-562	103 T C ---	---	CTCTTCACTCCCAACACTATATTGCTTACTTAATGGTTACAGATTAAAGCCAGAAAGGAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTTAAAT/CJAAATGGTCCTTTATTTAAAAAAA AAAGNTATCTAAAGAGAAACCATAATAATCTCTCAGGTAATTTATGGCCACAGCCAAACCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-597c	141 A G ---	---	GTGTAATTTGGTGGCTTGCAACTTTCCACAGTAACCTTTAGAATNTNAAAGGTGGAAGGTAAGG ATGAGGAAGAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATTCT GATACATG/A/GJTAATGACCCCTCCATGACTCTGGTACCTCATCTACCAATGTGAGAAATTATTAAC TTGATCTAATAATCTTCAAACTAATATACCTGAGAGAAATAAGTCTATTTAAT
WI-597b	141 A G ---	---	GTGTAATTTGGTGGCTTGCAACTTTCCACAGTAACCTTTAGAATNTNAAAGGTGGAAGGTAAGG ATGAGGAAGAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATTCT GATACATG/A/GJTAATGACCCCTCCATGACTCTGGTACCTCATCTACCAATGTGAGAAATTATTAAC TTGATCTAATAATCTTCAAACTAATATACCTGAGAGAAATAAGTCTATTTAAT
WI-597	136 A G ---	---	GTGTAATTTGGTGGCTTGCAACTTTCCACAGTAACCTTTAGAATNTNAAAGGTGGAAGGTAAGG ATGAGGAAGAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATTCT GAT/A/GJCATGATAATGACCCCTCCATGACTCTGGTACCTCATCTACCAATGTGAGAAATTATTAAC TTGATCTAATAATCTTCAAACTAATATACCTGAGAGAAATAAGTCTATTTAAT

WI-611	66 G C ---	---	TTCAAAATTAACACCATGGGTATATTAAATTTNGCTCTATCCATAGTTCTAACCCCTCTTCTCTG/ CJACAGTGAGACACCTGCCCTTCTATTGTCCTTGACGTATTACGTATTCGATCAGTCACCCATCTGGA ACCAAGGTTTCATTTCTGCTGACCCCTCCCTCCTCACCCTAGTTGGCTCTGACTTCTTCTTCTGCGCT GAACCTTCTCTGTGTGGCTGTCCGCTTCTCTGCTGCTGGCTTCCAAATAC
WI-681b	156 A G ---	---	TGAAGCCCTCTCTCTATACCCAAAGTGTCTTTATCTTAAATGCTGTGGTCAAGTATCTACCCCTTA GGGATATTGTGAGAAATCAATAAGTTTCATACAGGGGAAGCACCTTTGNCCTGGTATGTACATAAGCAA TCCATAATTGTTATAGCTATTJAGJTTATACATATGGCACCATTGGGACACAGATTATATATGTCAGA CACCACGNATGTCCTTTAAGATATGCAGCAAGCACAAATCTGTCAATGGTTT
WI-681	156 A G ---	---	TGAAGCCCTCTCTCTATACCCAAAGTGTCTTTATCTTAAATGCTGTGGTCAAGTATCTACCCCTTA GGGATATTGTGAGAAATCAATAAGTTTCATACAGGGGAAGCACCTTTGNCCTGGTATGTACATAAGCAA TCCATAATTGTTATAGCTATTJAGJTTATACATATGGCACCATTGGGACACAGATTATATATGTCAGA CACCACGNATGTCCTTTAAGATATGCAGCAAGCACAAATCTGTCAATGGTTT
WI-867b	119 G A ---	---	AATCTTAACAGCCCTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCTCCAAAGGCTCCCAAGTATCTGGCACATCTTCCCTTTTCATCTCCGJAJTTGTGTGTTTGGC CAAATAATATCTCCCCAGGGACGTCTCTTTCTAATCCCTGAAACCTGAGAAAATGTTATCTTATGCG AGTGCTATGGTTTGAATGTGTCCTCCCAAGCACACATTAGAAACTTA
WI-867	113 A G ---	---	AATCTTAACAGCCCTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCTCCAAAGGCTCCCAAGTATCTGGCACATCTTCCCTTTTCATCTCCGJAJTTGTGTGTTTGGC CAAATAATATCTCCCCAGGGACGTCTCTTTCTAATCCCTGAAACCTGAGAAAATGTTATCTTATGCG AGTGCTATGGTTTGAATGTGTCCTCCCAAGCACACATTAGAAACTTA
WI-867	119 G A ---	---	AATCTTAACAGCCCTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCTCCAAAGGCTCCCAAGTATCTGGCACATCTTCCCTTTTCATCTCCGJAJTTGTGTGTTTGGC CAAATAATATCTCCCCAGGGACGTCTCTTTCTAATCCCTGAAACCTGAGAAAATGTTATCTTATGCG AGTGCTATGGTTTGAATGTGTCCTCCCAAGCACACATTAGAAACTTA
WI-871b	123 C G ---	---	TCATCAGACCTGAGATTCAGCATGAAATCTACCAAAGGTACCACAAATGTAACTTGTCCAAAACGA ATCTCAGTTTCTGCATATGTAAATGGGAATGATAAGAGCACCCACCTACCTCATG[C/G]AACTGTT GAGAGAAATAATGAGACATTGTAAGTAAAGTTTGTAAATGCACCTGTTATGGCTGAAATTGTGTACCC TAAATTCATATGTTGAAGCCCTAACACCCCAATATGNCCTGTTATTTGTACATAA
WI-871	123 C G ---	---	TCATCAGACCTGAGATTCAGCATGAAATCTACCAAAGGTACCACAAATGTAACTTGTCCAAAACGA ATCTCAGTTTCTGCATATGTAAATGGGAATGATAAGAGCACCCACCTACCTCATG[C/G]AACTGTT GAGAGAAATAATGAGACATTGTAAGTAAAGTTTGTAAATGCACCTGTTATGGCTGAAATTGTGTACCC TAAATTCATATGTTGAAGCCCTAACACCCCAATATGNCCTGTTATTTGTACATAA

WI-884	198	T C ---	---	AGGTTCTGGACTTGATGCTGGGAAACAATTTGGTNGTGGAGAAATTCCTATTTTGAGTNTTTCACAGAT CAGTAGAGCCAAATGGGAAAGTATCCTAGTCCATCCCTTTATTAGGAACCTTTCCTGATCTATTGGGA ACTTCTCTCTAATAGATCAGGAAATCCACCTCATTTAATCATGGACAACNNAAGGAATA[T/C]G ATCCCGCATGCAACATTTTATTCAGTGAACATGATGAAATGAACATAAT
WI-921b	205	G A ---	---	CACATCCCAAGGGCTCTGGGGGANGAGCGGTGGGACGCTGCCGGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGCAGGGGCTCTGCTCTGAAGCCGACACTGCCAGGTGCACACAGGGACAGTTATACTGG CAGTGATGCCTCTCAGCCTGGCCCCCAAGAAAGTCTNGCCAGGAAAAAGCAGCATCCATCTAC TCT[G/A]GGGAGAGATCTGACAAATTTAATCAGGAGGAAGAAATTCCTCCGAG
WI-921	205	G A ---	---	CACATCCCAAGGGCTCTGGGGGANGAGCGGTGGGACGCTGCCGGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGCAGGGGCTCTGCTCTGAAGCCGACACTGCCAGGTGCACACAGGGACAGTTATACTGG CAGTGATGCCTCTCAGCCTGGCCCCCAAGAAAGTCTNGCCAGGAAAAAGCAGCATCCATCTAC TCT[G/A]GGGAGAGATCTGACAAATTTAATCAGGAGGAAGAAATTCCTCCGAG
WI-945c	90	G C ---	---	GGCTGGGATGAGAGGTTCTACTTGTGTTACTGGAGGTTTCACTGGCTTGTGCTAGAACTAGNAAAGNA GAAAGACACAGNGATTGGCTAAC[G/C]CATGGCAGTAGTGGCCCCCAAGGCCTGAGTAATAAGAAA AAATCATTAGATAAATGCTCATGACCAAAACAAGTTCAACANTAGGTGCAGCACANNNNGGTT TTCTCTGGTCATAGAAATCTCTTAAAGGGAAATCATGACAGATTTCTTGGCTTTA
WI-945b	90	G C ---	---	GGCTGGGATGAGAGGTTCTACTTGTGTTACTGGAGGTTTCACTGGCTTGTGCTAGAACTAGNAAAGNA GAAAGACACAGNGATTGGCTAAC[G/C]CATGGCAGTAGTGGCCCCCAAGGCCTGAGTAATAAGAAA AAATCATTAGATAAATGCTCATGACCAAAACAAGTTCAACANTAGGTGCAGCACANNNNGGTT TTCTCTGGTCATAGAAATCTCTTAAAGGGAAATCATGACAGATTTCTTGGCTTTA
WI-960b	167	C T ---	---	TTGCTTCAAGAAGTTCTTGTCTCAGGAAGTTATTCATTTCAGCAACCTAAATTTGTTTGTAGTACAT ATCAAGCACAGGGTTCTGAGCAATGTCTTAGGAAGACCATAAAGGTGAATAAATGAGTGTCTTCTACC CTGAGGAATTTATCAAGATGTTAAGTTATCT[C/T]CTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-960a	155	G A ---	---	TTGCTTCAAGAAGTTCTTGTCTCAGGAAGTTATTCATTTCAGCAACCTAAATTTGTTTGTAGTACAT ATCAAGCACAGGGTTCTGAGCAATGTCTTAGGAAGACCATAAAGGTGAATAAATGAGTGTCTTCTACC CTGAGGAATTTATCAAGATG/AJTAAAGTTATCTCCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-1121	181	T C ---	---	TCCCAGTGAATGGCTTTCAGTAGTTTATTATGATGCGCTAGGTACATTTGTTTTATTGTTCTG CGAATTGTTGATTACTTTGGGAGAAATGCICAACATAAATATGCTCTGACCCCTTTCTGTGTTTC CTTCTTAAGATACAAAATAAATGTAAACATTAGACCTCTCAGTA[T/C]GCTGTTTTTACTCTCCTCTG ATTTTTTTCCATTATTTTATGCTCIGGCTTCATTTTGTAATNG

WI-1147b	204 GA ---	---	TTTGCCATTATTTGAAGATAACCCACAOCTTGGTGCCAGGGTTTTCACAGGATTAGTGGTCAGTCA CATAGGCATATAGTACCTGATGCTCTATCCAGCCACGCAACTTCTCCTCCTCCTGCTGGCTC CTGAGCCAAAACAGGCATTTACCATAAATCACTTTGTAGGATGAACCTATCTGGCCAAACTGATA CIGAGCATGACCCACAGCCTCAGGTATATAAAACACTCTCATCAGGCAGA
WI-1158b	147 CT ---	---	GCATTGAGGGTTCGTTTAAATGACATTCACTGAGGCCCTGCTATGTCAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAATGAAAAACAATGATGGTCTCCTGAGTGTCTGAATCGCCAGGTGGC TAAGTGTGGGG[C/T]CTGGGGTCAGGCTGCCCTGGGTGCACATCCTGGCTCCAAACTGCTTTGCTATG GCT
WI-1158a	124 CG ---	---	GCATTGAGGGTTCGTTTAAATGACATTCACTGAGGCCCTGCTATGTCAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAATGAAAAACAATGATGGTCTCCTGAGTGTCTGAATG[C/G]GCCAGGT GGCTAAGTGTGGGGCTCTGGGGTCAGGCTGCCCTGGGTGCACATCCTGGCTCCAAACTGCTTTGCTATG GCT
WI-1304	124 TC ---	---	AAGTTTACAGAAAAAATACCAGAAAAAGTGACTTCAAGANTCAGCTGAGATAGAAACATATGCCCA TCATCTTCAANGTCCACAGACACTTATCCCTAGACAGCCATTCTTTTGAATGNT[C/G]NCANT AAAAATGATTGAAATTGGGAATAAGGCCCTCCCTCTAATGATTGACAGTGTAGACCTTGCCTAG G[C]
WI-1305d	202 CT ---	---	TTCTCAATCCAACTGCTGTGTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCAATTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTAAANTGNNATATG[C /T]AGGGCGANGTAATANGTATACAGNGANTCATACAGCCCTGCCTACCA
WI-1305c	46 CT ---	---	TTCTCAATTCCAAATCTGTGTGTACTTTTATTTCTTTCTTCCATT[C/T]ATGTTGGTAAATATAAAG ATGATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCAATTTNCAGAAAGATAAGGTTTTCCTC ACATCCACTGCTTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTAAANTGNNATA TGCAGGGCGANGTAATANGTATACAGNGANTCATACAGCCCTGCCTACCA
WI-1305b	153 TC ---	---	TTCTCAATTCCAAATCTGTGTGTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCAATTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTTCANTAAAT[C/T]NACTCCACTNATGCTNACAAAATNACACTGTTTAAANTGNNATA TGCAGGGCGANGTAATANGTATACAGNGANTCATACAGCCCTGCCTACCA
WI-1305	202 CT ---	---	TTCTCAATTCCAAATCTGTGTGTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCAATTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTAAANTGNNATATG[C /T]AGGGCGANGTAATANGTATACAGNGANTCATACAGCCCTGCCTACCA

WI-1306b	248 A G ---	---	TTCTGCATTGGAATAGTTGACTTCTATGAGNNGCAATAAATGGACAATCTTGNGNNNTNG GGCTGGGTGACTGTCCTGGTCAATTTAGAGCCATAGAGTGAAGTAGCCTGCAATAAAGAGGA AAGTGAAGCTAATCTGAAGCTGACCTAAGGNGAGAGTGCCCTNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGCCAGTTGAAATTTATCTTCTT[A/G]G[C]
WI-1306	240 A G ---	---	TTCTGCATTGGAATAGTTGACTTCTATGAGNNGCAATAAATGGACAATCTTGNGNNNTNG GGCTGGGTGACTGTCCTGGTCAATTTAGAGCCATAGAGTGAAGTAGCCTGCAATAAAGAGGA AAGTGAAGCTAATCTGAAGCTGACCTAAGGNGAGAGTGCCCTNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGCCAGTTGAAATTT[A/G]TCTTCTAGC
WI-1307b	118 T C ---	---	GACAAGGCTGGTACTAGTTTCCAATTCCTCAATCTATGTACACTTCTCCTCACTTTCTCAAGTGGACA GATTTTCTGCATTACTGCTGGGTTGGGGAGCAGTGGTGTAGGCAAT/CJGTGAGATTGCTTT CCTACCTCTTAATGTATCTTNCATTAATATGCTAAACCGGTACTGTGATCTATCACTGGTT TCCTTTGGTGTGTTGTTGCTGTTGTTTCTCCTGTAAAGNTGTTT
WI-1307	118 T C ---	---	GACAAGGCTGGTACTAGTTTCCAATTCCTCAATCTATGTACACTTCTCCTCACTTTCTCAAGTGGACA GATTTTCTGCATTACTGCTGGGTTGGGGAGCAGTGGTGTAGGCAAT/CJGTGAGATTGCTTT CCTACCTCTTAATGTATCTTNCATTAATATGCTAAACCGGTACTGTGATCTATCACTGGTT TCCTTTGGTGTGTTGTTGCTGTTGTTTCTCCTGTAAAGNTGTTT
WI-1325b	169 T C ---	---	GAGAGATGGCCAAAGACAAAGCAGAGGGAGAGAGAGCAACCTCTGTGGTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCATTAGGCAACTACAATGTGCTTGTCTCTCT/CJACCTCAGAACTTCTTGAGGGGCAGGC ATTATGATTCCCACTTACATCAGTGGGAATTTGGACTTGGTGAAGTTAGGTT
WI-1325	165 C T ---	---	GAGAGATGGCCAAAGACAAAGCAGAGGGAGAGAGAGCAACCTCTGTGGTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCATTAGGCAACTACAATGTGCTTGTCTCTCT/CJACCTCAGAACTTCTTGAGGGGCAGGC ATTATGATTCCCACTTACATCAGTGGGAATTTGGACTTGGTGAAGTTAGGTT
WI-1327b	162 T C ---	---	CTACGATAATTAGGTTGGCAGTGAGGGTATTAAAGCTGTGTAGTGCAGAAAGTCTGTTATTGTAAA ACACCAAGTGGGTTTAAATGGAATGCGTATGTGTAGTNCATATTCAGGACAGGCTGGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTG/CJGAAGTTGGGTAGTACCAGGCCTCCCCAAATGTAGT TCTTGNGCTGAAAGTCTCTCTTACTGAAGAGGCAATGGTTCATCTCTAAG
WI-1327	175 C G ---	---	CTACGATAATTAGGTTGGCAGTGAGGGTATTAAAGCTGTGTAGTGCAGAAAGTCTGTTATTGTAAA ACACCAAGTGGGTTTAAATGGAATGCGTATGTGTAGTNCATATTCAGGACAGGCTGGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTGTGAAGTTGGGTAGT/CJGTACCAGGCCTCCCCAAATGTAGT TCTTGNGCTGAAAGTCTCTCTTACTGAAGAGGCAATGGTTCATCTCTAAG

WI-1341b	136 G A ---	---	---	TATCAGCATGATTGGCTGTTGGACACAAAGTCAATTTGTACTTTGNTGCNNNTCCCTTTTCNTTT ACCTGATCCACTATCTTCTCAAGATCANGTTCAAAATTTGGCTTCTTGTNAATATACCCAAGC [G]AGGATTGTGATGGATCTGTTTATTTCTGTGCTTGAACAGCAGAGTCTCTGNGAGTNG GTTTCAGGATTGTCTCTGTTTCCCGAGCCACTTGCACATTAGCAAGTGT
WI-1349e	192 G C ---	---	---	CTGACAAATGTCTATCTCACTCTCTAAACCCACAGGTCTAGAAATCAGTTAGTACCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCAGGTGGTAGGTGCTGGCCTGTCAGTTTGATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTCTGAATTTCCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAAAATATGATAGAAATTTGTGAAGTACTAGATTTTCAGAAAAATA
WI-1349d	264 C A ---	---	---	CTGACAAATGTCTATCTCACTCTCTAAACCCACAGGTCTAGAAATCAGTTAGTACCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCAGGTGGTAGGTGCTGGCCTGTCAGTTTGATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTCTGAATTTCCATCTCTGAGTTCAAAATA ATTGAGAAAAATATGATAGAAATTTGTGAAGTACTAGATTTTCAGAAAAATATGAT
WI-1349c	192 G C ---	---	---	CTGACAAATGTCTATCTCACTCTCTAAACCCACAGGTCTAGAAATCAGTTAGTACCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCAGGTGGTAGGTGCTGGCCTGTCAGTTTGATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTCTGAATTTCCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAAAATATGATAGAAATTTGTGAAGTACTAGATTTTCAGAAAAATA
WI-1349b	264 C A ---	---	---	CTGACAAATGTCTATCTCACTCTCTAAACCCACAGGTCTAGAAATCAGTTAGTACCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCAGGTGGTAGGTGCTGGCCTGTCAGTTTGATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTCTGAATTTCCATCTCTGAGTTCAAAATA ATTGAGAAAAATATGATAGAAATTTGTGAAGTACTAGATTTTCAGAAAAATATGAT
WI-1349	264 C A ---	---	---	CTGACAAATGTCTATCTCACTCTCTAAACCCACAGGTCTAGAAATCAGTTAGTACCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCAGGTGGTAGGTGCTGGCCTGTCAGTTTGATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTCTGAATTTCCATCTCTGAGTTCAAAATA ATTGAGAAAAATATGATAGAAATTTGTGAAGTACTAGATTTTCAGAAAAATATGAT
WI-1403b	57 C T ---	---	---	TGGTATTTGGAATGGGTTCCAGACTCCGGTTCTGGCTCTGACCTTTGGTAAGTTG[C/TT]CCGAAT GCCACTTTATAAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAAATACGT AAAGTTTACATCAACATAATTTGCCCTGCATCATGCAATTTGGCAATATGTCACATAGCTGTCCTCA TAATCCCCAAAGTGCCAAAAAGGGTTGTATCTGATTTGT
WI-1403	58 T C ---	---	---	TGGTATTTGGAATGGGTTCCAGACTCCGGTTCTGGCTCTGACCTTTGGTAAGTTG[C/TT]CCGA TGCCACTTTATAAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAAATACG TAAAGTTTACATCAACATAATTTGCCCTGCATCATGCAATTTGGCAATATGTCACATAGCTGTCCTC ATAATCCCCAAAGTGCCAAAAAGGGTTGTATCTGATTTGT

WI-1417c	31 C T ---	---	CAGCCGGAAGAGATTACGTGAGAGATGTC/TJTGCCAGGGCGGAGATGTGAGCCACGGG GGTGACAGCATGCCCTGCTGGCATTGAGGGCCOCAGAAAGGAATCCAGTGGCCCTCTCAATGACTTG GGGTCTCGACTTCGGAAGTTTAAGGGCTCGGCTTCAAAAAGCTGGTCCGGTTTGAGCGGTTGC AGGCGAGGCCCTTAGGTCGGTATTATGTTTGTGTAAGAAAGTCGC
WI-1417b	31 C T ---	---	CAGCCGGAAGAGATTACGTGAGAGATGTC/TJTGCCAGGGCGGAGATGTGAGCCACGGG GGTGACAGCATGCCCTGCTGGCATTGAGGGCCOCAGAAAGGAATCCAGTGGCCCTCTCAATGACTTG GGGTCTCGACTTCGGAAGTTTAAGGGCTCGGCTTCAAAAAGCTGGTCCGGTTTGAGCGGTTGC AGGCGAGGCCCTTAGGTCGGTATTATGTTTGTGTAAGAAAGTCGC
WI-1729	172 A ---	---	CCATGAGCAACAGCATGTTCTACTCTGTGATGTATGTTAGGGGCGATGATATCTGATTTCTT TTTTATTCTCTCCAAAAGAAATTTTCAATTATGCAAAACATTATCAGGCAATGCAGCTCGTAATAAGA TGTGGAGAACTGAAAAGAGAGCTTACATGCACCCCAATAGCAAACTCTCCACACATTTCCAGCA GATGATGTGTCCTCCGTGGTNACTTCTCTCCACCACATCACTGTGTTTT
WI-1732b	122 T C ---	---	TGCCTACTTCTTGTTCATTCACCACCATACATTTGTAAATTGGAACCTCTAGGAGGTTAGAAGGA TATGCTGATCAAAAAAGGGACATATTCAGGAGTNTCCCTGGGTCAACCCCTTTTCAATCAGTCT CTGCCACATGTCTAGTAACGTGTAGTGATGGTGCATCAGTATAATCCTGAGCCTCCCAAGGTACAGC CTTCACTACTATTCAATCATATGGCTAAGGTATTCATCATATTTGGCTAAG
WI-1732	114 C T ---	---	TGCCTACTTCTTGTTCATTCACCACCATACATTTGTAAATTGGAACCTCTAGGAGGTTAGAAGGA TATGCTGATCAAAAAAGGGACATATTCAGGAGTNTCCCTGGGTCAACCCCTTTTCAATCAGTCT CTGCCACATGTCTAGTAACGTGTAGTGATGGTGCATCAGTATAATCCTGAGCCTCCCAAGGTACAGC CTTCACTACTATTCAATCATATGGCTAAGGTATTCATCATATTTGGCTAAG
WI-1750	97 A G ---	---	GCGAATTTAATGACTCCAAAAGGTAGTAATTCCTTCCCCCAAAAAGGTTTAAATCTGTGTGGA CATAATGTTTGAATTTGCAGTTCACCTTGGAG/GJTTAAGGTGTGCTGTTTCTGGCAAGAGTCAG TGGGAGTGTCCGGGAAAAGGGCTAAAGTCTTTGTAGTCAAGCAAAACCGGCTTGCACTCCTGACTGAG CTACATTCACTTTATGATCTCCAGCAGGTTCTTCCA
WI-1780	31 A G ---	---	GGTACACAAAGAAATGCTTCTGGAAATCTAC/GJTAGCGCCTTAACATTTGGCTGAGTATTAATC TGTACATGTGTATGTGAACCCACCATGAAGCTGGGCAAGAAACAAATCTTAGGAAAAGTACAATTAC TGGGAACTGTAGAACAATAATCTCATAGTTTACACATAGCTGGGAATCACTCATGTTCCCATCA ACTGGAGAGACCTTGTGAGTACAGAGGACATTCAAGAAATAATCAATAAAAAAT
WI-1803c	77 A G ---	---	CCACTCAGTAATAATAGTGTGGAGATAAGTATATGTTAGGCACATAATAATTTTTCAGGCAGAA CCATTATGAT/GJAGTAGGGTAGAGCATCACACTTGGGAGGACATATTCGGAGTNAATATCCTG GGTGCTAATTTCAAATATATCTACTAAAGCATGACTTCTAGAAAATTAATTAATCTTGTCTCTCAA GGAAATGGGAATACCTATAATACAGTCTTATTGAGGAAAATAACTGGAATCA

WI-1803b	77 A G ---			CCACTCAGTAATAAGTGTGGAGATAAGTATATGGTAGGCACATAATAATATTTTCAGGCAGAA CCATTATGATAGTAGGTAGGTAGAGCATCACACTGGGAGGACATATCTGGAGTNAGATATCCTG GGTGCTAAATTTCAAATATATCTACTAAAGCATGACTTCTAGAAAATACATTACTCTTGCTCCTCAA GGAATGGGAATACCTATAATACAGTCTTATTGAGGAAAATAACTGGAATCA
WI-1837b	112 C T ---			TTTACTTGGGATTTTTCATAGCTGATCATAAATTTACCAATTTGATAATTCACCTCTTTTCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGAAATAGACCCGTTTATAC/C/TTCGTGCCAGTTTATTTTT AAGGTTTTTTTTCATTGCACCTGATGCCAAAACAAACCTCAAAAGACCTTGAGTGAATTTTGAGCT CGTGAACAACCTGGGAAGTCTGGGGAACGTTTTCAGCTTCTGCTGGCT
WI-1837	112 C T ---			TTTACTTGGGATTTTTCATAGCTGATCATAAATTTACCAATTTGATAATTCACCTCTTTTCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGAAATAGACCCGTTTATAC/C/TTCGTGCCAGTTTATTTTT AAGGTTTTTTTTCATTGCACCTGATGCCAAAACAAACCTCAAAAGACCTTGAGTGAATTTTGAGCT CGTGAACAACCTGGGAAGTCTGGGGAACGTTTTCAGCTTCTGCTGGCT
WI-1840b	79 G T ---			TCACCTAGGGAGGTCGCTAAAAATGTAGCTTCATTAAAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCAC/TG/TGAGAACTCTGAATATTCAGCACATACAAGTGTGACAACCACTTGTTTAGTAT ATTTATCTCCAGAGTGTTTTGAATTTACTAAAAAGTTCTTAAAGAGCCATGAAGAATTATAAGACT ATCGCA
WI-1840	79 G T ---			TCACCTAGGGAGGTCGCTAAAAATGTAGCTTCATTAAAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCAC/TG/TGAGAACTCTGAATATTCAGCACATACAAGTGTGACAACCACTTGTTTAGTAT ATTTATCTCCAGAGTGTTTTGAATTTACTAAAAAGTTCTTAAAGAGCCATGAAGAATTATAAGACT ATCGCA
WI-1879b	110 C T ---			GGGCTCACTTTTCATCAGAGCACATATCACGTGATAGTGTCTCTCTTTTCATAACTACTCCCGG CACTGTAGGNTTTCTTTGAGGTAAAGGACCTGCCNTTTTAC/C/TGCTGCNAAATAAACTCCCAAAA AAGTGGTTAGTCCACAGGGTTTAAATAGTCTTGTGAATGAATTTCTGTGCGACCCCTGTGCCTTCT CAAGAAAAAATAAATGAAAAATCTCCACAGAGCCCTTTACCCACT
WI-1879	110 C T ---			GGGCTCACTTTTCATCAGAGCACATATCACGTGATAGTGTCTCTCTTTTCATAACTACTCCCGG CACTGTAGGNTTTCTTTGAGGTAAAGGACCTGCCNTTTTAC/C/TGCTGCNAAATAAACTCCCAAAA AAGTGGTTAGTCCACAGGGTTTAAATAGTCTTGTGAATGAATTTCTGTGCGACCCCTGTGCCTTCT CAAGAAAAAATAAATGAAAAATCTCCACAGAGCCCTTTACCCACT
WI-1900b	119 C T ---			TGTTCTCTGCTCCAGGCACCGGCTAAGTCTTGTCTGCATAATGAATAATCAACTGGACAACCCNG CTNAGGTAGGNTACCTNGGCAATTAGCCCCATCTTACAGCTGCAAAAGAGG/C/TGCTCTGAGAGGT AAAGTCCCTGCCCAACGCGCACAACTAGAGAGCAGCAACAGGTGTTTGAACCCAGCTCTGCT GACTTCAGATCTGTGCTTAAGTGCATGAGAAACCACTTTCTTTGCTCC

WI-1900	119	C T	---	---	TGTTCTCTGGTCCAGGCACCGGGTAAGTCTTGCTGCATAATGGAATAATCAACTGGACACACCCNG CTNAGGTAGNTACCTNGGCAATTAGCCCATCTTACAGCTGCAAAAGAGG[C/T]GCTCTGAGAGGT AAAGTGCCTGCCCAACCGGCACAACTAGAGAGCAGCCAAACAGGTGTTGAACCCAGCTCTGCCT GACTTCAGATCTGTGCTTAACCTGCCATGAGAAACCACTTTCTTTGCTCC
WI-1943c	165	C T	---	---	ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTCAGAGTCAAGC AGCAAGCCAAATGGTAGGAAAGACCAGCC[C/T]CTCTGAANCTGGTCCCACGTGGAGATAGTGAA TACAGGGCACCGNTGAGCATTCCAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1943b	165	C T	---	---	ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTCAGAGTCAAGC AGCAAGCCAAATGGTAGGAAAGACCAGCC[C/T]CTCTGAANCTGGTCCCACGTGGAGATAGTGAA TACAGGGCACCGNTGAGCATTCCAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1943	164	C T	---	---	ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTCAGAGTCAAGC AGCAAGCCAAATGGTAGGAAAGACCAGCC[C/T]CTCTGAANCTGGTCCCACGTGGAGATAGTGAA TACAGGGCACCGNTGAGCATTCCAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1960c	270	A T	---	---	CCAGGTGAGGCTGAAAGAAGGAAGGAGGCAATTGCTGTTGGAGTGAGGGATTCTGGAGAAGCACCCCT GCAGAGCTTCATTCTGTTTTCAAAAGTGTGCCATGCANGGTCNTCTGGGTTGTGAGCTCATNGCTGAG TTATCACAGCTCCTGATGACAGATCATGAAAAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGTCTGAAAACTTAAAAATGCACCTCCCAACTTT
WI-1960b	270	A T	---	---	CCAGGTGAGGCTGAAAGAAGGAAGGAGGCAATTGCTGTTGGAGTGAGGGATTCTGGAGAAGCACCCCT GCAGAGCTTCATTCTGTTTTCAAAAGTGTGCCATGCANGGTCNTCTGGGTTGTGAGCTCATNGCTGAG TTATCACAGCTCCTGATGACAGATCATGAAAAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGTCTGAAAACTTAAAAATGCACCTCCCAACTTT
WI-1977	203	T C	---	---	CTGATGCCAAGTGCAGCTTAGAGTNAGGAATCCAGAGAAAGTNTTGGATCTGGTAAGTAGGAGTCA TTCTGGGCATTCTCATAGAGTNTGTTTTTAGTCTCGTAATAACTGTTGGCCCTAGGAAGGTTGTT TTCTCTACTGGCTGTGAAAGCCTTTCCCATCGAGTGATACAGTACTTTCAGATTATGGAGATTTT /CTAACAAATCAACACTGGCTGAGGCTGTTGG
WI-2012	102	T C	---	---	AAATCTAGAAGCCAGAGTCAGCTCACGATTATAAAGTTGAAGTAATGCATTGTAGTTTCATGT TTTCTCTTAATTCTGCACAAACTAGCTAAAAATC[T/C]TTTAAATCAGTTACCAGAGGCAATACCT GGGTTAATGTAAGCACTCAAAAGTTATGTAGAGTAGTGTCTCTGAGTCACTTTTTTCTACTCTCATT GGCTTCAACCAATGCTTCCACTGGATC

WI-2013	127 C T	CTTTAGAGGTGGTCATTCGGTCCCTTCGGAAAGTGATTCGGTGTAAAGAAAAATAGATGCAACG TTGCTAAGTACACCTAACATTTAAACAGTCTCCAGCAGATAAATGCTGATACGACTTC/TCTCA CCAGAAAAAGAGAAATACCCATCATGAGGAAGAGAAATGACTTTTGTTCAGTTATGCTCCCGGGTCC CCTTCACTGGAGGATATCTACGCTTCAGCCCTGAGCCCTGGTTACTGCAATCC
WI-2032c	166 G A	ACCAGACATCCCATCAGGAGTTAGTCCCTCTGGCAAGCCAGCCCTGCCCCTCTGATTTCCCAAAAACC TCAATTTTCTTNACITACTATAATTTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACC ACATCACCCAACTGGTTTCTAGATGTACACG/AJTGTTGGACCTCTGTCTCAACCTCCGACTTTTCAC AGATCATTTGGTTAGGCTCACCTTCCCTGTAATTGCTTCTGTTTTTCAAAAGGG
WI-2032b	219 C G	ACCAGACATCCCATCAGGAGTTAGTCCCTCTGGCAAGCCAGCCCTGCCCCTCTGATTTCCCAAAAACC TCAATTTTCTTNACITACTATAATTTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACC ACATCACCCAACTGGTTTCTAGATGTACACG/TGGGACCTCTGTCTCAACCTCCGACTTTTCACAGA TCATTGGTTAGGCTCA/C/GCTTCTCTGTAATTGCTTCTGTTTTTCAAAAGGG
WI-2032	219 C G	ACCAGACATCCCATCAGGAGTTAGTCCCTCTGGCAAGCCAGCCCTGCCCCTCTGATTTCCCAAAAACC TCAATTTTCTTNACITACTATAATTTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACC ACATCACCCAACTGGTTTCTAGATGTACACG/TGGGACCTCTGTCTCAACCTCCGACTTTTCACAGA TCATTGGTTAGGCTCA/C/GCTTCTCTGTAATTGCTTCTGTTTTTCAAAAGGG
WI-2054b	188 C T	CGTTTCTTCTACATCTTGGGNNACATAAAGANGAAAGAGNAGCTGTCTTTTGTGGTAGTTTGTCT CAGAGCTGCCTAGAGCNAGGACAAGACAGGTGACCTTTCAAATACCTTACAGACTTAGGATTTGGA TTTTCATGGTGGTTGGCACAGCCAGGCTCAACAGAACTAATACCTGCT/C/GTTCTCTGCTCCAC CAGCCCTATCTTAGGCTCAAGGAGAAATTTTACTGGATGGGCTGTCTTT
WI-2054	183 T C	CGTTTCTTCTACATCTTGGGNNACATAAAGANGAAAGAGNAGCTGTCTTTTGTGGTAGTTTGTCT CAGAGCTGCCTAGAGCNAGGACAAGACAGGTGACCTTTCAAATACCTTACAGACTTAGGATTTGGA TTTTCATGGTGGTTGGCACAGCCAGGCTCAACAGAACTAATACCTGCT/C/GTTCTCTGCTCCAC CAGCCCTATCTTAGGCTCAAGGAGAAATTTTACTGGATGGGCTGTCTTT
WI-2573d	129 T C	TGGGATTAACCCCTGTTTCTTCTCCAGTTCAGTGTGCCCTTAATGTTGTGCTAGAAATTAACA TTAACAGCAGTAAAAATAGCTCTTAAATGCACTTGCCGTTCAAGGTGTTTCCGTGCTTT/CJ/GA TATCATCTGATCTTCCCAACCCAGGGCTTATTTATGCTAGGTAGGGGTAAAGCAACAGAGGCTGTGT GAAGTGAATGATTTGCTTGCACAAGGTCAATATGGCTGGGCTTGGACGAG
WI-2573c	165 A C	TGGGATTAACCCCTGTTTCTTCTCCAGTTCAGTGTGCCCTTAATGTTGTGCTAGAAATTAACA TTAACAGCAGTAAAAATAGCTCTTAAATGCACTTGCCGTTCAAGGTGTTTCCGTGCTTTTGTATAT CATCTGATCTTCCCAACCCAGGGCTTATTT/CJ/GCTAGGTAGGGGTAAAGCAACAGAGGCTGTG TGAAGTGAATGATTTGCTTGCACAAGGTCAATATGGCTGGGCTTGGACGAG

WI-2573d	129	T C ---				TGGGATTAACACCCCTGTTTCTCCCTCCAGTTCAGTGTGCCCTTAATGTTGTGCTAGAAATTAACA TTAACAGCAGTAATAATAGCTCTTAAATGCACCTTCCGTTTACAAAGGTGTTCCGTGCTT[C]/TGA TATCATCTGATCTTCCCAACCAGGGCTTATTATGCTAGTAAGGGTAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGACAAGGTCATATGGCTGGGCTTGGACGAG
WI-2573c	165	A C ---				TGGGATTAACACCCCTGTTTCTCCCTCCAGTTCAGTGTGCCCTTAATGTTGTGCTAGAAATTAACA TTAACAGCAGTAATAATAGCTCTTAAATGCACCTTCCGTTTACAAAGGTGTTCCGTGCTT[T]/GATAT CATCTGATCTTCCCAACCAGGGCTTATT[C]/TGCCTAGTAAGGGTAAGCAACAGAGGCTGTG TGAAGTGAATGATTGCTTGACAAGGTCATATGGCTGGGCTTGGACGAG
WI-2573b	165	A C ---				TGGGATTAACACCCCTGTTTCTCCCTCCAGTTCAGTGTGCCCTTAATGTTGTGCTAGAAATTAACA TTAACAGCAGTAATAATAGCTCTTAAATGCACCTTCCGTTTACAAAGGTGTTCCGTGCTT[T]/GATAT CATCTGATCTTCCCAACCAGGGCTTATT[C]/TGCCTAGTAAGGGTAAGCAACAGAGGCTGTG TGAAGTGAATGATTGCTTGACAAGGTCATATGGCTGGGCTTGGACGAG
WI-2573a	129	T C ---				TGGGATTAACACCCCTGTTTCTCCCTCCAGTTCAGTGTGCCCTTAATGTTGTGCTAGAAATTAACA TTAACAGCAGTAATAATAGCTCTTAAATGCACCTTCCGTTTACAAAGGTGTTCCGTGCTT[C]/TGA TATCATCTGATCTTCCCAACCAGGGCTTATTATGCTAGTAAGGGTAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGACAAGGTCATATGGCTGGGCTTGGACGAG
WI-2868b	60	A G ---				GACTTCATGCTCATGAACAAGCATTTGCTTAATTACAGACATTAAACAAGCTTTC[C]/G/CTC CCACTTCCCTCCCACTATCACTCAACCTCTTCATCCACTTTAAAGAGGTTCTTTAGGTCCTCTGCAT ATCATGGAAGCCAACTACTCTATTACGCTTTCCTCAATGATGCAGCCAGTTCGCTGCATACAGTTTGT CAGAAATGCTATATTATGGAACACAGCTGAAAAATGAAATATCGATATAC
WI-2868	60	A G ---				GACTTCATGCTCATGAACAAGCATTTGCTTAATTACAGACATTAAACAAGCTTTC[C]/G/CTC CCACTTCCCTCCCACTATCACTCAACCTCTTCATCCACTTTAAAGAGGTTCTTTAGGTCCTCTGCAT ATCATGGAAGCCAACTACTCTATTACGCTTTCCTCAATGATGCAGCCAGTTCGCTGCATACAGTTTGT CAGAAATGCTATATTATGGAACACAGCTGAAAAATGAAATATCGATATAC
WI-2870b	131	T C ---				CATGCTGTGTAACCTCTGTGCTGCTGCTGCTGCGGGGAAATTAGAGCAAGGAATTGTATAATCCTAGGC TTCAAGGAGCTTCTCATCTCATTTGAGGAGACAAAGATGAACATCAGGAATGACTGGATAATGA[T]/C/ AGAAATGAATAGAGCCCCATTTTAAATTATACAGAGCTTATGTCACACTTCCCTGCTGCCATCAG TGGGCTTTTACAAAGGAGGCTTT
WI-2870	131	T C ---				CATGCTGTGTAACCTCTGTGCTGCTGCTGCTGCGGGGAAATTAGAGCAAGGAATTGTATAATCCTAGGC TTCAAGGAGCTTCTCATCTCATTTGAGGAGACAAAGATGAACATCAGGAATGACTGGATAATGA[T]/C/ AGAAATGAATAGAGCCCCATTTTAAATTATACAGAGCTTATGTCACACTTCCCTGCTGCCATCAG TGGGCTTTTACAAAGGAGGCTTT

WI-2954c	49 T A ---	---	---	TTAGCACATATCTGTTGGGACTTAAGTGAGACAAGGCATAAAAAAT/AJ/CAGCACCTGGGGCA CAGAGGAGCTCTATGCATTNAAATCCTCATACCTACCCCTCCTCTCATTCATCAATGAGTCCTTTGAGT CCTTGGAAAGACTCTATCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA GAG
WI-2954b	41 A G ---	---	---	TTAGCACATATCTGTTGGGACTTAAGTGAGACAAGGC/AJ/AAAAAATCAGCACCTGGGGCA CAGAGGAGCTCTATGCATTNAAATCCTCATACCTACCCCTCCTCTCATTCATCAATGAGTCCTTTGAGT CCTTGGAAAGACTCTATCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA GAG
WI-2954a	38 G T ---	---	---	TTAGCACATATCTGTTGGGACTTAAGTGAGACAAGGCATAAAAAATCAGCACCTGGGGCA CAGAGGAGCTCTATGCATTNAAATCCTCATACCTACCCCTCCTCTCATTCATCAATGAGTCCTTTGAGT CCTTGGAAAGACTCTATCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA GAG
WI-2971b	62 T C ---	---	---	ATTACAAATCCTACCTAGCAACTGCTGACACTCCAGTTAGACTACCAGCATTTCTAAGAT/CJG CTGCCAGCACCAATAAGCTTTCTTTCAAAACAATTTGTGTAACCTCCTCCTCTTAATAAACCTAAC ATTTCCCTTTGTTCCCTGACATTCGAAGGCCACGCTGGTCTAGATGTATGCCAGATTGCAATCCT AGTTCTTTAATGTTATCTGAAGAAAACCTTTTACTTAGGATTGTCT
WI-2971	62 T C ---	---	---	ATTACAAATCCTACCTAGCAACTGCTGACACTCCAGTTAGACTACCAGCATTTCTAAGAT/CJG CTGCCAGCACCAATAAGCTTTCTTTCAAAACAATTTGTGTAACCTCCTCCTCTTAATAAACCTAAC ATTTCCCTTTGTTCCCTGACATTCGAAGGCCACGCTGGTCTAGATGTATGCCAGATTGCAATCCT AGTTCTTTAATGTTATCTGAAGAAAACCTTTTACTTAGGATTGTCT
WI-2995d	133 A T ---	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTNTATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAGGAGCTGGANTTTTTTTA /TJAAATCTTTCTTTCTGGTGTAAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGT
WI-2995c	151 G C ---	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTNTATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAGGAGCTGGANTTTTTTTA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
WI-2995d	133 A T ---	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTNTATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAGGAGCTGGANTTTTTTTA /TJAAATCTTTCTTTCTGGTGTAAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGT

WI-2995c	151 G C ---	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAGGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995d	133 A T ---	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAGGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995c	151 G C ---	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAGGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995b	151 G C ---	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAGGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995a	133 A T ---	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAGGAGCTGGANTTTTTTNA /JAAATCTTTCTTTCTGGTGGTTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAG GAATGAGACAGAACTAGCAGAAAGTGTT
WI-3147	85 C T ---	---	---	GTGGTGCAGTTTCATCCTCTGGAGCTCCCTGTGAGATCAGACTGGAGCCAGTCCAGCTTGAGACAC ATCTCAGTTAGCTCCTT[C/T]CCTGCCATATCCTGTGTTTCTTACTCCTATCTCCTGAGACTTCTCCT GAATGAATTACATGCACCTCAATCCCTGCCTCAGTCTGCTTTNAGGGAACITTGACCTAAGACAGAA ATCTTAGTACCAATACTTTGCAAGG
WI-3234b	68 T C ---	---	---	ATTCTGTAATGTTTTCAGTCTTCCAGTAAATTCITTTATTGAGGTCCATGTCCATTACCTCTACTTA T/C]GACAAGCAAGAACAAACAGAAAGCCCTCTGTTTGGCAATCTGGCCTCTTATAAATACTTTCTG TATATTTTAAACAAGTACTGTAGAGTNATGAATCATACATCCTTAATAAGCATATCAAAATTTTAC TCAGTAATTCAGAAGAAAGGACAAATGGAATGTACTTATTTTATATCTTAT
WI-3234	68 T C ---	---	---	ATTCTGTAATGTTTTCAGTCTTCCAGTAAATTCITTTATTGAGGTCCATGTCCATTACCTCTACTTA T/C]GACAAGCAAGAACAAACAGAAAGCCCTCTGTTTGGCAATCTGGCCTCTTATAAATACTTTCTG TATATTTTAAACAAGTACTGTAGAGTNATGAATCATACATCCTTAATAAGCATATCAAAATTTTAC TCAGTAATTCAGAAGAAAGGACAAATGGAATGTACTTATTTTATATCTTAT

WI-3292b	106 G A ---	---	---	GTITGCTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTTAGCTCTGCACTCATCC TCCCTGTCCCGTCCCAAGCCCTATGTTACTGGTATGCTGATGGATTGGATGGATGATTCTT GCCATGAATATTTCCATTGTTTCTCATTAAATGATTAATTAATTAAGTAAATATATTNCCATGA GACACAATGGAAAAATGGAACACATTCATGGAAAAAACCCATTCCAATC
WI-3292	106 G A ---	---	---	GTITGCTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTTAGCTCTGCACTCATCC TCCCTGTCCCGTCCCAAGCCCTATGTTACTGGTATGCTGATGGATTGGATGGATGATTCTT GCCATGAATATTTCCATTGTTTCTCATTAAATGATTAATTAATTAAGTAAATATATTNCCATGA GACACAATGGAAAAATGGAACACATTCATGGAAAAAACCCATTCCAATC
WI-3355	19 G C ---	---	---	CCATGAACCATGGGCTACA[G/C]ATATTCCTAAACITCAGAGTCCCTCTTACTGGAGAGGGATCCA CTTTTAAATATGATTTCTTGAAGTGGCTGCATATACTTCCCTCCAAGCACCTTAAACATCATCAGAA AAAAAATCATCAAAAAGTCGAAGTTAGTTTNAATTACCTTCACCTTTTCAATGGAAAACTTTATAA ACTGTGGATCAATTTATATTACTTTTGGATCAGTTTAGATGACTTTNAGTTG
WI-3408	194 G A ---	---	---	CCATGAAGAATGAGTTCCCTCCCTCCCTGGTCACTGCTAAGAAATAGCACACCCCTTGAGAAATTNACT TAGCACGTGGCATTGTAATGGCTGGATTCTCCGCTCTAAGACACACCTTTATGCTTTTCAAGCTTT CTGGAATTGGGATGAATCTNACATTCATGTGCACCCCTCGTGTGGGATCATTCTCC[G/A]TGCCCC ATCTCTGGNAGAAAGCCACTGGGAAGTCGAAGGAGTCACTTCAATCAGG
WI-3505b	131 G A ---	---	---	TAACTTATGCCTCATCTGGCTTACTGCTTAGTTCCCATTTTGTGCATCAGTGCACCTTAAAAAATTATTT GAAAAATTGCCATTTTAAATATCTTTGGAACTTCTTAACACATTAACCTATTTTNAACCAAAC[G/A] AGGTGATTCTTATGGGAAAATATATACAGCAAGAAAAAANANGGAAAAAATGTTGATGATACCT GTITAAITGGGAAAATATGTTGCATAT
WI-3505	131 G A ---	---	---	TAACTTATGCCTCATCTGGCTTACTGCTTAGTTCCCATTTTGTGCATCAGTGCACCTTAAAAAATTATTT GAAAAATTGCCATTTTAAATATCTTTGGAACTTCTTAACACATTAACCTATTTTNAACCAAAC[G/A] AGGTGATTCTTATGGGAAAATATATACAGCAAGAAAAAANANGGAAAAAATGTTGATGATACCT GTITAAITGGGAAAATATGTTGCATAT
WI-3564b	177 C T ---	---	---	GCTAGTAAGGTTCCACCTAAATGGTTCCAAGTCAGGAGAGTCACTAAATGTTTGGAAAAATAAAGT GAAATCAATGTGTCTCCAGTGTATTCACATGGCAGAGTGCACAGAGGGCTTGAGCGTCTGAGCG TGGAGTTCACTGGTTGACTAACGTTAACATGCTGCTGT[G/C]TAAACAAGTGTGTTGTTGTTGTCATC AGTGTACACATGCTACCTTCTTCAAAAAACAAA
WI-3564	177 C T ---	---	---	GCTAGTAAGGTTCCACCTAAATGGTTCCAAGTCAGGAGAGTCACTAAATGTTTGGAAAAATAAAGT GAAATCAATGTGTCTCCAGTGTATTCACATGGCAGAGTGCACAGAGGGCTTGAGCGTCTGAGCG TGGAGTTCACTGGTTGACTAACGTTAACATGCTGCTGT[G/C]TAAACAAGTGTGTTGTTGTTGTCATC AGTGTACACATGCTACCTTCTTCAAAAAACAAA

WI-3649	64	A G	---			AATGTCCATGCTGTGACTGACCTGTCTAACACCTTTTCTAGTATTCCTTTAGTGAAGATTACAC[G AGACCAGTTTGCCTTACCTTAGTAGGGCCCAATGATAGACTTTTATAGGTCTACACAAAGGTACCTGC ACAGCCACATCATATGTCACAGTATGGTTGCAAAAGGACCTGTCTAGACTCTTTCTGCCTGCCCTTGCTC TTCTGTGTTTACCATAATATGATGACATGCAAAACCTCAGAGCCTTTTA
WI-3674b	133	G C	---			ACAGTACACATGGCCCCATTATGGAACAATCATCTGACTTATGTTACCTGAGAAGTCCCTCTCTAA ATTTAACTACCAGGGGAGTCTTTTATAGTAATTAATATGTTTATTTAGAAAAATAACAAAATIG /CJAAGAAAAAATGATAGTCAAGTTGTAGACACTATTTAAAATTGTAACCTGGTCAAAATGATTGT AATCTTAATTAATTGTTTTATGTTTTNATTACTGCCAATCACAGCCAAG
WI-3674	133	G C	---			ACAGTACACATGGCCCCATTATGGAACAATCATCTGACTTATGTTACCTGAGAAGTCCCTCTCTAA ATTTAACTACCAGGGGAGTCTTTTATAGTAATTAATATGTTTATTTAGAAAAATAACAAAATIG /CJAAGAAAAAATGATAGTCAAGTTGTAGACACTATTTAAAATTGTAACCTGGTCAAAATGATTGT AATCTTAATTAATTGTTTTATGTTTTNATTACTGCCAATCACAGCCAAG
WI-3682	137	G A	---			CAATATAGACCAATGACTGCCACAAGAGAAATAGTGGATCTACATTTAGAAACCCACATGTTTT ATTGGCTCTCTCTCTCTCTCTCTTTTATAGCTCTCTCCAACCAATTCACCTTTATCTTTTCAA TIG/AJAGCATTTGTCCAAATTAAGTCAATGAAAAATATGTACATTTTTCACAAGTATACATTAA GCCCTGCAAAAGTCTTATGCTAT
WI-3854b	194	G A	---			GGTATGTTGAGGTCAGCTAATGGTCACTGTGGTTGGAGTGAATCTAAATGGATTTTTGCCCTTGA CAAAGACCAAGGACAACCTGAGGACTTCTGCATGGTCTACCTCACTTAGGCTTCTTGATTAACTC TGGTTCAAGGAAGGCAAGGCGAGTTATGACCACCTTTACAACTGAGGAAATCAAAGCAACG/AJAGAA GTTAAATGGCCTGTCCCACTCCACAGAAATGGTTATAACAGAGTCAGAGCCA
WI-3854	194	G A	---			GGTATGTTGAGGTCAGCTAATGGTCACTGTGGTTGGAGTGAATCTAAATGGATTTTTGCCCTTGA CAAAGACCAAGGACAACCTGAGGACTTCTGCATGGTCTACCTCACTTAGGCTTCTTGATTAACTC TGGTTCAAGGAAGGCAAGGCGAGTTATGACCACCTTTACAACTGAGGAAATCAAAGCAACG/AJAGAA GTTAAATGGCCTGTCCCACTCCACAGAAATGGTTATAACAGAGTCAGAGCCA
WI-4039	210	G A	---			AGCCAGCCACATCATGTTGAGTCTGCTCATCTTCCATCTTATTTCTCTACTGSCCTTCACCTT CCATTAAACAAGAACTCTGTGATTACATTGATGTTTGTTGTTACACTACAGAATCCAAGATGACCTC CCCATCTCAAGGTCAACTAATTACACCTTAATCTATTGCAATCTTTGTCATTACCATAACATATT CATGGG/AJTTCTGGGATAAGGGGTAGACATTTTATGGGAGGCATTA
WI-4110b	130	T C	---			GAAAAATGATGTTTTTGATTTCCCTTCCATCTTCAGATTATTGGAGTGTATTAGAAAACTGATAGT AACCTTTTATTGATGAAACTCTGCTATAATTAACCTTCCCTTCTCTGCTTTATTTGCTT/CJACA GTTTAGGTAAATAAAGATGCCCAAGAAATTCAGTATTCAGTACAGTAAAAAGTAGCAACCATGGG GTAGGGACAAGTNCAGAAAAAGGAGGAGGTTGGGGGTTTTCTGGGAAGA

WI-4110	130	T C ---	---	GAAAAATGATGTTTGAATTCCTTCCTATCTTCAGATTATGGAGTGTCTTATAGAAAACTGATAGT AACCTTTTATTTGATGAAACTCTGTCTATAATTAACCTTCCTCTTCCTGCTTTATTTGCGC[T/C]ACA GTTTAGGTAAATAAAGATGCCAAGAATTCAGTATTCAGTACAGTAAAAAGTAGCAACCATGGG GTAGGGACAAGTNCAGAAAAGGGAGGAGGTTGGGGGTTTCTGGGAAGA
WI-4119b	168	GA ---	---	ACCTCTCTATGCCTGAAAGCCCTCATGAGTGTCCAGCAAGGGCTTGGGTGGGAAAAGTAATAATAG AATGGAAGGATAAATAAAGGTAACTACGGGGAAGAACAGCAAGACAGACAGACAGAAGGGGTT AGAGGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA[G/A]CAAGGTACCAAATTTGTTTTCTTCA TGAGACCGTCTGCATTCTTTGTTTTTAAAGGGCTCTGTGATCATCATCTTCA
WI-4119	168	GA ---	---	ACCTCTCTATGCCTGAAAGCCCTCATGAGTGTCCAGCAAGGGCTTGGGTGGGAAAAGTAATAATAG AATGGAAGGATAAATAAAGGTAACTACGGGGAAGAACAGCAAGACAGACAGACAGAAGGGGTT AGAGGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA[G/A]CAAGGTACCAAATTTGTTTTCTTCA TGAGACCGTCTGCATTCTTTGTTTTTAAAGGGCTCTGTGATCATCATCTTCA
WI-4123b	51	T G ---	---	CAAAGTCAGATTTGATTATTCAGGATAACAATTTTGAATAAGAAAGTG[T/G]TTAAACTATTT CAAATAACAATAAAGAAAACATGATGAAATTCCTCGTTACATAATTTGATAGAATTTAGTGGG TTCTCCATGACATTGGCTTGTCTTCTCAACAGTGGGTGGTGGATGTTTCTTAAGCTTTCTC AGGCACAAACAACAGTGAAGAAACCTTAGCAACATTTCTGCTGAATGTGTG
WI-4123	51	T G ---	---	CAAAGTCAGATTTGATTATTCAGGATAACAATTTTGAATAAGAAAGTG[T/G]TTAAACTATTT CAAATAACAATAAAGAAAACATGATGAAATTCCTCGTTACATAATTTGATAGAATTTAGTGGG TTCTCCATGACATTGGCTTGTCTTCTCAACAGTGGGTGGTGGATGTTTCTTAAGCTTTCTC AGGCACAAACAACAGTGAAGAAACCTTAGCAACATTTCTGCTGAATGTGTG
WI-4149b	145	GC ---	---	TTGTACATGTTTCATTCCTCCCTCCCATCTTTCTGCTTATAAGAACCTCGCTTCTCTCCAAGT CTTACTTCTCCACCTGAGCCACAGATCTCTTTATTTCCATCAAGCTTTCTCAGCATCTCTATATACT GTGCTGT[G/C]CCTTGGAAGAAGCCAGAGCCGAGCATACCAACATGATCTTTTGTGAACTGTAGT AGGAGAGACAAGACAGATGTGCGGGTCCCATGATATAAGGTAATTG
WI-4149a	137	T C ---	---	TTGTACATGTTTCATTCCTCCCTCCCATCTTTCTGCTTATAAGAACCTCGCTTCTCTCCAAGT CTTACTTCTCCACCTGAGCCACAGATCTCTTTATTTCCATCAAGCTTTCTCAGCATCTCTATATAC[T/C]GTGCTGTGCTTGTGAAGAAGCCAGAGCCGAGCATACCAACATGATCTTTTGTGAACTGTAG TAGGAGAGACAAGACAGATGTGCGGGTCCCATGATATAAGGTAATTG
WI-4182	188	GA ---	---	TAACACACTTTTCATTTGGTTTCTTACTGCGAGTTAAAGGACCATCCATTATATACAATCCCTC AGTTCTATGCTTTAGAGTNCATTTATAGGACTACTGAAAAATTCAGAGGGAATTAAGTCTGAGTA GGGGAATGAGTTAAATAATCTACCACATGCCAATTTGCAGGGGACTGTGGTTAA[G/A]ATGCTCTCT TGCCCCCTCCCAAGTCTTAAATTCCTAG

WI-4230	93	T	---	---	AGAGACGTTGAATGGGGACATCTTTTCATTTTCGATTTTAGTTTAACTTTGATAAGAATTGATGAAA GTTTGTACATTCAGATTATCTTTATAGCAGCAGAAGCTGGCAATAATAACAGCACACTGACT TTTCCATGGTAAAAAGAGTTAGAGAAAAACAGCCTATTTTCTTAATGTTAAATGTAATCTGAAT ACATTTAAATGGAGGAGAATGAATAGTGACCTTTTGAATTTTGAATTTATGG
WI-4241	118	C	T	---	GAAAAATCCATTGAAGTTTGACCTTGAACCTGATCTCATTAATACCTTTTNCCTTGTAGTGGTTGATTT CATTTTGGACAACAGACAGACGAAAAATTTCCACTTAAAAATTAATTTCTC/C/TJAGATATCTATGAT TTAGCACTGTTAGCACCCAGAAACTGTGAAATTAATCTCTAGATATCTCTCAGAAATCTAGGATGGAAG AA
WI-4271b	151	A	---	---	CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAAGACTAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGTCCCTGGAGGATTAAAGATCAAAATAAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGAGTNTACAGGGAGCCCCCAACCTCCCCCTTTGTCTCAGG CTCTAGAAAGTCCAGTCAGGGGC
WI-4271	151	A	---	---	CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAAGACTAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGTCCCTGGAGGATTAAAGATCAAAATAAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGAGTNTACAGGGAGCCCCCAACCTCCCCCTTTGTCTCAGG CTCTAGAAAGTCCAGTCAGGGGC
WI-4389b	156	G	A	---	AATCGAAACATTGATTTTGTAAAGGAACCACTATTATGATATTTTGCCCCAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGATAGAAAGGATATTATTGCATAACCTTTGGA AGGTAAGATGTGAACCTATACA/G/ATJNGCAAGGAAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAACCTGGAAGCGGTAA
WI-4389	156	G	A	---	AATCGAAACATTGATTTTGTAAAGGAACCACTATTATGATATTTTGCCCCAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGATAGAAAGGATATTATTGCATAACCTTTGGA AGGTAAGATGTGAACCTATACA/G/ATJNGCAAGGAAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAACCTGGAAGCGGTAA
WI-4488	31	A	G	---	GATGACAATTATTGTGATTGGCATTTTAA/A/GJGTACCATTCCATTTCTCTGGCTTTCGTGTGTT TGTTGTTGAGAAGTCAGGGGTAGTCGTATTGCTCCTTTTCTAGTCTCTCAGTAGGAAGACTGATC CTAAACAACCTAATTACCCATGCCAAAGTACGTCCAACTGATCTTTAAGAACAATAAAATCAAAATTG TATTATCCTATGCTTAAATGCTCAG
WI-4491	145	G	C	---	ACCATCAATGTATCACCTTCTAAAAATTTATTAGATGATTAACTGGCTCTGTAAAAATAAAAAACCT GTCTTGGACATTGAAAAATAAACATTACTATTGGTCATTTTCTGCTACTTACAAAGGTACTGCACTA AACAAGTTAAG/G/CJGTTTTTGGAGGGGAAAAATCATAAAAATGCATAAAAAATTTCTACCACCTGTCA TTCTTGCCCCATAAATAAAAAATTTTACATGCGCT

WI-4584	144	A G ---	---	TTGGTTGGCA TTTAGCCTCATAACAAC TATTACAATCAATAATGTTACTCTATTATTTACAAACAAG AAAAATGAGGCTTAACATCACACTTCTGCTTAGTCGACAGCAAGATTTGAACCCAGGAATCCATT CACCGGTAC[A/G]TGCTACCTGGTAAAAAATGTTTAAATAATCTATGGCATTAGATTTCAAAGA GTCTAATGTGGTTTGAAATAGGTGCTTTAATTTGTTTATCAGTATGC
WI-4639	185	C T ---	---	TTTCTGCATTGAATGTTGATGTCAGACTTCAGAGGAACCCAGGAATCTCATTTTATTAGTACAATA TGGTGGCCAGGTGCTCAGGCCCTATTATCAGAGAGATCTCAGTTTAACTTCCAAATTCACCACTTTAC TGACCATATGACTTGGGGAACATTATCTCACCTATCTGAGTCTGTATCC[C/T]CATCTTTAAATTTGTA AATTTAAGGACACCTCATCATAGTAATATTGTGAGGATAAAATGAAATAA
WI-5327	63	A ---	---	AAATGAATCGGCTTTAGAGCAATACCAGTAAGGCTGGTGCAGGATGGTGGCTGAGAGA[A/-] JGATTACTCATAAAAGCATATTAAATTTTATAAATATGGAATAATTAAGTAGATAATTAATGTGAAT TGAGTTGAAGTTGCATGAGAGTAGGAGGAGGTAGTTCTACTTATAGGGTTTATATAAGTNTGCT TCAATAGATGGCTCTTCGGATGACATGATGAATGTTCTAAGCAGACAG
WI-5390	87	C T ---	---	GCTTTGAGAAATGAAAGGGGAGCCTGGACCATTGCAGGGCTTCTCATCTCTGATTATTTTGTGTAT TTATTGTTCACTTATTAT[C/T]GCTGCTCCCTTCTGCTGATGCTTGTGTCATGAACAATGAATTC CCAGTGCCTGGCCGATTCGTGGCTCCTAGAGGTGTCAGAAAAAAGTTTCGGTGAATAGAATTG ACGAATGGTTTCAGAAATGAAACCTGTGAATCTATGGAAGACAAACGAAT
WI-5404b	87	G A ---	---	CCTTGCCTGCTTTATGCATAATGAGAAATAGAGTTGACTCTCCTGTCAAGAAATCAATTTAAGCAGT GCAACATATTATTAATTT[G/A]AAAGAAACTTGTTTCTGAAACTTTGTAATCTTTGTAGTNAATTTG AATCTTCTCTCAGCAGTTCCATGGTCGTGAATCCACCCCATCTCTTTTACCAGTAGCAAGATT GCTACTTATATGGAGGGTTTATAGAGTTCAACAA
WI-5404	87	G A ---	---	CCTTGCCTGCTTTATGCATAATGAGAAATAGAGTTGACTCTCCTGTCAAGAAATCAATTTAAGCAGT GCAACATATTATTAATTT[G/A]AAAGAAACTTGTTTCTGAAACTTTGTAATCTTTGTAGTNAATTTG AATCTTCTCTCAGCAGTTCCATGGTCGTGAATCCACCCCATCTCTTTTACCAGTAGCAAGATT GCTACTTATATGGAGGGTTTATAGAGTTCAACAA
WI-5545b	77	A C ---	---	TAGGAAAGGGGATGGTATGGCCTCTGAGACATTTAAATCTATCTTTCACCACCTCACACTGCCGCCA TATCTCCTC[A/C]CCAAACCTCTGTTTCTGACAGCAAGTTCCATCAGTTGATATGGACTATTT GTTGCAAAACAATTTGTTAAAGATTTGGCTGACTTTGGCTGAATTTGCTACAACCTCCAAAAAGANTC GAGATACACCATGAATTTTATTTTCATTTC
WI-5545	77	A C ---	---	TAGGAAAGGGGATGGTATGGCCTCTGAGACATTTAAATCTATCTTTCACCACCTCACACTGCCGCCA TATCTCCTC[A/C]CCAAACCTCTGTTTCTGACAGCAAGTTCCATCAGTTGATATGGACTATTT GTTGCAAAACAATTTGTTAAAGATTTGGCTGACTTTGGCTGAATTTGCTACAACCTCCAAAAAGANTC GAGATACACCATGAATTTTATTTTCATTTC

WI-5860b	134	A G ---	---	ACTCAAGTTGGGGATAAAATCAGAAGTTCTATGTACAACCTAAATTTTGCTAAGATTTTATTGT TTCTTTTATATAAAATTATGGATTGTTTTTACTTCCCTAACCAACCTTCTAACTGAGGAACAC/A GJTATACTGGAATCATGTGAAGACATTCTAAAGGGTACCCAGGTGCACATAGTTTTAAGGGAATCA ATTCCAAATCATCAACTTCTGTAT
WI-5860	134	A G ---	---	ACTCAAGTTGGGGATAAAATCAGAAGTTCTATGTACAACCTAAATTTTGCTAAGATTTTATTGT TTCTTTTATATAAAATTATGGATTGTTTTTACTTCCCTAACCAACCTTCTAACTGAGGAACAC/A GJTATACTGGAATCATGTGAAGACATTCTAAAGGGTACCCAGGTGCACATAGTTTTAAGGGAATCA ATTCCAAATCATCAACTTCTGTAT
WI-6106	208	C G ---	---	GCAACAACCTATTATACCTGATTCACCCAGGTCTACTAACATTAAATCAACCTAACCAATAC TATATATTGTCCTGTTCTGAATTTATTTCAITTAGAATCTGATGAGATTAGCATGGATAAGTGCAG TGCAGAGATAGTAACACACTGCTCTTTTGTCTCCAGGAGTCTCAATGTGAAGTATAATTTACAGAG TAATTTC/GJATAGTAGGTACCCACCAAGTCTATATTGTATGTGAAGGAAAG
WI-6109d	129	T C ---	---	AAGATAGACAAACATATGCCAGACCACAAACACACAGACCTGTCATATTTCTGAGAGAAATGTAC ATTGAGTCTCCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGGAAGGAAAAAACCT/CJ AAACCTATATTNCTGCTTGTGTCATCTTTAAATGTATAATGTGGGAGAGAGGAATTTTGATGT GNAAAATTATCCCTGAAAAATTTTATACCA
WI-6109c	147	T C ---	---	AAGATAGACAAACATATGCCAGACCACAAACACACAGACCTGTCATATTTCTGAGAGAAATGTAC ATTGAGTCTCCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGGAAGGAAAAAACCTAA ACCCTATATTNCTGTC/CJCTTGTCATACTTTAAATGTATAATGTGGGAGAGAGGAATTTTGATG TGNAAAATTATCCCTGAAAAATTTTATACCA
WI-6109b	147	T C ---	---	AAGATAGACAAACATATGCCAGACCACAAACACACAGACCTGTCATATTTCTGAGAGAAATGTAC ATTGAGTCTCCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGGAAGGAAAAAACCT/CJ AAACCTATATTNCTGCTTGTGTCATCTTTAAATGTATAATGTGGGAGAGAGGAATTTTGATGT GNAAAATTATCCCTGAAAAATTTTATACCA
WI-6109a	129	T C ---	---	AATGCCTATCACCTTCCATCATGCTGCATAACTGATTGATTCATAATGCTTATTGTTAGCACCTGTC TTCCAAACACATGCTGTTTTGTTCAATGA/T/CJGCATATCCCAAGTGCCTTAGACAATGCTCCCATAC AGTGAACAGATTTTGACTAAACACATACTTGTTAAATCAATAAAATTAATCAACTTGGCATATGCAGG GAAC
WI-6112	96	T C ---	---	

WI-6244	103	T C	---	---	TAATTGCACAACCTTACATATCAGGGTTTCTGATTGAAAGGAAGAATATTCTCTTTTAGTGATT GCTTAATATTAAATTCATAATAAGTGCACCATCTCTTCGCTCCTTATAAATGTGTTTGAAGAAGG AAATTGAGTGTGGGAATTAAGCAACCAAGGAGACATTTTATATACTCTACAGTGGGGAAGACTT CCTATTCTTCCCAAGGATGGATACATTCTAC
WI-6268	124	C T	---	---	CTGGCCTTATAATCCAAAGTTAGGATTAACTTACCCCACTTAATAGACTTCCAGACAGTTGCAGTT GTCTACAAGATTTCCTCTAGTAGGGCTTTGGGTGTGGCACCGTTTGGCTCATTCTCTACTCCCT GGGTCTATTGACTTTCAGGGAGCCTAGAAGAGCTGGACAAACCTGCTCTCTTGCAGAAAGAGTCG GGTTCCAAAGATTTCGTACGATTTTITA
WI-6336b	234	C T	---	---	AGGTGCCATTTAATCCATTCAAATTTGGAAGCTACATCTTCAAGGGTCTGAGAGAGCTCACTCCCCC ATATATCCCCCTTTACATGTTTCTTATAAGACATACAGTTTAAATCAATTAACAACTAAACAGCTT ATATACTGGCAATATATTACAGATGGGTTTATGTCAGAGTAATAGATCAGATGAAATGGACCATGTG GTACCCAGTGCATTATGCTTGGTAGAGCCCTCTGAGGACACTGACAGT
WI-6336	234	C T	---	---	AGGTGCCATTTAATCCATTCAAATTTGGAAGCTACATCTTCAAGGGTCTGAGAGAGCTCACTCCCCC ATATATCCCCCTTTACATGTTTCTTATAAGACATACAGTTTAAATCAATTAACAACTAAACAGCTT ATATACTGGCAATATATTACAGATGGGTTTATGTCAGAGTAATAGATCAGATGAAATGGACCATGTG GTACCCAGTGCATTATGCTTGGTAGAGCCCTCTGAGGACACTGACAGT
WI-6381	92	C A	---	---	TTGGATACAAAAATTCAGTTACACAATCAGTAGCATTCAAAATTAGTTATGAGTATTTATACAATTA CAAAAAATGNTTCATGTTTAAACA[C/A]GTATTTTAAAGCTCAAAACATTTTAAACAGGCACAA ATTCTAANGGCATATGCATTCCACCATGGGCTTTTGAATGTCTCTCACTCCCACTTCACAATCAAAATC TACAGANGGGCAAAAGATCAGAGTTTACAG
WI-6436	198	C G	---	---	GGTTGAGGCATTGGGAAAGGCAGAAATGAGGCAGTAGAAAAATGGACATTTTAGGAAAAGAGAAGT TCAGAGGCAAGTCATGACAGACAGGAAATACAAGGCTTAGGAAGACAGTAGTCTCTGTGGTTGAA ATTTGGTGTCTATAATAAGAAGTTAGACTTTGGGTGTAGTAGTTGATAGTAGTAGGAGCGTT[C/ G]ATTGGGTGATTCACACAGACAAGGTGATGTTCTAAGATTGATATTTATGT
WI-6449	186	C T	---	---	GAGGCCTCTTTGCTTTTCTCAGTCAAGGCTGTATCCAGGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTGTTGTTCTGATTGGTTGGTGTCTCAGACTGCCAGATTGTTAAATATTTGAAAATC GTATCTGGTTCTATTATCATCTGCAATCTCTGATCTTATGCTGGCTCTATTCTCTATCTCTCTGA TCTTATGTCAGACCTGAAGTTCTCTCTAATTTTCTGIGGGIATTATA
WI-6449	186	C T	---	---	GAGGCCTCTTTGCTTTTCTCAGTCAAGGCTGTATCCAGGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTGTTGTTCTGATTGGTTGGTGTCTCAGACTGCCAGATTGTTAAATATTTGAAAATC GTATCTGGTTCTATTATCATCTGCAATCTCTGATCTTATGCTGGCTCTATTCTCTATCTCTCTGA TCTTATGTCAGACCTGAAGTTCTCTCTAATTTTCTGIGGGIATTATA

WI-6463	72 T C ---	---	---	GCTGGAGAGAAAGACCTCCAAAAGAAAGAACTAAATCAGAGTCTCTTGAGCAAGAGGAATTTGAAA AGAACATTCGTGAAAAAATTAAGTAGAACTCAAGAGCCAAAAAGTCCCAATTTGTGTCCATTA TAAGAAATATTTGAATGGAAATCTTAAGAAATGATTTTATGATCAGTTAAATGTTCTTCCTCCTC CAGTCCCATTTATGACATCCGCATGCTG
WI-6474b	76 C T ---	---	---	AAGCAGTAAATCTTCCATCATGGATGCCAGTGGTAAATGTTATAGAACTTCAGAGGANAC AGAGGCAAA[C/T]GTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGCCTTAGAGCC AAGAAAAAGTAGGATTTTGAAGGCACAGAGAAAGGGGTGACTAGAGGAGAACTATGTAAGCAG AGGTATAGAGGAACCTAAAGTATAAAAGAGTGAGCCATAACTTAGGGTACCATAA
WI-6474	76 C T ---	---	---	AAGCAGTAAATCTTCCATCATGCCATGGATGCCAGTGGTAAATGTTATAGAACTTCAGAGGANAC AGAGGCAAA[C/T]GTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGCCTTAGAGCC AAGAAAAAGTAGGATTTTGAAGGCACAGAGAAAGGGGTGACTAGAGGAGAACTATGTAAGCAG AGGTATAGAGGAACCTAAAGTATAAAAGAGTGAGCCATAACTTAGGGTACCATAA
WI-6478b	175 T A ---	---	---	GAACTCAATTAACCTTTCACAACTGAGAAATCGGATTTGGAGATCTGCAAGCTGAGGTGAGATT TTGGACCTTGGTGATCCAAATGGGGAATGCCACGCTTCGAGGCTGTCTATATGCTTATTTTGTGA CACTGTCTATTTACCTCCCAATAGTGGAGAAATCAGAGT[A/G]CTCCTTGTCAAGTGTGCTACAGA GAAGATATACAGGATGGAAGGACAGCTCCTCGTAGGACCTAGACACAACCTG
WI-6478	175 T A ---	---	---	GAACTCAATTAACCTTTCACAACTGAGAAATCGGATTTGGAGATCTGCAAGCTGAGGTGAGATT TTGGACCTTGGTGATCCAAATGGGGAATGCCACGCTTCGAGGCTGTCTATATGCTTATTTTGTGA CACTGTCTATTTACCTCCCAATAGTGGAGAAATCAGAGT[A/G]CTCCTTGTCAAGTGTGCTACAGA GAAGATATACAGGATGGAAGGACAGCTCCTCGTAGGACCTAGACACAACCTG
WI-6559	149 G A ---	---	---	CACATTTTGAATGCAACTGAGAAANTGGTTTNTAGGCCTACCTTTTATTTAAGAGTACATCTGGCTC CAATGTTACCCCAACATGCAAAACATAAGGCAACAACTCTGATCATTTTATAGGNTCCCAAGCCCA TTAGCAATATCTTA[G/A]TCAAAATTTTAAAAAGAGAACAGGAAATAGGAAGGCCCTAACAGAGGAG TTAAATAATTTGTGCAAAACTTATCAGTTCTTC
WI-6564b	54 G A ---	---	---	TTCTTTATGGTCTACCAATGTGACTCTTTACCCAGGCCCCACTGTTCTCTATGC[G/A]CACTGGCTTTG TAGGCATTACATCATATGCTGTGCTCGTGAATAATCTCAATTAATTTCTCCTNCCCTATTCCTTTCCAT GCTCGCCTCATTTNCTCAGAAATGGAAGGCATTGATTATNATTTTTTTGTTGGGTCTGTGTAAAG GTTCTTGGCAGGAGAACATGCATATGACTTTAAATAAAGACCAACA
WI-6564	54 G A ---	---	---	TTCTTTATGGTCTACCAATGTGACTCTTTACCCAGGCCCCACTGTTCTCTATGC[G/A]CACTGGCTTTG TAGGCATTACATCATATGCTGTGCTCGTGAATAATCTCAATTAATTTCTCCTNCCCTATTCCTTTCCAT GCTCGCCTCATTTNCTCAGAAATGGAAGGCATTGATTATNATTTTTTTGTTGGGTCTGTGTAAAG GTTCTTGGCAGGAGAACATGCATATGACTTTAAATAAAGACCAACA

WI-6608b	46 C ---			CTAATCACAGTAGCACTGAACATGGCTCTAGTGAGTGGGCCTCAGT[C/- JAGTTCAGGCAGCTAAAGGGAGGGGATTTCTCTCTAGTCTCTCCCTAGAGCTAAATATGCATCTGG GAAAAATTAGGCTCTGGAGCACAGAGGATTTTCTAGAGGAAAAAGAACTGAACCTCCAGCACTAG GTAAACTGCAAAAAGAAAAACACCTGTGCCCCAGGCACCTAGCTACAAGGCCACACCAGAAAAAGGAA AGC
WI-6608	46 C ---			CTAATCACAGTAGCACTGAACATGGCTCTAGTGAGTGGGCCTCAGT[C/- JAGTTCAGGCAGCTAAAGGGAGGGGATTTCTCTCTAGTCTCTCCCTAGAGCTAAATATGCATCTGG GAAAAATTAGGCTCTGGAGCACAGAGGATTTTCTAGAGGAAAAAGAACTGAACCTCCAGCACTAG GTAAACTGCAAAAAGAAAAACACCTGTGCCCCAGGCACCTAGCTACAAGGCCACACCAGAAAAAGGAA AGC
WI-6666	68 C A ---			GTTAGACAGTATCCAGCAAAAAGGTTATTTATACCTCTACTTTTCCAAAACGAGGAAACCTCCCC AIC/AJAAATCCCATCAACACACAGTCATGCTGGAAGGCATCTGTCTTACTCTGTGGTTTCATGTAA ATGTTGGGGTGACTCATTCGGCTCTCTNTTCTCAAGTCCAGGCTCTTGGGTAGACCAAACTA ATACAAATGTTAGACACACAAGAGA
WI-6670b	120 A G ---			AGATTACATAATTATCTAGGGGCCATGTAGGGTTNGGAGGAGTGTCTTTCTATCTGCAGCCAAA CAGAAATACGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAATGAAC/A/GJTTGTTAGCCA GCATTGCCATTGAGGGCCGGAGTCAGGGTTTGTGGGCCAGAGTTTAGACAATTTGGGGAATCTGA AAAAAAAAGAAATACAGAAATTTGTAACACACAGACACAGAACTCTTAGAAGGGAT
WI-6670	120 A G ---			AGATTACATAATTATCTAGGGGCCATGTAGGGTTNGGAGGAGTGTCTTTCTATCTGCAGCCAAA CAGAAATACGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAATGAAC/A/GJTTGTTAGCCA GCATTGCCATTGAGGGCCGGAGTCAGGGTTTGTGGGCCAGAGTTTAGACAATTTGGGGAATCTGA AAAAAAAAGAAATACAGAAATTTGTAACACACAGACACAGAACTCTTAGAAGGGAT
WI-6704c	33 T C ---			TTTGAAAATAAATTATGCACCAATGTTTAACT/CJACATATATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAGTTTTCATGACACACCGNCA CTATTGCTCTTTAAATATGTTGTACATGTCATCATTAATCGATTCTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6704b	33 T C ---			TTTGAAAATAAATTATGCACCAATGTTTAACT/CJACATATATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAGTTTTCATGACACACCGNCA CTATTGCTCTTTAAATATGTTGTACATGTCATCATTAATCGATTCTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6704	28 T C ---			TTTGAAAATAAATTATGCACCAATGTTTAACT/CJAACTACATATATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAGTTTTCATGACACACCGNCA CTATTGCTCTTTAAATATGTTGTACATGTCATCATTAATCGATTCTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG

WI-6710	106 G A ---			CCATGGACAGTTTAAATTAGGAAGCTTCGACTTGTAGAAATACAGAGGAAGTCCAGTTATCTACCT ATTCCTTAAACACACATTTTGTAGGCTGGAATGATTCCC[G]ATAGTAAACATCAACATCCACACCT GCATAACATCGCTCCCAAGTGACTATTATTAAGTGTGACACAGGATGTACACAGTGAGCCTC ATCCAGTCCAAATGGAGGAGTTGACTTAGACCTTCCTTGGACAGGAAGGTC
WI-6766b	148 G C ---			AAACAAATGGTGCAATTCGATAATTTGGTGCAGTATAAAACAATACAATAGTTTCATATAAC ATTGATATGGACAAAATACACANGATCCTTTCTTGTCTACGGAAATNCTGCAGATCCTTATGT GCCACACTTAAAN[G]CJAAAGTCAACGTTTCTCTTAGGNTCTGCACACATATTATCACTGA GAATTTGGTCAACAGTGGAGNGAACTTACCAAATCCCAGTTCCTCTTC
WI-6766	148 G C ---			AAACAAATGGTGCAATTCGATAATTTGGTGCAGTATAAAACAATACAATAGTTTCATATAAC ATTGATATGGACAAAATACACANGATCCTTTCTTGTCTACGGAAATNCTGCAGATCCTTATGT GCCACACTTAAAN[G]CJAAAGTCAACGTTTCTCTTAGGNTCTGCACACATATTATCACTGA GAATTTGGTCAACAGTGGAGNGAACTTACCAAATCCCAGTTCCTCTTC
WI-6787b	97 A G ---			ACAGATAAAAGTCTTTATCCCTGTATGTTTACATAAGAAAGTCTTTACAGACTTTTTTTATACA ATACCTGTGCAGCAATGTTCAAATTTCAAC[G]ATTTTACTGCATAAGATATCTTCATGTACAACGTG ATGCTTTGTCTTCTTGGGAAGGACGCTTAAAGACCTATGATAACACACATCCACATGACAAAAGGA GAGTGAATAGGGCAGAGTAGANTACTCACAGGAAAGAGTAAATTCAGGT
WI-6793	105 C G ---			GAACCCACAGGTCCTGTTATTTTATTAAGGAGCATTTACATTATGATAGCAAGTTTCAACACATTCA TCAACAGGCGGCTTCAAATCAATCAATCAGTCAACCCCTC[G]GAGTTAGAAAGTAGAGTCAAGGAA GAGCTGCTGGCTGTAGGAAGTAGGTTAATGCCCTTAATCCCTTAATCCCGGAAAGGGCAGACTGAAGCCA GAGCCAGANTCCTGGCAATTCACAGTTTCTCATCACAGGTAAAGGCAAC
WI-6810b	37 T C ---			CACAATAATAAAATCACTCCCTACCTACCTTGAAAACCTTATTCJAGAAGCATTTTAAATTTACAACACA AAGCTCAACGNAACCTACAATAAGTCTAGTCTGTGTACGNGCCAAAGGATAAGGCTGAACAATA AATTAACCCCTTAAATGTCTATGNACAAGTACAATTTCTTTTGAGTTCTGCAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGATCCAGCGGCAATGAAGTTAAT
WI-6810	37 T C ---			CACAATAATAAAATCACTCCCTACCTTGAAAACCTTATTCJAGAAGCATTTTAAATTTACAACACA AAGCTCAACGNAACCTACAATAAGTCTAGTCTGTGTACGNGCCAAAGGATAAGGCTGAACAATA AATTAACCCCTTAAATGTCTATGNACAAGTACAATTTCTTTTGAGTTCTGCAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGATCCAGCGGCAATGAAGTTAAT
WI-6817b	145 C A ---			GCATGATTAAACCAGTGCAGAAAATACCAAGTACATTGGGTGAACGATGAGCTAGCTGTCTAGTA TTTGCTTTTGTATCCAGTTAAGACCATCAGCATATACAATCACTCACTCACTCACTCACTCACT GCAGGGTAAAC[C]ATGTGGATACCCCTGTGTGCTCTACTINGCCCTCCAAAGGCATCAGGGGATCATCA AAGATGTTGGACACCTTGTGTTCAATCTTGGTTACAGTGGGCTGTGCAG

WI-6817	145 C A ---				GCATGATTAAACCAGTGCAGAAAAATACCAAGTACATGGGTGAACGATGAGCTAGCTGTCTAGTA TTTGGCTTTTGTAAATCCAGTTAAGACCATCAGCATATACAACATCATCACTAACTCAACAATGTAGCT GCAGGGTAAC[C]ATGTGGATACCCGTGTGCTCTACTNGCCTCCAAAGGCAATTCAGGGGATCATCA AAGATGTTGGACACCTGTGTCAAACTTGGTTCAGGTGCGGCTGTGCAG
WI-6819b	221 C ---				GATGGAAGGCCATTTATTTCTCTAAATTTAAATAGAAGACTTTAATGGAACATTTTAGTAC CATCATGTCACCCCTGAATGCCAGCAATACCTCGACTTTTACACAGCAGGAAGCCTAGTAAAGCCC CGTCAGTAGTACACATTTCTCTATGGTCCCTCAACAGTTTGGTTCATATACAAAATTTCTGCTATTTG CTTAGCAACAGCAATAACTTTTGTGTTTCTCTATATGACACCTAATATCCAG
WI-6819a	175 G T ---				GATGGAAGGCCATTTATTTCTCTAAATTTAAATAGAAGACTTTAATGGAACATTTTAGTAC CATCATGTCACCCCTGAATGCCAGCAATACCTCGACTTTTACACAGCAGGAAGCCTAGTAAAGCCC CGTCAGTAGTACACATTTCTCTATGGTCCCTCAACAGTTTGGTTCATATACAAAATTTCTGCTATTT TTGCTTAGCAACAGCAATAACTTTTGTGTTTCTCTATATGACACCTAATAT
WI-6826b	154 A G ---				GCAAAAAGCTTTATTGGCTCCCAAAATATCCCTTTTAAACTCCTCTCTCTCTGCTCAGTG GAACAACACATTTGAATTCAGATTTGCAGTTTATAGCATTTTCCCTAAGAACCATAATAATAC ATGCAAAACCTTGACAT[AG]GAGCTTAAATAATCAAAATGCAATATAGATTGGGTGCACGTG TAAGCTGAATTGCAATATGGCAACACACACTGGACTGGGTATACGTTG
WI-6826	154 A G ---				GCAAAAAGCTTTATTGGCTCCCAAAATATCCCTTTTAAACTCCTCTCTCTCTGCTCAGTG GAACAACACATTTGAATTCAGATTTGCAGTTTATAGCATTTTCCCTAAGAACCATAATAATAC ATGCAAAACCTTGACAT[AG]GAGCTTAAATAATCAAAATGCAATATAGATTGGGTGCACGTG TAAGCTGAATTGCAATATGGCAACACACACTGGACTGGGTATACGTTG
WI-6857a	122 T C ---				AGTGCAAACTATTTGAACAAAAGTAACTATGAGTCACAGCATTGAGCAAGACATCAGACACGGA AGAGTGAACATATTCCTAAGTAAATACAGCAGATGAGATGCTCTCACATGTAT[C]ATTTAAT TATTCATGCTTTTCAATAGTCTCTTAGTCAACTTTGAGTGAATTTCCACAAATATATAGCAGCTCA AACACAAATGCAGGAGCACAATGGCAAAGTTTGGCAACTGTTTGGGCTAATT
WI-6865	153 G A ---				TTATAGAATACTTATGGGGCATACNGTAAATGAACCTGCAACCTTAAATCTAAACAACAGCTTG TTTGTGGTTCGTCCTGAAATCCTCCCTGCTCACAACAGCCAGCTACTNGGTTTCTAAAGACGTA ATTTGTCAGGCAACTTC[G]ATGAGGCCATTCGTGCGAGAAGAGGGAGAGCTGTTTGT TTACCTGTAGTATGAAGATATCTTTGGCTGTGTAGAACTGAGCTCAATAA
WI-6909	73 C T ---				ATTGAAAACCTGGTAGCAACAGATAAATACAATAGAGCCTGGATATAAAATGAGAGAAGATGC AGACTT[C]TAAAGCTTATAGAGAAAGTCAAAAGGAGCAAGTTTGAATCAGATTTTATGATAC GGAAAAAAATTTCCTTTTTGGCAACAGGATTATTCGAATATAAATCTGCCAGTGCCCAATCAG AACACCATTTCCACAATATTTGCAIGCCCCCTAGTTGCCATTTTATACATAIC

WI-6910b	163 G T ---	---	---	CACTCAAAAGCCTTTATTCATTGATTTACAAAGCTGTACAATAATTTACAAAGTTTAGGCATTAAATCCCA TATTGACATGAATGCTGTGGAGAGCTTAAAAATAAATATGTGGCACATAGCTTAATAATACACATCAT GGCTCTTTACACTTAAGCCATTACCAATA[G/I]TGAGATGTAATGGAGAATTTAATGTGGTAGAAAA GTCAGAGTGGCTGACCAGTCCCGGACCTCCATGTGAATGACTCTTCCTTGGC
WI-6915	144 A ---	---	---	GCTGTTTTTTTGTTGTTTTTAAGTGACACCTTGGCCTTGTGGCATTTCTTCACATTATCTTACCC AAAAGTGCCTTTGGGCCAGCCACTGACTGATTTAAACCAGAAATGTGGTTTTAAACAATGTGGT CGTGGTAATCAGGTGATTTNATTTCTATTGGTAGTATTTTCAGATTCCCAACAAAGAACATG TATTGCTTTGTAATTTGAAAAAAAATCAACACAGGATAGTAAAGATAT
WI-6928b	175 T C ---	---	---	CAATCAAAAAGTTCCAAAGTTCAAAGCTGGGATGAAAAGCCAGGCTTCTGACTTGCACCTGTGTCAC ACTGGATTTTNCCTCTGATCCAGCTGCAGCTCCCATAGAAGTTCACTCTTAATTTTCATGTCCCATG CTTTGTCTTGGTCCCTGTGAGGAAAGGGTCAGCTAAAGG[I/C]AACTGTTCTATAAGGATGGGTAGG TATCTGGCAAGATATTTCTCTGAAATAGTAAACGTGACCTTAGAAGTTA
WI-6928	175 T C ---	---	---	CAATCAAAAAGTTCCAAAGTTCAAAGCTGGGATGAAAAGCCAGGCTTCTGACTTGCACCTGTGTCAC ACTGGATTTTNCCTCTGATCCAGCTGCAGCTCCCATAGAAGTTCACTCTTAATTTTCATGTCCCATG CTTTGTCTTGGTCCCTGTGAGGAAAGGGTCAGCTAAAGG[I/C]AACTGTTCTATAAGGATGGGTAGG TATCTGGCAAGATATTTCTCTGAAATAGTAAACGTGACCTTAGAAGTTA
WI-6955b	79 G A ---	---	---	TTTTATGAACATTTCCAGATCCCTCATATCACAGCACATCAATAGCAGTATGTACATAGACTGA CTTTTATAGAC[G/A]NGTCATGTCCCAAATTTCCCAATCCTAGGTAAAGATATCAAGTTACAAANTAC AAGTCCGNTAATTAACATAGGTAGTATATTAAACAAAATGNGTTTTTNGCAAATTTATGTGAAT AAGGCTTTAACCAAAGC
WI-6955	79 G A ---	---	---	TTTTATGAACATTTCCAGATCCCTCATATCACAGCACATCAATAGCAGTATGTACATAGACTGA CTTTTATAGAC[G/A]NGTCATGTCCCAAATTTCCCAATCCTAGGTAAAGATATCAAGTTACAAANTAC AAGTCCGNTAATTAACATAGGTAGTATATTAAACAAAATGNGTTTTTNGCAAATTTATGTGAAT AAGGCTTTAACCAAAGC
WI-6957	47 C G ---	---	---	AACTAAAAACCCCTTATTGCTCCAAAGTGTGGCAAAATAGAAAAT[G/G]TTTCAATTACATTAGG AAATCGGGTGGATAACGGAGTATAGTTATCCACTTAAGAAGCATTCAGTCAAAATAATCACAAAA ACAAATTCAGATTGCTTGGATCTTGGTCATTTATGGCTTGAAGAAGTGGATTTGAAAACCCACTTTAGG CTAAATAAATGTATGAATAATGCATAGACTGTGTATCTAGAAAATCATGC
WI-6996c	242 G T ---	---	---	ACTTCTAGTGCCTCTGTACCACCACTCTAATGCCTCTGGTCCCGCACTTCTGTATGTCGCTAGGCGT TAAATCTGCCTGGCTCCCTCTGCTCTTCAGACCCAGAGGAGAGAGCGGCGAGTTCCTG CAGGAGAGAGGAGGGCTGTGGACCCAAAGGCTCAGTCCTCTGCTCTCAGGACCCCTGTCTGACT CTCTCCTGATGGTGGCCCTCTGTGCTCTCTCTCTTCC[G/I]GTCCGGATC

WI-6996b	242 G T ---	---	---	ACTTCTAGTGCCTCTGTTACCAACACCTCTAATGCCCTCTGGTCGCCGACCTTCTGATGTCCGTAGGCCT TAAATCTGCCTGGGTCCCTCCCTCTGTCTTCCAGCACCCAGAGGAGGAGAGAGCCGCGAGTTCCCTG CAGGAGAGAGAGGGGCTGCTGGACCCAAAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGCTCTGCTGACT CTCTCCTGATGGTGGGCCCTCTGTGCTCTCTCTCCGCTGCTCGGATC
WI-6996	228 T G ---	---	---	ACTTCTAGTGCCTCTGTTACCAACACCTCTAATGCCCTCTGGTCGCCGACCTTCTGATGTCCGTAGGCCT TAAATCTGCCTGGGTCCCTCCCTCTGTCTTCCAGCACCCAGAGGAGGAGAGAGCCGCGAGTTCCCTG CAGGAGAGAGAGGGGCTGCTGGACCCAAAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGCTCTGCTGACT CTCTCCTGATGGTGGGCCCTCTGTGCTCTCTCTCCGCTCGGATC
WI-7021b	112 G A ---	---	---	TGGGAGACAGGGAGATGCTGCAGTTCCTCCAAAGAGAAGGTTCTTCCAGAGTCATCTACCTGAGTCT CTGAAGCTCCCTGTCTGAAAGCCACAGACAATATGGTCCCAAATGAGTCCCAAATGAGTCCCACTCTGCTG CTTCAGCTCTCTTGACATCAAGGCTCTTCGTTCCACATCCACACAGCCAATCCAAATTAATCAAAACC ACTGTTATTAAACAGATAATAGCAACTTGGGAAATGCTTATGTTACAGGTTA
WI-7021	108 A G ---	---	---	TGGGAGGACAGGGAGATGCTGCAGTTCCTCCAAAGAGAAGGTTCTTCCAGAGTCATCTACCTGAGTCT CTGAAGCTCCCTGTCTGAAAGCCACAGACAATATGGTCCCAAATGAGTCCCAAATGAGTCCCACTCTGCTG CTTCAGCTCTCTTGACATCAAGGCTCTTCGTTCCACATCCACACAGCCAATCCAAATTAATCAAAACC ACTGTTATTAAACAGATAATAGCAACTTGGGAAATGCTTATGTTACAGGTTA
WI-7056c	118 C T ---	---	---	GGCAGTAGGAACCAACAGTGTGGGTTCTGCTGGACCTTGGAGACCTGCATCCAGGATCGGGTGG CCCTGCAGCCTCCTCCACCTCACTCCATGACAGCGCTAAACGTTGGTGA/C/TGGTGGGAGCCTCT GGGCTGTTGAAGTCACCTTGITGTTCCAAAGTTCCAAACAACAGAAAGTCATTCTCTTTTAA ATGGTCTTAAGTTCAGCAGATGCCACATAAGGGGTTGCCATTGATA
WI-7056b	118 C T ---	---	---	GGCAGTAGGAACCAACAGTGTGGGTTCTGCTGGACCTTGGAGACCTGCATCCAGGATCGGGTGG CCCTGCAGCCTCCTCCACCTCACTCCATGACAGCGCTAAACGTTGGTGA/C/TGGTGGGAGCCTCT GGGCTGTTGAAGTCACCTTGITGTTCCAAAGTTCCAAACAACAGAAAGTCATTCTCTTTTAA ATGGTCTTAAGTTCAGCAGATGCCACATAAGGGGTTGCCATTGATA
WI-7091b	153 A C ---	---	---	AATTCGCTGAAAAGGAACCTACCTATCCTTACATTTACCTTACCTACTAATGTCTCTTAACATCTTAGAG GTCCATGGAGAAGGCATATGGAGAACATGTTTTACTGCTCTATAAATAGTATCCCAATCACTGTG CTTAATTTAAATAGCATT/C/TCTTATCATTTATCAGCCCTTTATGTATTTCCAAAGTAAATATTA ACATATTATTCATTGGTCTCTTTTTATCTGGTCTATATGAATGCTAT
WI-7091	153 A C ---	---	---	AATTCGCTGAAAAGGAACCTACCTATCCTTACATTTACCTTACCTACTAATGTCTCTTAACATCTTAGAG GTCCATGGAGAAGGCATATGGAGAACATGTTTTACTGCTCTATAAATAGTATCCCAATCACTGTG CTTAATTTAAATAGCATT/C/TCTTATCATTTATCAGCCCTTTATGTATTTCCAAAGTAAATATTA ACATATTATTCATTGGTCTCTTTTTATCTGGTCTATATGAATGCTAT

WI-7136	58 T C ---			TGTGAAGCCACATTTTCCAACATGAGCCTCATGAAGCCCACTAAGTGTATTGAACGTGTC/CAATTCTCTCAATAACTCAGTGTAGCACTTTAAAGTCTGAAGGACAGCAACATGAAAAGAGCATATCAATGTGTGGAGAAAGGAAGGGTGGCTTTTAAATTTATTTCTTCATCTTTTATAACAAGAAAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGTAGCTTCTCTATATATG
WI-7146c	210 A G ---			GGGACGCTGTGTTTGGCTCAATTTGGGTTTGTGGTCACATGGAGCTCTCCATTTCGTTTAGCTGAATAATGAGTTGTTCTAGAGGAGACAGCCTGTCTCTCTCTGTTGCCCCCAAGCCCATGCGCTGCCGTGGTGGCAGCTGGGGCTGTGGATGGAGGGTCCCAACATGGATGTGTGGCCCTCTCTCCGATGOC AACGC/A/GJTTTCATGTACAAGGCCCTCTGCAACTGGAGAGAAATTA
WI-7146b	210 A G ---			GGGACGCTGTGTTTGGCTCAATTTGGGTTTGTGGTCACATGGAGCTCTCCATTTCGTTTAGCTGAATAATGAGTTGTTCTAGAGGAGACAGCCTGTCTCTCTCTGTTGCCCCCAAGCCCATGCGCTGCCGTGGTGGCAGCTGGGGCTGTGGATGGAGGGTCCCAACATGGATGTGTGGCCCTCTCTCCGATGOC AACGC/A/GJTTTCATGTACAAGGCCCTCTGCAACTGGAGAGAAATTA
WI-7146	202 G A ---			GGGACGCTGTGTTTGGCTCAATTTGGGTTTGTGGTCACATGGAGCTCTCCATTTCGTTTAGCTGAATAATGAGTTGTTCTAGAGGAGACAGCCTGTCTCTCTCTGTTGCCCCCAAGCCCATGCGCTGCCGTGGTGGCAGCTGGGGCTGTGGATGGAGGGTCCCAACATGGATGTGTGGCCCTCTCTCCGATG/AJCAAACGAGTTTCATGTACAAGGCCCTCTGCAACTGGAGAGAAATTA
WI-7153	161 A T ---			ATATTACAACCTGCTTTTAGCTGATCTCCATCTCAATGACTCTTTTCTTTTATATGTTAAACATATATAAATGGCAACTGATAGTCAATTTTGATTTTATTCAGGAACATCTGAAATCTGCTCAGAGCCTATGTGCATAGATGAACNNNNNNNNN/ATJAAAAAAGTTATTTAACAGTAATCTATTTACTAATTATAGTACCTATCTTTAAAGTATAGTACATTTTACATATGTAATGGTATGTTT
WI-7155	156 T G ---			TAGAATAGATGGGTCAATCTCTTTGGCTTCTGGCTTCCAGCCCTCATGGTTGGCATCACATATGCCCTGCATGCCATTAAACACAGCTGGCCCTACCCCTAATATGATCCTGTGCTCTAAATTAATATACACAGTGGTTCCCTCCCTGT/GJTAAGACTAATGCTCAGATGCTGTTACGGATATTTATATTTCTAGTCTCACTCTCTGTCCCAACCTTCTCTCTCCCACTCCAG
WI-7169b	161 A G ---			AGCTCCACCCAGATGCAGATTTGTGTTTGTGTTTCTGTTATCACTGTACACAGCTTATAACATGTATGCTTTTCAGAAATACAGTTGTCTAGCCCAAGCCATCAAGTGTCTGAAATTCATATTTGTTTATGCAAAACAGCAAACTTTTATTTAAGTAGAT/A/GJGGAGAATATGTTTAAATATTTAGGAATCCTAGACCATA TTTTCAAGTCATCTTAGCAGCTAGGATCTCAATGGAAGTGTATATATA
WI-7175b	194 C T ---			CTCCTAGACTAGTGCCTTACCTTTTATTAATGAAGTGTGACAGGAAGCCCAAGGCGAGTGTCTCACCAATAAATTCAGAGAAGTCAGTTGGAGAAATGAAGAAAGGCTGGCTGGAATCACTATAACCATCAGTTACTGGTTTCAGTTGACAAATATATATGTTTACTGCTGTCTATGCTCCATGCTA/C/TAAGAT AATTTATTTTGTATTTTGAATAAAAAACATTTGTACATCTCTGATACGGG

WI-7175	194 C T ---	---	CTCTAGACTAGTGCCTTACCTTTAATGAAGTGTGACAGGAGCCCAAGGCGAGTGTCTCACCACCA ATAACTTCAGAGAAGTCAGTTGGAGAAATGAAGAAAGGCTGGCTGAAATCACTATAACCATC AGTTACTGGTTTCAGTTGACAAATATATAATGGTTACTGCTGTCATTTGCCATGCCTAIC/TAAGAT AATTTATTTGTATTTTGAATAAANAACATTTGTACATCTCTGATACTGGG
WI-7178b	273 G A ---	---	TGTATCAGGTGACGGGACTTGGACAGGAGTCAGTGTCTGGCTTTTCTCTGAGCCCGAGCTGCCTGGAG AGGGTCTCGCTGTCAGTGGCTGCTAGGGGACAGACAGCCAGTGAACCCAGAAAGCATAACACCA ATCCAGGGCTGGCTCTGCACCTAAGAGAAAATGCACATAATGAATCTCGTTCCCAAGAACTACCC CCTTTTCAGCTGAGCCCTGGGACTGTTCCAAAGCCAGTGAATGTGAAGGAA
WI-7178	273 G A ---	---	TGTATCAGGTGACGGGACTTGGACAGGAGTCAGTGTCTGGCTTTTCTCTGAGCCCGAGCTGCCTGGAG AGGGTCTCGCTGTCAGTGGCTGCTAGGGGACAGACAGCCAGTGAACCCAGAAAGCATAACACCA ATCCAGGGCTGGCTCTGCACCTAAGAGAAAATGCACATAATGAATCTCGTTCCCAAGAACTACCC CCTTTTCAGCTGAGCCCTGGGACTGTTCCAAAGCCAGTGAATGTGAAGGAA
WI-7182b	116 A C ---	---	GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGGTCAACAAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAAATTTATTCACAGTTCCTCTGCAACCCACTCTGAGCCT[AC]TCTCTCCTCTATTT TACTTGAGGCTGCCAATTACAGCCCGACGTTTCAGCTCAAGAGATGCCTTAAGATAATTTATGTGAGG CCACTTGGTAGCAAGATGGCAGCTATTCTCTGAAGCCCTAGTACCCCAATT
WI-7182	106 C A ---	---	GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGGTCAACAAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAAATTTATTCACAGTTCCTCTGCAACCCCA[AC]TCTGAGCCTATCTCTCCTCTATTT TACTTGAGGCTGCCAATTACAGCCCGACGTTTCAGCTCAAGAGATGCCTTAAGATAATTTATGTGAGG CCACTTGGTAGCAAGATGGCAGCTATTCTCTGAAGCCCTAGTACCCCAATT
WI-7191b	273 T A ---	---	ATAATTGCTTGTTTTCTAGCCTGGCAAGATATTTTATAAAGAGGGATAACAATGCTGATTACTAC CTTTTAAATATTTTAGATAAATGCACAGCACACAGCACCATCTAAGCATTAGTGATGGGTAGC TGATGTCAAGCTTCATGTGATTTTAAAGCACTCTAGAACAAATGAAGCTTCTTGGCATATTTTAAGGAG CTCCCAAATGTGTACCTATTAAATTTGTAACCTAGCAAGTAGAAGACCAATT
WI-7199c	112 T C ---	---	CCCAGTGGTGAACAGAACCTCCCAATTTGAGTTGCACCCCTCCCTGTGGCCCTTATGAGCTCAGCCTC GCTTTGAGGTACCCACCGTCTGTGAGCTCCTGACCTATGAGCT[TC]GGGGCCCTGACTAGGAAAGT TGGGAGTTAAGGAGGAAATAGCATTCCTTAATGTTTTGTTTGGTGTCTGAAATTCCTTTATTAT AGTCCCTATAGTTTTACTCCTCAGTTCCTCACCATCATCACTGTCTAA
WI-7199b	112 T C ---	---	CCCAGTGGTGAACAGAACCTCCCAATTTGAGTTGCACCCCTCCCTGTGGCCCTTATGAGCTCAGCCTC GCTTTGAGGTACCCACCGTCTGTGAGCTCCTGACCTATGAGCT[TC]GGGGCCCTGACTAGGAAAGT TGGGAGTTAAGGAGGAAATAGCATTCCTTAATGTTTTGTTTGGTGTCTGAAATTCCTTTATTAT AGTCCCTATAGTTTTACTCCTCAGTTCCTCACCATCATCACTGTCTAA

WI-7216c	237	T C ---	---		TGACACTAACACTCTAATTCAGCGAATGTTGGAACACCATGACCTCCTCTGTGTGCTCTTCTCCCC AAGGACAAAATGTAGAAAGATGTGAGATAACTTACTCAAGATTCCCTCCAGAAAAATACGTATGT TTAAAAACCCCTTCTGCTATACATAGGAAAAGACACACATCCACCTAAAAATTGACTGTACTGTTTAA CTGTCAATTCTCCTGAGGCTAAACACAGTTGTTTT[C]C[CTTGTAATCACIT]
WI-7216b	237	T C ---	---		TGACACTAACACTCTAATTCAGCGAATGTTGGAACACCATGACCTCCTCTGTGTGCTCTTCTCCCC AAGGACAAAATGTAGAAAGATGTGAGATAACTTACTCAAGATTCCCTCCAGAAAAATACGTATGT TTAAAAACCCCTTCTGCTATACATAGGAAAAGACACACATCCACCTAAAAATTGACTGTACTGTTTAA CTGTCAATTCTCCTGAGGCTAAACACAGTTGTTTT[C]C[CTTGTAATCACIT]
WI-7220b	147	A T ---	---		AGGATGATGCTCCAAAGGGGACCTTGAACCTATTACACCATATTGTCTCTTTAAGCTGGCAACCCCA TCATTAAATAGCACATAAAATAGCAATCATATGGGATAAGTAGTACAGCTTCAGTAATCAATGGGCA GTGGCACTAGAA[A/T]AATCTTGAGCACAGTGAATGACCTATCCTGCAACATCTAATGGATCTCTA AAGGGTAACAAACCCCTATAAATTCTGGCTTACTGCACATATTAGTGTGTTT
WI-7220	140	A T ---	---		AGGATGATGCTCCAAAGGGGACCTTGAACCTATTACACCATATTGTCTCTTTAAGCTGGCAACCCCA TCATTAAATAGCACATAAAATAGCAATCATATGGGATAAGTAGTACAGCTTCAGTAATCAATGGGCA GTGGCACTAGAA[A/T]AATCTTGAGCACAGTGAATGACCTATCCTGCAACATCTAATGGATCTCTA AAGGGTAACAAACCCCTATAAATTCTGGCTTACTGCACATATTAGTGTGTTT
WI-7226	232	C ---	---		GATCGAATTTTCAGATGATTCGGAATTTTCATTGAGGTATTTGTAAGTAGGACATATATATGTATA TACATATCACCTCCTATTCTTAATTTTGTAAATGTTAACTGGCAGTAAGCTCTTTTGTATCATTT CCCTTTCCATATAGGAAACATAAATTTGAAAGTGGCCAGATGAGTTTATCATGTCAGTGAAAAATAA TTACCCACAAATGCCACCAGTAACCTAACGATTCTTCACITCTTGGGGTTT
WI-7228b	254	G A ---	---		ATAGCTTCAGATTACAAAGGCCAAGGGTAATAGAAATGCATACCAAGTAATGGCTCCAATTTCATAA TATGTTCCAGGAGATTACAATTTTGTCTCTTGTCTTTGTAATCTATTAGTTGATTTTAAATTA CTTTCTGAATAACGGAAGGATCAGAAAGATATCTTTTGTGCTTAGATTGCAAAATCTCCAATCCACA CATATTGTTTAAAATAAGAAATGTTATCCAACCTATTAAAGATATCTCAATGTT
WI-7228a	163	G A ---	---		ATAGCTTCAGATTACAAAGGCCAAGGGTAATAGAAATGCATACCAAGTAATGGCTCCAATTTCATAA TATGTTCCAGGAGATTACAATTTTGTCTCTTGTCTTTGTAATCTATTAGTTGATTTTAAATTA CTTTCTGAATAACGGAAGGATCAGAAAGATATCTTTTGTGCTTAGATTGCAAAATCTCCAATCC ACACATATTGTTTAAAATAAGAAATGTTATCCAACCTATTAAAGATATCTCAATGTT
WI-7233c	213	CT ---	---		CGATCGTACTGCCAGTAGCATTTGTCTGTCTGCGGCTTGTGTTGACATCCATTTCAATTGTTACA GATGTGAACITTTATCTTGTCACTAATTATATTTAAATTTATTTCTAGGAAGTCAAAAAATATAA TAAAGGTTGAGCCCTCTACTTCTTCTGCCCACCTTTTGTGGCAATATTAAGTGAACGTGCTAATA GTGTAAGTAC[CT]GTGCACAAAACCACTGCCCAGATAACGAGGGGCTG

WI-7233b	213	C T	---			CGATCGTACTGCCAGTAGCATTTGTCTGTCTGTCGGTCTGTGTGTACATTCATTTCAATTGTTACA GATGTGAACATTATTCCTTGTCACATAATTAATTAATAATTTCTAGGAAGTCAAAAAATATAA TAAAGGGTTGAGCCCTCTACTTCTCTGACCCTTTTGTGGCAATATTAAAGTGAAGTGCCTAATA GTGTAAAGTAC/TGTGCACAAACCACCTGCCAGATAACAGAGGGGCTG
WI-7233	211	T C	---			CGATCGTACTGCCAGTAGCATTTGTCTGTCTGTCGGTCTGTGTGTACATTCATTTCAATTGTTACA GATGTGAACATTATTCCTTGTCACATAATTAATTAATAATTTCTAGGAAGTCAAAAAATATAA TAAAGGGTTGAGCCCTCTACTTCTCTGACCCTTTTGTGGCAATATTAAAGTGAAGTGCCTAATA GTGTAAAGTAC/TGTGCACAAACCACCTGCCAGATAACAGAGGGGCTG
WI-7238	128	T C	---			GGGTCTACAGACAGCTCACCATTTTGTCTGTATCTGTAAACACATTTTGTCTTAGTCTTTTCTTG TAAATTGATGTTCTTTAAATCGTTAATGTATAACAGGGCTTATGTTTCAAGTTGTTT/CJCGTT CTGTTTTAAACAGAAAAATAAAGGAGGTGAAGTCTCTTTCTCATTTCAAAGTTGCTACCAGTGTAT GCAGTAATTAGAACAAAGAGAAACATTCAGTAGAACATTTTATGCTA
WI-7252f	520	T C	---			CCACAGGATCCAGCCAAAGCGGGCCCTCCGCCCCCTCCACTCGCAGCAGACGCCGGGGACAGAG GCCTGCCCCGGCGCGOCAGCCCCGGCCCTGGCTGGAGGCTGCCCCGGCCCCCTGGTCTCTGGTCCG GACACTCTAGAACGCGACGCCCTAGAGCCTGCCTGGAGCGTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACTCAGTCATTAGACTCCTCTCCA
WI-7252e	552	T C	---			CCACAGGATCCAGCCAAAGCGGGCCCTCCGCCCCCTCCACTCGCAGCAGACGCCGGGGACAGAG GCCTGCCCCGGCGCGOCAGCCCCGGCCCTGGCTGGAGGCTGCCCCGGCCCCCTGGTCTCTGGTCCG GACACTCTAGAACGCGACGCCCTAGAGCCTGCCTGGAGCGTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACTCAGTCATTAGACTCCTCTCCA
WI-7252d	540	T C	---			CCACAGGATCCAGCCAAAGCGGGCCCTCCGCCCCCTCCACTCGCAGCAGACGCCGGGGACAGAG GCCTGCCCCGGCGCGOCAGCCCCGGCCCTGGCTGGAGGCTGCCCCGGCCCCCTGGTCTCTGGTCCG GACACTCTAGAACGCGACGCCCTAGAGCCTGCCTGGAGCGTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACTCAGTCATTAGACTCCTCTCCA
WI-7252c	552	T C	---			CCACAGGATCCAGCCAAAGCGGGCCCTCCGCCCCCTCCACTCGCAGCAGACGCCGGGGACAGAG GCCTGCCCCGGCGCGOCAGCCCCGGCCCTGGCTGGAGGCTGCCCCGGCCCCCTGGTCTCTGGTCCG GACACTCTAGAACGCGACGCCCTAGAGCCTGCCTGGAGCGTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACTCAGTCATTAGACTCCTCTCCA
WI-7252b	540	T C	---			CCACAGGATCCAGCCAAAGCGGGCCCTCCGCCCCCTCCACTCGCAGCAGACGCCGGGGACAGAG GCCTGCCCCGGCGCGOCAGCCCCGGCCCTGGCTGGAGGCTGCCCCGGCCCCCTGGTCTCTGGTCCG GACACTCTAGAACGCGACGCCCTAGAGCCTGCCTGGAGCGTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACTCAGTCATTAGACTCCTCTCCA

WI-7252a	520	T C ---	---	CCACCAGGATCCACAGCCCAAGCGGCCCTCCCGGCCCTTCCACTCGACGACAGCGCGGGGACAGAG GCTGCCCGGGGGCCAGCCCGCCGCGCTGGGCTCGAGGCTGCCCGGCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGCGCCCTAGAGCCTGCTGGAGCGTTCTAGCAAGTGAGAGAGATGGGAG CTCTCTCTGGAGGATGCAGGTGAACCTCAGTCATTAGACTCTCTCTCCA
WI-7265m	252	T A ---	---	AACCTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTCCACCATTTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTTGTATTTATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGGCTTT/
WI-7265l	231	T A ---	---	AACCTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTCCACCATTTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTTGTATTTATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGGCT
WI-7265k	121	T G ---	---	AACCTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTCCACCATTTCTGTGGTTCATTGTAT GTTAAGGAAACCAAGCATATAGATGCATTAGTATTTTGTATTTATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGGCT
WI-7265j	174	T A ---	---	AACCTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTCCACCATTTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTTGTATTTATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGGCT
WI-7265i	227	T C ---	---	AACCTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTCCACCATTTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTTGTATTTATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGGCT
WI-7265h	80	T A ---	---	AACCTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTCCACCATTTCTGTGGTTCATTGTAT GTTAAGGAAACCAAGCATATAGATGCATTAGTATTTTGTATTTATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGGCT
WI-7265g	170	T G ---	---	AACCTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTCCACCATTTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTTGTATTTATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGGCT

WI-7265f	231 T A ---			---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCAATTTTACCCATTCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCAATAGTATTTGTTTATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGTATTTTCTTTT/AJ/AGGAGTAAAGATTGGCT
WI-7265e	227 T C ---			---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCAATTTTACCCATTCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCAATAGTATTTGTTTATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGTATTTTCTTTT/CJT/TAAGGAGTAAAGATTGGCT
WI-7265d	174 T A ---			---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCAATTTTACCCATTCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCAATAGTATTTGTTTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTTAAAGGAGTAAAGATTGGCT
WI-7265c	170 T G ---			---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCAATTTTACCCATTCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCAATAGTATTTGTTTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTTAAAGGAGTAAAGATTGGCT
WI-7265b	121 T G ---			---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCAATTTTACCCATTCTGTGGTTCAATTGTAGTT GTTTAAAGGAAACCAAGCATATAGATGCAATAGTATTTGTTTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTTAAAGGAGTAAAGATTGGCT
WI-7265a	80 T A ---			---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCAATTTTACCCATTCTGTGGTTCAATTGTAGTT GTTTAAAGGAAACCAAGCATATAGATGCAATAGTATTTGTTTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTTAAAGGAGTAAAGATTGGCT
WI-7281b	183 C ---			---	GATCACCCAGCCACAAGCCCTTCGAGGGCCCTATACCATGGCCACCTTGGAGCAGAGGCCAAGC ATCTCCCTGGGAAGTCTTTCTGGCCAAGTCTGGCCAGCCTGGCCCTGCAGTCTCCCATGAAGGCCA CCCCATGGTCTGATGGGCATGAAGCATCTCAGACTCCTTGGCAAAAACGGAGTCCGAGGCCGCGAG GTGTTGTAAGACCACTCGTCTGTGGTTGGGGTCTCTGCAAGAGGCCCTCTC
WI-7281	171 C A ---			---	GATCACCCAGCCACAAGCCCTTCGAGGGCCCTATACCATGGCCACCTTGGAGCAGAGGCCAAGC ATCTCCCTGGGAAGTCTTTCTGGCCAAGTCTGGCCAGCCTGGCCCTGCAGTCTCCCATGAAGGCCA CCCCATGGTCTGATGGGCATGAAGCATCTCAGACTCCTGAGTCTC/AJ/TTGGCAAAAACGGAGTCCGAGGCCG CAGGTGTTGTGAAGACCACTCGTCTGTGGTTGGGGTCTCTGCAAGAGGCCCT

WI-7282b	159	G C ---	---	TGTCACCTGGCACATTCATTTTCTCAGTTGAAGAAGAGAAAAATTTGAAAAATGTCCTTATGCTTTTAGA GTTGCAACCTTAAGTATATTTGGTAGGGTGAGTGTTCCTCACTCAAAATATGTCAACTTNNNNNNNT AGGCCCTTTCATAAAAAACCAAACT[G/C]TAGCAAGATGCAAAATGCATGGCAAAATCTGTCGGTCTCCA GTTGGTTATCTGAATAGTGTACCAATTCACCAAGACAGTGTGAGATTGG
WI-7292	92	T C ---	---	CTTGATTACTCCACTGAGGTGGAGCATCTCCAGTCTCCCCAAATATATCTCCCCACTCCACTAC TCTCTTCTCCACTTCATTTTCQ[C/T]TGTCTCTCTCTAATTCAGTGTTTGGAGGCTGACTTG GGGACAACGTATTATTGATATTATTGCTGTTTCTCTCTCCCAATAGAAGAAATAGTCATGGAGCC TGAAGGTGCTAGTTGACTTACTGACAAAAGGCTCTAGTTGGCTGA
WI-7301f	133	A G ---	---	AACTATGGCAGTGGTCTGGTTATAGTAGAGCGGGGTATGGTGGTGACCAAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTTGGAGGATATGATGTTACAATGAAGGAGGAAATTTG[A/G]CGGTAGTAACATATGGTGGTGGGAACATAATGATTTTGGAAATACAGTGGACAACAGCA ATCAAATTATGGACACATGAAGGGGGCAGTTTGGTGGAAAGCTCGGGCAG
WI-7301e	94	T G ---	---	AACTATGGCAGTGGTCTGGTTATAGTAGAGCGGGGTATGGTGGTGACCAAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGT[G/T]TGGAGGATATGATGTTACAATGAAGGAGGAAATTT TGACGGTAGTAACATATGGTGGTGGGAACATAATGATTTTGGAAATACAGTGGACAACAGCAA TCAAATTATGGACACATGAAGGGGGCAGTTTGGTGGAAAGCTCGGGCAG
WI-7301d	138	A G ---	---	AACTATGGCAGTGGTCTGGTTATAGTAGAGCGGGGTATGGTGGTGACCAAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTTGGAGGATATGATGTTACAATGAAGGAGGAAATTTGA CGGT[A/G]TAACATATGGTGGTGGGAACATAATGATTTTGGAAATACAGTGGACAACAGCAA TCAAATTATGGACACATGAAGGGGGCAGTTTGGTGGAAAGCTCGGGCAG
WI-7301c	211	A C ---	---	AACTATGGCAGTGGTCTGGTTATAGTAGAGCGGGGTATGGTGGTGACCAAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTTGGAGGATATGATGTTACAATGAAGGAGGAAATTTGA CGGTAGTAACATATGGTGGTGGGAACATAATGATTTTGGAAATACAGTGGACAACAGCAATCA AATTATGGAC[A/C]CATGAAGGGGGCAGTTTGGTGGAAAGCTCGGGCAG
WI-7301b	182	C T ---	---	AACTATGGCAGTGGTCTGGTTATAGTAGAGCGGGGTATGGTGGTGACCAAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTTGGAGGATATGATGTTACAATGAAGGAGGAAATTTGA CGGTAGTAACATATGGTGGTGGGAACATAATGATTTTGGAAAT[A/C]TAGTGGACAACAGCAA TCAAATTATGGACACATGAAGGGGGCAGTTTGGTGGAAAGCTCGGGCAG
WI-7301	88	GT ---	---	AACTATGGCAGTGGTCTGGTTATAGTAGAGCGGGGTATGGTGGTGACCAAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGT[G/T]CGGTGTTGGAGGATATGATGTTACAATGAAGGAGGAAATTT TGACGGTAGTAACATATGGTGGTGGGAACATAATGATTTTGGAAATACAGTGGACAACAGCAA TCAAATTATGGACACATGAAGGGGGCAGTTTGGTGGAAAGCTCGGGCAG

WI-7301	205 A C ---	---	---	AACATGGCAGTGGTCTGGTTATAGTAGAGAGGGGGTATGGTGGTGACAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGGAGGATATGATGTTACAATGAAGGAGGAAATTTTGA CGGTAGTAACATATGGTGGTGGGAACTATAATGATTTGGAATACAGTGGACAAACAGCAATCA AATTGATGGACACATGAAAGGGGGCAGTTTGGTGGAAAGCTCGGGCAG
WI-7314c	49 G A ---	---	---	CTCTCCTTTTCTTCAGATCTGCTCCTGGGTTTAAITGGGAGGTCA[G]ATTGTTCTACCTCACTG AGAGGGAACAGAAAGGATATTGCTTCCCTTTGCAGCAGTGAATAAAGTCAATTAATAACTTCCCAGG ATTTCTTTGGACCCAGGAACAGCCATGTTGGGTCCTTCTGTGCACATGAACGCTTCTTTCCCAGGA CAGAAATGTGTAGTCTACCTTATTTTTTATTAACAAAACCTTGTTTTT
WI-7314b	49 G A ---	---	---	CTCTCCTTTTCTTCAGATCTGCTCCTGGGTTTAAITGGGAGGTCA[G]ATTGTTCTACCTCACTG AGAGGGAACAGAAAGGATATTGCTTCCCTTTGCAGCAGTGAATAAAGTCAATTAATAACTTCCCAGG ATTTCTTTGGACCCAGGAACAGCCATGTTGGGTCCTTCTGTGCACATGAACGCTTCTTTCCCAGGA CAGAAATGTGTAGTCTACCTTATTTTTTATTAACAAAACCTTGTTTTT
WI-7314	36 A G ---	---	---	CTCTCCTTTTCTTCAGATCTGCTCCTGGGTTTAAITGGGAGGTCA[G]ATTGTTCTACCTCACTG AGAGGGAACAGAAAGGATATTGCTTCCCTTTGCAGCAGTGAATAAAGTCAATTAATAACTTCCCAGG ATTTCTTTGGACCCAGGAACAGCCATGTTGGGTCCTTCTGTGCACATGAACGCTTCTTTCCCAGGA CAGAAATGTGTAGTCTACCTTATTTTTTATTAACAAAACCTTGTTTTT
WI-7321b	199 C T ---	---	---	ACTCAGGGAAGGGATGCCCCATTAAAGTGACAAAAGGGTGGGTGGGACCATGGCATGAGGAAG AAACAAGGTCCCTGAGCAGGCACAAGTCTGACAGTCAAGGGACTGCTTTGGCATCCAGGGCTCCA GTCACCTCACTGCCATACATTAGAAATGAGACAATCAAGNNNNNNNAGGGTGGCACACCCATC[C /TGTGTTGCTGGGGTGTGGCAGCCACATCCAAAGACTGGAGCAGCAGGCTGGCCA
WI-7321	199 C T ---	---	---	ACTCAGGGAAGGGATGCCCCATTAAAGTGACAAAAGGGTGGGTGGGACCATGGCATGAGGAAG AAACAAGGTCCCTGAGCAGGCACAAGTCTGACAGTCAAGGGACTGCTTTGGCATCCAGGGCTCCA GTCACCTCACTGCCATACATTAGAAATGAGACAATCAAGNNNNNNNAGGGTGGCACACCCATC[C /TGTGTTGCTGGGGTGTGGCAGCCACATCCAAAGACTGGAGCAGCAGGCTGGCCA
WI-7336b	248 A C ---	---	---	AGACATTCCTCGTTCCCTGAAAGACTGAAGAAAGTGTAGTGCATGGGACCCACGAAACTGCCCTGGC TCCAGTGAACCTTGGGCACATGCTCAGGCTACTATAGGTCCAGAAAGTCTTATGTTAAGCCCTGGCAG GCAGGTGTTTATTAAATTCGTAATTTTGGGGATTTTCAAAAGATAATATTTACATACACTGTATGT TATAGAACTTCATGGATCAGATCTGGGGCAGCAACCTATAAATCA[A/C]CA
WI-7338c	221 A G ---	---	---	CTCTTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACCTTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATATTGGCAAAAGGTGCTTTACCTTGAGC CATTATTTGTGCAGAGAACAACAAAGAAACAGAAATCAATATATAAATTCAAAGACTATCTGCAGCTA GTGTGTTTCTTCTTACACACACACATCAACACAGACATCAGAAATTTCTGTT

WI-7338b	125 A C ---	---	CTCTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAAATATTTGGCAAAAGGTGCTTTTAC/CJCCCTTG AGCCATTATTTGTGCAGAGAACAAAAGAAACAGAAATCAATATATAAAATTCAAAGACTATCTGCAG CTAGTGTTTCTCTTACACACATATACACAGACATCAGAAAATTCGTGTT
WI-7338	125 A C ---	---	CTCTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAAATATTTGGCAAAAGGTGCTTTACCTTGAGC CATTATTTGTGCAGAGAACAAAAGAAACAGAAATCAATATATAAAATTCAAAGACTATCTGCAGTA GTGTTTCTCTTACACACATATACACAGACATCAGAAAATTCGTGTT
WI-7338	221 A G ---	---	CCTATGTCAATGAAATGCTAGGGGCCAGGGAACAAAATTTTAAATAATAAAATTCACCATAG CAATACAGAAATAACTTTAAATACCATTAATACATTTGATTTTCAATGTGAACAGGTATTTCTTCA CAGATCTCATTTT/AJAAAAATCTTAATGATTTTATTTACTACTGTTTAAAGGGGATGTTA TTTTAAAGCATATACCATACACTTAAGAAAATTTGAGCAGAAATTTAAAAAAGAA
WI-7384c	146 T A ---	---	CCTATGTCAATGAAATGCTAGGGGCCAGGGAACAAAATTTTAAATAATAAAATTCACCATAG CAATACAGAAATAACTTTAAATACCATTAATACATTTGATTTTCAATGTGAACAGGTATTTCTTCA CAGATCTCATTTT/AJAAAAATCTTAATGATTTTATTTACTACTGTTTAAAGGGGATGTTA TTTTAAAGCATATACCATACACTTAAGAAAATTTGAGCAGAAATTTAAAAAAGAA
WI-7384b	146 T A ---	---	CCTATGTCAATGAAATGCTAGGGGCCAGGGAACAAAATTTTAAATAATAAAATTCACCATAG CAATACAGAAATAACTTTAAATACCATTAATACATTTGATTTTCAATGTGAACAGGTATTTCTTCA CAGATCTCATTTT/AJAAAAATCTTAATGATTTTATTTACTACTGTTTAAAGGGGATGTTA TTTTAAAGCATATACCATACACTTAAGAAAATTTGAGCAGAAATTTAAAAAAGAA
WI-7384	145 T A ---	---	TGAAATCCTGGGCTCTTGGCCTGCTGCTAGCTGGTTTATTTTACTTTGCCCTCCCCACTTTTTT TGAGATCCATCCTTTATCAAGAAAGTCTGAAGCGACTT/AJAAAGGTTTTTGAATTCAGATTTAAAAA ACCAACTTATAAGCATTGCAACAGGTTACCTCTATTTGCCACAAGCGTCTCGGGATTGTGTTGA CTTGCTGCTGCCAAGAACTTTTCCCTCCCAAGATGTGATGTTATGG
WI-7388c	106 A T ---	---	TGAAATCCTGGGCTCTTGGCCTGCTGCTAGCTGGTTTATTTTACTTTGCCCTCCCCACTTTTTT TGAGATCCATCCTTTATCAAGAAAGTCTGAAGCGACTT/AJAAAGGTTTTTGAATTCAGATTTAAAAA ACCAACTTATAAGCATTGCAACAGGTTACCTCTATTTGCCACAAGCGTCTCGGGATTGTGTTGA CTTGCTGCTGCCAAGAACTTTTCCCTCCCAAGATGTGATGTTATGG
WI-7388b	106 A T ---	---	CTTGCTGCTGCCAAGAACTTTTCCCTCCCAAGATGTGATGTTATGG

[illegible]

WI-7499a	33 A G ---	---	CAATTCATAACCACTAGTCTGNTGCCTAA/GJCCATTCCAGACAAACATCCACTTCGAAGTTTAAATGCATAAGTCAGATAGCAATCCTTCAGTTGCCCCAGAGGCACATCACGTTCTTTGAATGCTTCATTATAGTCTCTTCATTAGCAATCAGTGAGGCAATACACTGGCATCATGATCCCTTTTTTTAGGAACTCTGTACAAAATCCCTTTGAAAATATAAATTTTGGAAATGAGTGATGA
WI-7506b	118 A C ---	---	TGGGAATAGTAAGAGAAAGATGGAAAGGTGACCAAAACAATATAGAGGCAGAGGCCCAAGTGAATGCATCCCAGCAGCAGACCACCTTNAAAAAGTAGTCTGGTGTGCTGATTGCCCTAGC/A/CJGGAGAGTTGAGTGCCACAGGTAAGAATGAGTGAAGAGGAAAAAATCATGTGTCATGTATGCAGTAATTAATCTATGTCA GAAGAAAATATTTTAAAATATTGGACCACCTCTTGTTCTACCATCCCTACCCACT
WI-7506	118 A C ---	---	TGGGAATAGTAAGAGAAAGATGGAAAGGTGACCAAAACAATATAGAGGCAGAGGCCCAAGTGAATGCATCCCAGCAGCAGACCACCTTNAAAAAGTAGTCTGGTGTGCTGATTGCCCTAGC/A/CJGGAGAGTTGAGTGCCACAGGTAAGAATGAGTGAAGAGGAAAAAATCATGTGTCATGTATGCAGTAATTAATCTATGTCA GAAGAAAATATTTTAAAATATTGGACCACCTCTTGTTCTACCATCCCTACCCACT
WI-7534b	143 C T ---	---	TGTGAATTCCTAGCTCTGGAAGGTGTTATGCTTTGCGGGTTCTTGATGTTCGCAGTGTACCCCAAGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCGTGGAAACACATCCCGGTGATAGAATTGCTAAATGTGTC/JGTGAAATAGTTAGAAATTTTCTTAAATATGTTTCTTATTCGTGAAAAATTCGGAGAGTGTCTGCTAAAATGGATTGGTGTGATCTTTTGGTAGTTGTAATT
WI-7534	135 T C ---	---	TGTGAATTCCTAGCTCTGGAAGGTGTTATGCTTTGCGGGTTCTTGATGTTCGCAGTGTACCCCAAGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCGTGGAAACACATCCCGGTGATAGAATTGCT/JCAAATTCGTGAAATAGGTTAGAAATTTTCTTAAATATGTTTCTTATTCGTGAAAAATTCGGAGAGTGTCTGCTAAAATGGATTGGTGTGATCTTTTGGTAGTTGTAATT
WI-7543b	162 G A ---	---	GGGAAAGAATAAAATTAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGGAGACTTTGAAGACCAGTCTGTTTGAGGGAGCCCCACTTGAAAGGAAGTCTAAGAGTGAAGTAGGTGACTTTGAAC TAGATTGCATGCTTCCTCTCTTGCTCTTG/AJGGAAGACCAGCTTGCAGTGACAGCTTGAGTGGGTTCTCTGCAGCCCTCAGATTATTTTCTCTGGCTCTGGATGTAGTCAGTTA
WI-7543	162 G A ---	---	GGGAAAGAATAAAATTAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGGAGACTTTGAAGACCAGTCTGTTTGAGGGAGCCCCACTTGAAAGGAAGTCTAAGAGTGAAGTAGGTGACTTTGAAC TAGATTGCATGCTTCCTCTCTTGCTCTTG/AJGGAAGACCAGCTTGCAGTGACAGCTTGAGTGGGTTCTCTGCAGCCCTCAGATTATTTTCTCTGGCTCTGGATGTAGTCAGTTA
WI-7555c	60 T C ---	---	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCAAAAATTTGTAGAGGTC/JCTTA AAAAGAAAGTGGTATGTTGTGTGATGATCAGCACTAAGTCTGCTGCTGTTAAAGCCACTTGGGTCATAAAGAGGGAGTAAAAATGAAGTCTGACTAGAAATCTATTGCAGAGGCCAAGTACATTTAGTATGGCATTGAGTTGTGATATAGTTTTCATTGATGTCATTTGAAATTCAG

WI-7576b	168 A T ---	---	AATGATGATGATAATGATGATGACGACGACGATGATGCTTGTAAACAGAAACATAAGAGAGC CTTGGTTCATCAGTGTAAATAATTTTGAAGGCGGTACTAGTTCAGACACATTTGGAAGTTTGTGT TCTGTTTGTAAACCTGGCATCTGACACAAAATATGTTGAAGGCTTATTCTACATTTACCTAC TTTGTAACTGAGAGAGACAAAGCAANNNNNNNNAAGAAAAATAAAC
WI-7577g	77 T C ---	---	AACCATGTTCCCTTCTCTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTTAA AAATATGCATCAATCGTCTCTCATTACTTTCTCTGAGGTTTGTAAACAGTAGGAGTTAAT AAAGAACTTCAATTTGGTTTACACGTAGGAAAGAGAGCATCAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577p	50 GC ---	---	AACCATGTTCCCTTCTCTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTTAA TAAATATGCATCAATCGTCTCTCATTACTTTCTCTGAGGTTTGTAAACAGTAGGAGTTAAT AAAGAACTTCAATTTGGTTTACACGTAGGAAAGAGAGCATCAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577o	157 G A ---	---	AACCATGTTCCCTTCTCTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTTAA AAATATGCATCAATCGTCTCTCATTACTTTCTCTGAGGTTTGTAAACAGTAGGAGTTAAT AGAAGTTCAATTTGGTTTACAC[GTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACT ATTGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577n	48 A G ---	---	AACCATGTTCCCTTCTCTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTTAA TAAATATGCATCAATCGTCTCTCATTACTTTCTCTGAGGTTTGTAAACAGTAGGAGTTAAT AAAGAACTTCAATTTGGTTTACACGTAGGAAAGAGAGCATCAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577m	84 G A ---	---	AACCATGTTCCCTTCTCTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTTAA AAATATGCATCAATCGTCTCTCATTACTTTCTCTGAGGTTTGTAAACAGTAGGAGTTAAT AAAGAACTTCAATTTGGTTTACACGTAGGAAAGAGAGCATCAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577l	93 T C ---	---	AACCATGTTCCCTTCTCTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTTAA AAATATGCATCAATCGTCTCTCATTACTTTCTCTGAGGTTTGTAAACAGTAGGAGTTAAT AAAGAACTTCAATTTGGTTTACACGTAGGAAAGAGAGCATCAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577k	154 C A ---	---	AACCATGTTCCCTTCTCTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTTAA AAATATGCATCAATCGTCTCTCATTACTTTCTCTGAGGTTTGTAAACAGTAGGAGTTAAT AGAAGTTCAATTTGGTTTAC[ACGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACT ATTGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC

WI-7577j	117 A G ---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATATCAAAACCCCAACATAAGTGTTCCTTTCCTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAGTA/GJACAGTAGGAGTTAAT AAAGAAGTTTCATTTTGGTTTACACGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTC
WI-7577i	77 T C ---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATATCAAAACCCCAACATAAGTGTTCCTTTCCTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAGTTTCATTTTGGTTTACACGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTC
WI-7577h	50 G C ---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATATCAAAACCCCAACATAAGTGTTCCTTTCCCTT TAAAAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAGTTTCATTTTGGTTTACACGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTC
WI-7577g	157 G A ---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATATCAAAACCCCAACATAAGTGTTCCTTTCCCTT AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AGAAGTTTCATTTTGGTTTACAC/GJTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTC
WI-7577f	48 A G ---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATATCAAAACCCCAACATAAGTGTTCCTTTCCCTT TAAAAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAGTTTCATTTTGGTTTACACGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTC
WI-7577e	84 G A ---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATATCAAAACCCCAACATAAGTGTTCCTTTCCCTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAGTTTCATTTTGGTTTACACGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTC
WI-7577d	93 T C ---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATATCAAAACCCCAACATAAGTGTTCCTTTCCCTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AGAAGTTTCATTTTGGTTTACACGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTC
WI-7577c	154 C A ---	---	AACCATGTTCCCTTCTTCTAGCACCAAAATATCAAAACCCCAACATAAGTGTTCCTTTCCCTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AGAAGTTTCATTTTGGTTTACACGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTC

WI-7577b	117 A G ---	---	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTTCTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTTCTCTGAGGGTTTGTAGTA/GIACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAAAGTGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTCTGAAATTGACTGTATTTC
WI-7577	107 G A ---	---	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTTCTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTTCTCTGAG/GIAGTTTGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAAAGTGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTCTGAAATTGACTGTATTTC
WI-7619q	106 C G ---	---	ACAAGGCGACTTGAAGAGGACGCGAGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAGAC AGAGAAGGGCCCAATGGGTCTATCCCTCCCTAACGAGACT/C/GTCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGATGGGGCCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTTCATCTTTTCCCT CTCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619p	150 T C ---	---	ACAAGGCGACTTGAAGAGGACGCGAGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAGAC AGAGAAGGGCCCAATGGGTCTATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGATGGGGCT/CCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTTCATCTTTTCCCTCTCT TCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619o	228 A G ---	---	ACAAGGCGACTTGAAGAGGACGCGAGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAGAC AGAGAAGGGCCCAATGGGTCTATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGATGGGGCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTTCATCTTTTCCCTCTCT CGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619n	237 G C ---	---	ACAAGGCGACTTGAAGAGGACGCGAGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAGAC AGAGAAGGGCCCAATGGGTCTATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGATGGGGCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTTCATCTTTTCCCTCTCT CGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619m	99 C T ---	---	ACAAGGCGACTTGAAGAGGACGCGAGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAGAC AGAGAAGGGCCCAATGGGTCTATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG TGGCAGGAAGATGGGGCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTTCATCTTTTCCCTCTCT TCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619l	189 T A ---	---	ACAAGGCGACTTGAAGAGGACGCGAGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAGAC AGAGAAGGGCCCAATGGGTCTATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGATGGGGCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTTCATCTTTTCCCTCTCT TCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC

WI-7619k	90	C G	---			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCC[C/G]CTCCCTAACGAGACTCTGTGCTGGGGTGCCTAATTAC ATGGCAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCCCTCT
WI-7619j	206	T G	---			CTCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCCCTCTCT
WI-7619i	106	C G	---			CGCTT[G]TCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCCTAATTACATGG ATGGCAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCCCTCT
WI-7619h	150	T C	---			CTCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCCCTCTCT
WI-7619g	228	A G	---			TCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCCCTCTCT
WI-7619f	237	G C	---			CGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCCCTCTCT
WI-7619e	99	C T	---			CGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCCTAATTACATGG TGGCAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCCCTCT
WI-7619d	189	T A	---			TCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTCCATCTTTTCCCTCTCT

WI-7619c	90 C ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGCTCCAGAGGACAAACCCCAATACAGGAGAACGACACAAGAC AGAGAAGGGCCCAATGGGGTCATCC[C/G]CTCCCTAACGAGACTCTGTGCTGGGGGTGCTAATTAC ATGGCAGGAAGATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCTCCCTTTTTCATCTTTTTCCT CTCTCGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619b	206 T G ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGCTCCAGAGGACAAACCCCAATACAGGAGAACGACACAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCTCCCTTTTTCATCTTTTTCCTCTCT CGC[T/G]TCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619	189 T A ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGCTCCAGAGGACAAACCCCAATACAGGAGAACGACACAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCTCCCTTTTTCAT[T/A]CTTTTTCCTC TCTCGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7626d	105 A G ---	---	---	CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACACAAAAGCAACAGTAA TCTATGTGTTTCTGTAAACAAATTGGGATCTGTCTTGGC[A/G]TTAAACACATCATGGACCAATGTG CCATACTAATGATGAGCAATTTAGCACAAATTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCAATTTCTTTGGACTGTTCA
WI-7626c	155 C T ---	---	---	CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACACAAAAGCAACAGTAA TCTATGTGTTTCTGTAAACAAATTGGGATCTGTCTTGGCATTAAACACATCATGGACCAATGTGCCA TACTAATGATGAGCAATTTAGC[A/T]ACAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCAATTTCTTTGGACTGTTCA
WI-7626b	28 T A ---	---	---	CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACACAAAAGCAACAGTAA TCTATGTGTTTCTGTAAACAAATTGGGATCTGTCTTGGCATTAAACACATCATGGACCAATGTGCCA CCATACTAATGATGAGCAATTTAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCAATTTCTTTGGACTGTTCA
WI-7626	144 T C ---	---	---	CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACACAAAAGCAACAGTAA TCTATGTGTTTCTGTAAACAAATTGGGATCTGTCTTGGCATTAAACACATCATGGACCAATGTGCCA TACTAATGA[T/C]GAGCATTTAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCAATTTCTTTGGACTGTTCA
WI-7689c	134 A G ---	---	---	TCCCATACCGCTGATCTCAGGCTCTCTGCTGCCGCCCAACCCAGATGGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTCTAGGACGCCACCCAGCAAAAGGTTGTTCTCTAA[A/ G]TAAGGGGAGATCACACTGGGCGAGCTGATACAAATTCAGACTGTGTAAAAAGAGAGCTTAAT GATAATATTGTGGTGCCACAAATAAATGGATTTATTAGAAATTCATATGAC

WI-7689b	134 A G ...	---	TCCATAACCGCTGATTCTCAGGGTCTCTGCTGCGGCCACCCAGATGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGAGCCACCCAGCAAAAGGTTGTTCTCTAAJA /GJTAAGGGCAGAGTACACTGGGGCAGCTGATACAAATTGCAGACTGTGTAAAAAGAGAGCTTAAT GATAATATTGTGGTGCCACAAATAAAATGGATTATTAGAAATTCATATGAC
WI-7689	121 G A ...	---	TCCATAACCGCTGATTCTCAGGGTCTCTGCTGCGGCCACCCAGATGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGAGCCACCCAGCAAAAGGTTGTTCTCTAA AATAAGGGCAGAGTACACTGGGGCAGCTGATACAAATTGCAGACTGTGTAAAAAGAGAGCTTAAT GATAATATTGTGGTGCCACAAATAAAATGGATTATTAGAAATTCATATGAC
WI-7690	45 G A ...	---	TGGAGAACATTCAATCTTCCGTCACCTATTCATCAATGAAGATTAGJACTGAGATCCAGAGAGG CTGGATGACTTGTCTCAAGTTCAACAGCATGGTAGTGGCAAGAGAGGTCAGAGTCTGGCCCTTGAT GCCAGCTCAGTGCCACAAAGCTCAGTAGGAGGATGTTCCAGTGGATGAGGGCCACCAGGAAGCAC AGGTCCAAAGGCTGGTCCACACTTATCAGCAGCAACAACCTGTCAGTTCATCC
WI-7703b	164 T C ...	---	ACAGAAAGTTGAATTTACATGGCTGGAGCTAGAAATTTGATATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTATTTTAAATTTGGTTTTCACATTGGAACAAGTCAGTCAATTCAGATATGATTCAAA TGCTATAAACCAAACTGATGTAAGTAAATTCJGGTCTCTCACTTGTGTTTATTTAACCTCTAAATTC TTCAATTTAGGGTAGCATTTGTGTTGAAGAGGTTTTAAAGCTTCCATTGT
WI-7703	156 T C ...	---	ACAGAAAGTTGAATTTACATGGCTGGAGCTAGAAATTTGATATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTATTTTAAATTTGGTTTTCACATTGGAACAAGTCAGTCAATTCAGATATGATTCAAA TGCTATAAACCAAACTGATGTT/CJAAAGTAAATGGTCTCTCACTTGTGTTTATTTAACCTCTAAATTC TTCAATTTAGGGTAGCATTTGTGTTGAAGAGGTTTTAAAGCTTCCATTGT
WI-7743e	106 C A ...	---	TTAAATGAGTGTGTTTGTACACCGTTGGGGATTGGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAATTCGTACCTACTGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAG GAGGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAACG
WI-7743d	275 C T ...	---	TTAAATGAGTGTGTTTGTACACCGTTGGGGATTGGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATTCGTACCTACTGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAACG
WI-7743e	106 C A ...	---	TTAAATGAGTGTGTTTGTACACCGTTGGGGATTGGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAATTCGTACCTACTGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAG GAGGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC

WI-7743d	275 C T ---	---	---	TTAAATGAGTGTGTTGTACCCGTTGGGGATTGGGGAAGACTGTGGCTGTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTCACTGGGGTCTGGGGCTCGAGGCTCATCCGAGGAGGGTTCAGGAGAG GGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7743e	106 C A ---	---	---	TTAAATGAGTGTGTTGTACCCGTTGGGGATTGGGGAAGACTGTGGCTGTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAATCTGCTACCTCACTGGGGTCTGGGGCTCGAGGCTCATCCGAGGAGGGTTCAGGAG GAGGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7743d	275 C T ---	---	---	TTAAATGAGTGTGTTGTACCCGTTGGGGATTGGGGAAGACTGTGGCTGTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTCACTGGGGTCTGGGGCTCGAGGCTCATCCGAGGAGGGTTCAGGAGAG GGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7743c	106 C A ---	---	---	TTAAATGAGTGTGTTGTACCCGTTGGGGATTGGGGAAGACTGTGGCTGTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAATCTGCTACCTCACTGGGGTCTGGGGCTCGAGGCTCATCCGAGGAGGGTTCAGGAG GAGGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7743b	275 C T ---	---	---	TTAAATGAGTGTGTTGTACCCGTTGGGGATTGGGGAAGACTGTGGCTGTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTCACTGGGGTCTGGGGCTCGAGGCTCATCCGAGGAGGGTTCAGGAGAG GGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7743	106 C A ---	---	---	TTAAATGAGTGTGTTGTACCCGTTGGGGATTGGGGAAGACTGTGGCTGTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAATCTGCTACCTCACTGGGGTCTGGGGCTCGAGGCTCATCCGAGGAGGGTTCAGGAG GAGGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7743	275 C T ---	---	---	TTAAATGAGTGTGTTGTACCCGTTGGGGATTGGGGAAGACTGTGGCTGTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTCACTGGGGTCTGGGGCTCGAGGCTCATCCGAGGAGGGTTCAGGAGAG GGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7758	144 A G ---	---	---	TGACATTTATTCAAAAGTTAAAGCAACACTTACAGAAATTAAGAGAGGTATCTGTTTAAACATTTCC TCAGTCAAGTTTCAGAGTCTTCAGAGACTTCGTAATTAAGGAACAGAGTGAGACATCATCAAGTG GAGAGAAATCAGTAAAGTTTAAAGTGCATTAATAATTTTAAACAGAAATTAAGTAGATTTTAAAA GATAAATGTGTAATTTGTTTATTTTCCCAATTTGGACTGTAACTGACTGCC

WI-7765b	126	G C ---	---		ACAGGGCTTTGGCAGGTGACGCCCCACTGCGTTTGACCTGCCTCCCTTCATGTCATGGAATTCCTCTCATCTGGAACCATCAGAAACACCTCAGACTGGGACTTGCAAAAAGGGTCAGTATGG[G/C]TTAGGGAAACATTCACCTTGGAGTCAAAAATCTCAATCTCCCTATCTTTGCCACCCCTCATGCTGTGTGACTCAAAACCAATCACTGAACCTTTGCTGAGCCTGTAAATATAAAGGTCTCGGA
WI-7773b	237	C G ---	---		TTAATTTACTGATTCAGCAAGACCAATCATTTGTATCAGATTATTTTAAAGTTTATCCGTAGTTTGTATAAAGATTTTCTTATTCCTTGGTTCTGTGAGAGAACCTAATAAGTGTACTTTGCCATTAAAGGCACTAGGGTTCATGCTTTTACCCTTTNNNNNNNNTTGTAAGTCTAGTTACCTACTTTTCTTTGATTTTCGACGTTTGACTAGCCATCTCAAGCA[C/G]TTTCGACGTTTGA
WI-7774b	170	T C ---	---		TGCAACCTCTTTTGGTATGGGAGCCTGCTGGTCAGCACTCCAGTAGCGAGAGACGGCACCCAGAAATCAGATCCAGCTTCGGCATTGATCAGACCAACAGTGTCTTTCCGGGGAGGAAACACTTTTTTAAATTACCCCTTTGAGGACCCACTTTAATCTGTTT[C]ATACCTTGTCTTATAATGAGCGACTTAAATGATTGAAATAATGCTGTCTCTTTAGTAGCAAGTAAATGTCTTGCT
WI-7785c	165	G ---	---		GCAGAGACCTTCCAAGGACATATTGCAGGATCTGTAAATAGTGAACATATGGAAGTATTAGAAATAATTTATGCTGTAAATACTGTAATGCAATGGAAATAAACTGTCTCCCCATTGCTCTATGAAACTGACATTGGTCAATGTGAATANNNNNNNNNGCCAAAGGCTAATCCAATATTATATCACATTTACCAATAATTTATTTGTCCATTGATGATTTATTTGTAAATGTATCTTGGTGTGC
WI-7785b	165	G ---	---		GCAGAGACCTTCCAAGGACATATTGCAGGATCTGTAAATAGTGAACATATGGAAGTATTAGAAATAATTTATGCTGTAAATACTGTAATGCAATGGAAATAAACTGTCTCCCCATTGCTCTATGAAACTGACATTGGTCAATGTGAATANNNNNNNNNGCCAAAGGCTAATCCAATATTATATCACATTTACCAATAATTTATTTGTCCATTGATGATTTATTTGTAAATGTATCTTGGTGTGC
WI-7785	156	- T ---	---		GCAGAGACCTTCCAAGGACATATTGCAGGATCTGTAAATAGTGAACATATGGAAGTATTAGAAATAATTTATGCTGTAAATACTGTAATGCAATGGAAATAAACTGTCTCCCCATTGCTCTATGAAACTGACATTGGTCAATGTGAATANNI- /TJNNNNNNNGCCAAAGGCTAATCCAATATTATATCACATTTACCATAATTTATTTGTCCATTGATGATTTATTTGTAAATGTATCTTGGTG
WI-7789c	84	G A ---	---		TCTCCCCCTCATCCAACCTCCGAAAGTCTGAATCTCCCAAGGAGGGCCACCATCTTACAGAGACTCTCCCTGACGGTGGAATTTAA[G/A]TTTAGGGTCCCTAAAGCATTTGACACACAGTTGTTGAATGACTGACCCAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGTCCCTTCAGGCCCGCTGCCCTAGGATATGCCCTCTGGTGACTCGGGGGCTGTCTCAGACGACTAGCCCAAGGACCCATCT
WI-7789b	84	G A ---	---		TCTCCCCCTCATCCAACCTCCGAAAGTCTGAATCTCCCAAGGAGGGCCACCATCTTACAGAGACTCTCCCTGACGGTGGAATTTAA[G/A]TTTAGGGTCCCTAAAGCATTTGACACACAGTTGTTGAATGACTGACCCAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGTCCCTTCAGGCCCGCTGCCCTAGGATATGOCCTCTGGTGACTCGGGGGCTGTCTCAGACGACTAGCCCAAGGACCCATCT

WI-7789	73 GA ---	---	---	<p>TCTCCCTCATCCAACTCGAAAGTCTGAATCTCCCAAGGAGGGCACCATCTTACAGAGACTCTCCC TGACG[G/A]TGGAAATTAAGTTAGGGTCCCTAAAGCAATTTGACACACAGTTGTTGAATGACTGAC CCAAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGCTCCCTTCAGGCCCGCTGCCCTAGGATAT GCCCTCTGGTACTCGGGGCTGTCTCAGACGACTAGCCAGGACCCATCT</p>
WI-7790b	190 CT ---	---	---	<p>AATTGTCAGTCACCTCTTCAAACCTTACAGTCTTCTTAAGGTACTCTTCATGAGATTCATCCATT TACTAATACTGTAATTTTGGTGACTAGGCTTGCCTATGTGCTTATGTAGCTTTTACTTTTATGG TGTGATTAATGGTGATCAAGGTAGGAAAAGTTGTTCTATTTCTTGAAGCTC[G/TT]CTATACITTT AAGATACTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTAAC</p>
WI-7790	190 CT ---	---	---	<p>AATTGTCAGTCACCTCTTCAAACCTTACAGTCTTCTTAAGGTACTCTTCATGAGATTCATCCATT TACTAATACTGTAATTTTGGTGACTAGGCTTGCCTATGTGCTTATGTAGCTTTTACTTTTATGG TGTGATTAATGGTGATCAAGGTAGGAAAAGTTGTTCTATTTCTTGAAGCTC[G/TT]CTATACITTT AAGATACTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTAAC</p>
WI-7795b	81 CA ---	---	---	<p>CAGATGTTCTGGTAAACTGATTGCTGGCAACACAGATTCTCTGGCTCATATTTCTTTCTCTCAT CTTGATGATGATC[G/A]GTCATCATCAAGAAATTTAATGATTAAATAGCATGCCCTTCTCTCTCTCT TAATAAGCCACATATAAATGACTTTTCTCCAGAAAATTTCTCCTTGAGGAAAAATGTCCAAAA TAAGATGAATCATTAAATACCGTATCTTCTAAATTTGAAATATAATCTG</p>
WI-7795	81 CA ---	---	---	<p>CAGATGTTCTGGTAAACTGATTGCTGGCAACACAGATTCTCTGGCTCATATTTCTTTCTCTCAT CTTGATGATGATC[G/A]GTCATCATCAAGAAATTTAATGATTAAATAGCATGCCCTTCTCTCTCTCT TAATAAGCCACATATAAATGACTTTTCTCCAGAAAATTTCTCCTTGAGGAAAAATGTCCAAAA TAAGATGAATCATTAAATACCGTATCTTCTAAATTTGAAATATAATCTG</p>
WI-7814c	41 GA ---	---	---	<p>TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCG[G/A]TTTCATTTAGTCATGTGACCCTC TGCTTGTTGTTCCACAGCCTGCAAGTTCAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAAATCTTTAGAGAAGTATACATAAGTTAGGATAAAAAATATGGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTGATATTTTAAAGAAATAACAGAA</p>
WI-7814b	41 GA ---	---	---	<p>TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCG[G/A]TTTCATTTAGTCATGTGACCCTC TGCTTGTTGTTCCACAGCCTGCAAGTTCAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAAATCTTTAGAGAAGTATACATAAGTTAGGATAAAAAATATGGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTGATATTTTAAAGAAATAACAGAA</p>
WI-7814	28 GA ---	---	---	<p>TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCGTTTCATTTAGTCATGTGACCCTC TGCTTGTTGTTCCACAGCCTGCAAGTTCAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAAATCTTTAGAGAAGTATACATAAGTTAGGATAAAAAATATGGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTGATATTTTAAAGAAATAACAGAA</p>

WI-7830d	150	C T	---			GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTAGTAAGAGAAGTCTGTCTGTGATGA TGGATAGGGGGCAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAACG ATCCATAACTTTAGT[C/T]TAAATGTACACATTCGATTTTGATAAAATTAATTTGTGTTCCCTTTG AGGTTGATCGTTGTGTTTGTGTCGCACTTTTACTTTTTGCGGTGGA
WI-7830c	54	G A	---			GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTAGTAAGAGAAGTCTGTCTGTGATGA TGATGGATAGGGGGCAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAAC ACGATCCATAACTTTAGTCTTAATGTACACATTCGATTTTGATAAAATTAATTTGTGTTCCCTTTG AGGTTGATCGTTGTGTTTGTGTCGCACTTTTACTTTTTGCGGTGGA
WI-7830b	134	G A	---			GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTAGTAAGAGAAGTCTGTCTGTGATGA TGGATAGGGGGCAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAAC G/AJATCCATAACTTTAGTCTTAATGTACACATTCGATTTTGATAAAATTAATTTGTGTTCCCTTTG AGGTTGATCGTTGTGTTTGTGTCGCACTTTTACTTTTTGCGGTGGA
WI-7830	44	A G	---			GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTAGTAAGAGAAGTCTGTCTGTGATGA TGATGGATAGGGGGCAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTCGATTTTGATAAAATTAATTTGTGTTCCCTTTG AGGTTGATCGTTGTGTTTGTGTCGCACTTTTACTTTTTGCGGTGGA
WI-7865e	25	C T	---			CCACTTCCTATCTGATTTTCCAG[C/T]AAATGAGGAGGCAATTCCTAGTCTCCACAAACATCTA GCCATCTAAATGGAGAGATGAATCATTCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGG GGTATGCTACTCATAAGATTTGAGGGTGTCTCCAACTGAAATCTCAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7865d	191	C T	---			CCACTTCCTATCTGATTTTCCAGCAATGAGGAGGCAATTCCTAGTCTCCACAAACATCTA ATCTAAATGGAGAGATGAATCATTCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGGT ATGCTACTCATAAGATTTGAGGGTGTCTCCAACTGAAATCTCAATGTTCTCAGT[C/T]GAAAAAC CTGAAATCACATGCCTATGTAAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7865c	25	C T	---			CCACTTCCTATCTGATTTTCCAG[C/T]AAATGAGGAGGCAATTCCTAGTCTCCACAAACATCTA GCCATCTAAATGGAGAGATGAATCATTCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGG GGTATGCTACTCATAAGATTTGAGGGTGTCTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7865b	191	C T	---			CCACTTCCTATCTGATTTTCCAGCAATGAGGAGGCAATTCCTAGTCTCCACAAACATCTA ATCTAAATGGAGAGATGAATCATTCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGGT ATGCTACTCATAAGATTTGAGGGTGTCTCCAACTGAAATCTCAATGTTCTCAGT[C/T]GAAAAAC CTGAAATCACATGCCTATGTAAGGAAAGTGCTATTACCCAGTAAACCCAAA

WI-7865	25 C T ...	---	CCACTTCCTATCTGATTTTCCAG[C/T]AATGAGGCGAGCAATCTAGTCTTCCACAAAACATCTA GCCATCTAAATGGAGAGATGAATCATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGG GGTATGCTACTATAAGATTCAGGGTGCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7865	191 C T ...	---	CCACTTCCTATCTGATTTTCCAGCAAAATGAGGCGAGCAATCTAGTCTTCCACAAAACATCTAGCC ATCTAAATGGAGAGATGAATCATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGGGT ATGCTACTATAAGATTCAGGGTGCTTCCAACTGAAATCTCAATGTTCTCAGTA[C/T]GAAAAAC CTGAAATCACATGCCTATGTAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7867c	92 A C ...	---	TTCAACACCTGCTTCCACCCCTCCACCATCTGTGCAATCACTTCACCCCTCAGCCTCAGTCTCCCG CTAACAAATTACCTGTCAAGAGG[C/G]AGTGCAGCTCAGGTGGATTAAATGGGTTTAAATATGGC CTGTTGAGTTTAAATGTTGATTTCTTTAAGTAACCATTTCTGTTCTTGGCTATAAAATCTATGT CTATATGCTATGCTTAAATTTGGATGATGAAGGCAACTTGGATTAAAGG
WI-7867b	92 A C ...	---	TTCAACACCTGCTTCCACCCCTCCACCATCTGTGCAATCACTTCACCCCTCAGCCTCAGTCTCCCG CTAACAAATTACCTGTCAAGAGG[C/G]AGTGCAGCTCAGGTGGATTAAATGGGTTTAAATATGGC CTGTTGAGTTTAAATGTTGATTTCTTTAAGTAACCATTTCTGTTCTTGGCTATAAAATCTATGT CTATATGCTATGCTTAAATTTGGATGATGAAGGCAACTTGGATTAAAGG
WI-7868c	173 C T ...	---	TTGATCGATCTTTCCACCCCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCCGGCTTT CACCCAACTGCTCCCTGATCCTCCATCAGGGCCAGATCTCCACGTCTCCATCTCAGTACACAAT CATTAAATTTCCCTGCTTACCCCTATTCAAGCA[C/T]TAGAGGCCAGAAAATGGGCAAAATTAT CACTAACAGGCTTTTGACTCAGGTTCCAGTAGTTCACTTCAATGCTAGAT
WI-7868b	173 C T ...	---	TTGATCGATCTTTCCACCCCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCCGGCTTT CACCCAACTGCTCCCTGATCCTCCATCAGGGCCAGATCTCCACGTCTCCATCTCAGTACACAAT CATTAAATTTCCCTGCTTACCCCTATTCAAGCA[C/T]TAGAGGCCAGAAAATGGGCAAAATTAT CACTAACAGGCTTTTGACTCAGGTTCCAGTAGTTCACTTCAATGCTAGAT
WI-7868	66 T C ...	---	TTGATCGATCTTTCCACCCCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCCGGCTTT [C/T]CACCCAACTGCTCCCTGATCCTCCATCAGGGCCAGATCTTCCACGTCTCCATCTCAGTACAC AATCATTTAATTTCCCTGCTTACCCCTATTCAAGCAACTAGAGGCCAGAAAATGGGCAAAATTAT CACTAACAGGCTTTTGACTCAGGTTCCAGTAGTTCACTTCAATGCTAGAT
WI-7870b	85 T C ...	---	ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCACTATTAACTCTGCAGTATTAGAAGGG GTGGGTGGCGGGAATCC[T/C]ATTATCAGACTCTGTAAATTGAATATAATGTTTACTCAGAGGA GCTGCAAAATTGCTGCAAAAATGAAATCCAAATGAGCACTAGAAATTTAAACATCATTTACTGCCAT CTTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATATCAATTTG

WI-7870	76 C T ---	---	ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCACTATTAACTACTCTGCAGTGATTAGAAAGG GTGGGGTGG[C/7]GGGAATCCTATTATCAGACTCTGTAATGAATATAATGTTTTACTCAGAGGAG CTGCAATTGCCTGCAAAAATGAAATCCAATGAGCACTAGAAATATTTAAACAATCATTACTGCCATC TTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATCAATTG
WI-7889c	54 C ---	---	TTAGGTCTCATGCCACTCCOCAGGAGCAGCTGGCACTGACAGCCTGGGGGGCGCTCTCCCCCTG CAGCGTGCAGGACTCTAGCTCATGAGTGAAAGTCACTACAGGACTGGCGGGCCAGGGCCTCT GGCTTCCCTGCCCAATCCTCCCTGGAGAAGGACATGGGAATGAATTGAAATGGGGCGCTGGACACC TACAGCAGCAGCATGTCCCTCCAAGGCTGCTTCTCCAGAGCACAAGAG
WI-7889b	54 C ---	---	TTAGGTCTCATGCCACTCCOCAGGAGCAGCTGGCACTGACAGCCTGGGGGGCGCTCTCCCCCTG CAGCGTGCAGGACTCTAGCTCATGAGTGAAAGTCACTACAGGACTGGCGGGCCAGGGCCTCT GGCTTCCCTGCCCAATCCTCCCTGGAGAAGGACATGGGAATGAATTGAAATGGGGCGCTGGACACC TACAGCAGCAGCATGTCCCTCCAAGGCTGCTTCTCCAGAGCACAAGAG
WI-7894c	142 A G ---	---	AGCCACCCCAATAAATGTTATCCAGAAGCTGTTATGCTCTGTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACCTTATGCTCTATTGTTGTGAATTTATTTGCGTATAC ATTATC[A/G]TATGTAAAATTTGCAATTTTATTGAAAATTTGTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAAATTTAACCGCTATAGAGTATCCATA
WI-7894b	142 A G ---	---	AGCCACCCCAATAAATGTTATCCAGAAGCTGTTATGCTCTGTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACCTTATGCTCTATTGTTGTGAATTTATTTGCGTATAC ATTATC[A/G]TATGTAAAATTTGCAATTTTATTGAAAATTTGTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAAATTTAACCGCTATAGAGTATCCATA
WI-7900e	84 C T ---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAAGTGGCCATG[C/7]CCTGCCATTGAACAGTGATTAGTTTGAAGCCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTTGAACCCAGTGAAA TATGATGATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900d	128 C T ---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAAGTGGCCATG[C/7]CCTGCCATTGAACAGTGATTAGTTTGAAGCCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTTGAACCCAGTGAAA TATGATGATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900e	84 C T ---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAAGTGGCCATG[C/7]CCTGCCATTGAACAGTGATTAGTTTGAAGCCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTTGAACCCAGTGAAA TATGATGATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC

WI-7900d	128 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTTGAACACAGTGATTAAGTTTGATCAAGCCCATGGTGA[C/T]ACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTTGAACCCAGTGAAA TATGATGATTTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900e	84 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGCCATTGAACAGTGATTAAGTTTGATCAAGCCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTTGAACCCAGTGAAA TATGATGATTTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900d	128 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTTGAACACAGTGATTAAGTTTGATCAAGCCCATGGTGA[C/T]ACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTTGAACCCAGTGAAA TATGATGATTTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900c	84 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGCCATTGAACACAGTGATTAAGTTTGATCAAGCCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTTGAACCCAGTGAAA TATGATGATTTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900b	128 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTTGAACACAGTGATTAAGTTTGATCAAGCCCATGGTGA[C/T]ACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTTGAACCCAGTGAAA TATGATGATTTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900	84 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGCCATTGAACACAGTGATTAAGTTTGATCAAGCCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTTGAACCCAGTGAAA TATGATGATTTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7901c	33 C T	---	---	AGACTTAGGTACAAATTGCTCCCTTTTATATAT[C/T]JAGACACACACAGGACACATATATTAACAG ATTGTTTCATCATTTGCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAACATGGTAAGAC CCTTTTAAACAACCTCCAGGCGCTGGTTGGCGGCTGGGTTATTGGGCGAGCGCGGTGGTGGT CACTCAGTCGCTCTGCATGCTCTGTCTATACAGACAGGTAACTAGTCT
WI-7901b	33 C T	---	---	AGACTTAGGTACAAATTGCTCCCTTTTATATAT[C/T]JAGACACACACAGGACACATATATTAACAG ATTGTTTCATCATTTGCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAACATGGTAAGAC CCTTTTAAACAACCTCCAGGCGCTGGTTGGCGGCTGGGTTATTGGGCGAGCGCGGTGGTGGT CACTCAGTCGCTCTGCATGCTCTGTCTATACAGACAGGTAACTAGTCT

WI-7901	33	C T	---	AGACTTAGGTACAAATTGCTCCCTTTTATATA/C/TJAGACACACAGGACACATATATTAACAG ATTGTTTCATCATTTGCATCTATTTTCCATATAGTCATCAAGAGACCATTATTAACACATGGTAAGAC CCTTTTAAACAAACTCCAGGCCCTTGTTGCGGTCGCTGGTTATTGGGCAGCGCGCTGGTGGT CACTCAGTCGCTCTGCATGCTCTCTGTCTATACAGACAGGTAACCTAGTTCT
WI-7901	271	T G	---	AGACTTAGGTACAAATTGCTCCCTTTTATATACAGACACACAGGACACATATATTAACAGATT GTTTCATCATTTGCATCTATTTTCCATATAGTCATCAAGAGACCATTATTAACACATGGTAAGACCCT TTTTAAACAAACTCCAGGCCCTTGTTGCGGTCGCTGGTTATTGGGCAGCGCGCTGGTGGTGCAC TCAGTCGCTCTGCATGCTCTCTGTCTATACAGACAGGTAACCTAGTTCTGTGT
WI-7926c	150	C A	---	CATTCCGCATCTGTCAACCAGGACAGAAAGCATGGACAGGATGAGCTTTACAAAGATGATGCAC TTGGAGATCAGAAAATTCATATTTAAGCAAAGTGATACAAACACAGTGATTTGGGAATGCCTTCATT TACAATGCAATACTTAC/AJA/TTTTAACTCTTGTAGGAGAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAATTACACTGTGGAA
WI-7926b	28	A T	---	CATTCCGCATCTGTCAACCAGGACAGAAAGCATGGACAGGATGAGCTTTACAAAGATGATGCAC ACTTTGGAGATCAGAAAATTCATATTTAAGCAAAGTGATACAAACACAGTGATTTGGGAATGCCTTC ATTTACAATGCAATACTTACATTTTAACTCTTGTAGGAGAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAATTACACTGTGGAA
WI-7926	150	C A	---	CATTCCGCATCTGTCAACCAGGACAGAAAGCATGGACAGGATGAGCTTTACAAAGATGATGCAC TTGGAGATCAGAAAATTCATATTTAAGCAAAGTGATACAAACACAGTGATTTGGGAATGCCTTCATT TACAATGCAATACTTAC/AJA/TTTTAACTCTTGTAGGAGAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAATTACACTGTGGAA
WI-7947b	203	G T	---	AAGAGCCAGAGGTCAAAAAGGCCAACACACCACTAAGCAGCCAGACCCACAGGCCAGGTCCTGT GCTATCACAGGGTCACCTCTTTACAGTTAGAAAACACAGCCAGGCCACAGAAATCCCATCCCTTCC TGAGTCATGGCCTCAAAAATCAGGGCCACCATTTGCTCAATTCAATCCATAGATTTCGAAGCCACA GA/G/TJCTCTCCCTGGAGCAGCACTATGGGCAGCCCGAGTGTGCCACCTG
WI-7947	203	G T	---	AAGAGCCAGAGGTCAAAAAGGCCAACACACCACTAAGCAGCCAGACCCACAGGCCAGGTCCTGT GCTATCACAGGGTCACCTCTTTACAGTTAGAAAACACAGCCAGGCCACAGAAATCCCATCCCTTCC TGAGTCATGGCCTCAAAAATCAGGGCCACCATTTGCTCAATTCAATCCATAGATTTCGAAGCCACA GA/G/TJCTCTCCCTGGAGCAGCACTATGGGCAGCCCGAGTGTGCCACCTG
WI-7963b	145	T C	---	CATGTGCTGCATGAAGAGCTAATTTAAAAAGCAAAGTAAGACTAATTTTAAAAATAAAAAATGCC ACAAATTCATTTTCTCCTTAAGTATTACAATGGAGTTTATCTCGCTTAAAGTGGAGAAAT TGAGTGAATGAT/CJA/TTTTGTAAATTTAGGATAAGATCCAAAGTATTTTCCCCAACTCTGTTCCG CCATAAAGTTAGGCATGAGGAGGAGCACTCATTAAAGGCAGAGACGGAAAA

[illegible]

WI-8021b	57	C T	---			ACAATCTCAGAAGGACTGTGCAAGTCAATGAGTCGCTTGTGAATTCATCTCGAAAC[CT]GATCCC ACGCTTAGAACCTTCACCACAAGGAGTTTCTTGTAGTGATTCTCAAAAGTCTGGTAGGCATTGGA ACTGGTCTTTCACITTAGAGATCTTCTTTTGGCCCTCTATCAAGTCAGCACACACCTTTTCCAAG GATTTACGTTGGGCTTGTAGGGGTGATTGGAATTCGGTGAATTGCCA
WI-8021	57	C T	---			ACAATCTCAGAAGGACTGTGCAAGTCAATGAGTCGCTTGTGAATTCATCTCGAAAC[CT]GATCCC ACGCTTAGAACCTTCACCACAAGGAGTTTCTTGTAGTGATTCTCAAAAGTCTGGTAGGCATTGGA ACTGGTCTTTCACITTAGAGATCTTCTTTTGGCCCTCTATCAAGTCAGCACACACCTTTTCCAAG GATTTACGTTGGGCTTGTAGGGGTGATTGGAATTCGGTGAATTGCCA
WI-8024c	206	A G	---			CTGAAATTTACTATGCTCTCCACAACAAGAGCTCCCATTTCCACAGACACAGTCAATGTCAATCA GCTTGATTCAGGAGGACAGGGCAGAGGGATCCAGTGGCACTTCCCATGGGAAGACAGAAGAGAGT GGCCCCAGAGATGGAAGGACCCAGTGTATCACCACAACCACTTTTCAGCCGCTCTAGCCTCTAA TTCCC[A/G]CTAGAACAGCTGGCCCTGGTCGTCACTACACAAGGAAGAGC
WI-8024b	206	A G	---			CTGAAATTTACTATGCTCTCCACAACAAGAGCTCCCATTTCCACAGACACAGTCAATGTCAATCA GCTTGATTCAGGAGGACAGGGCAGAGGGATCCAGTGGCACTTCCCATGGGAAGACAGAAGAGAGT GGCCCCAGAGATGGAAGGACCCAGTGTATCACCACAACCACTTTTCAGCCGCTCTAGCCTCTAA TTCCC[A/G]CTAGAACAGCTGGCCCTGGTCGTCACTACACAAGGAAGAGC
WI-8077	167	A G	---			GAATGAGCCTTCTAGCGCGAGGAGCTGCTGCTGTTGTGGCTGCACATGCATCTATGGAATGC TTTTGGCCAAAGCGGGGCACTGAGGACTAAGCTCTGANNNNNNNNATCTGCCCCAACTCCTTTCT AAGGAGCTGGGTGTATGCTGCTACAAACCA[A/G]TAATTCATCAGATGGATTTTATTAAACGTT GTGATTTGACTTACTTTTCCAACTGACTCTGGCATACAAGGGAAAAA
WI-8118f	114	G C	---			TCTAGGTTTAAATCAAGCAATTTGCANTTTGGATTTGGAATGACCACCTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACTGGCAATACAGAATGTAGCTTGTTCGCTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCTCT AAAAATCAGACTCATTGTGACCAGTAGCTTGAGGACTCAAGCTGAATGA
WI-8118e	40	A G	---			TCTAGGTTTAAATCAAGCAATTTGCANTTTGGATTTGGAATGACCACCTCCCTTGCTAAGGAAGC TATGTACTTCATGCTGTGGAACTGGCAATACAGAATGTAGCTTGTTCGCTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCTCT AAAAATCAGACTCATTGTGACCAGTAGCTTGAGGACTCAAGCTGAATGA
WI-8118d	118	T G	---			TCTAGGTTTAAATCAAGCAATTTGCANTTTGGATTTGGAATGACCACCTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACTGGCAATACAGAATGTAGCTTGTTCGCTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCTCT AAAAATCAGACTCATTGTGACCAGTAGCTTGAGGACTCAAGCTGAATGA

WI-8118c	44 C T ---			TCTAGGTTTAATCAAAGCAATTGTCANTTTGGATTTTGGAAATGA/C/TJCACTCCCTTGCTAAGGAAGC TATGTACTTCATGCTGTGGAACTGGCAAATACAGATGTAGCTTGTTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTTCGTATTCCTGCTCCTCCTATTCCTTCCCT AAAAATCAGACTCATTGTGACCAAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118b	88 T C ---			TCTAGGTTTAATCAAAGCAATTGTCANTTTGGATTTTGGAAATGACCACTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAAATC/CJGGCAAATACAGAAATGAGCTTGTTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTTCGTATTCCTGCTCCTCCTATTCCTTCCCT AAAAATCAGACTCATTGTGACCAAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8171d	299 C T ---			TTTTCTCTCTCCGGGGGACCAAGGTACCTTCTGGGGCATACAACATGGCAGAGGGCTCGGGAAG AGGGGTAGGAGGACCGAGCAGCATTCTCTGTAGAGGAAGACAGGAAAGGAGACCCCTCTTGGCACACA TTTATGGAGGTTGTCCCTGAAGAGAAAGGCGAGGTGGGAGAGGTTCCCTGTACTTAAGAGAAGGC ACCAGTGGGCAAGAGACAAATGAAGAGGATGATGATAAAAACAATCACGGCA
WI-8171c	46 A G ---			TTTTCTCTCTCCGGGGGACCAAGGTACCTTCTGGGGCATACAAC/A/GJTGCGAGCAGGGCCTCGGG AAGAGGGGTAGGAGGACCGAGCAGCATTCTCTGTAGAGGAAGACAGGAAAGGAGACCCCTCTTGGCAC ACATTTATGGAGGTTGTCCCTGAAGAGAAAGGCGAGGTGGGAGAGGTTCCCTGTACTTAAGAGAA GGCACCAGTGGGCAAGAGACAAATGAAGAGGATGATGATAAAAACAATCAC
WI-8171a	46 A G ---			TTTTCTCTCTCCGGGGGACCAAGGTACCTTCTGGGGCATACAAC/A/GJTGCGAGCAGGGCCTCGGG AAGAGGGGTAGGAGGACCGAGCAGCATTCTCTGTAGAGGAAGACAGGAAAGGAGACCCCTCTTGGCAC ACATTTATGGAGGTTGTCCCTGAAGAGAAAGGCGAGGTGGGAGAGGTTCCCTGTACTTAAGAGAA GGCACCAGTGGGCAAGAGACAAATGAAGAGGATGATGATAAAAACAATCAC
WI-8171b	298 T C ---			TTTTCTCTCTCCGGGGGACCAAGGTACCTTCTGGGGCATACAACATGGCAGAGGGCTCGGGAAG AGGGGTAGGAGGACCGAGCAGCATTCTCTGTAGAGGAAGACAGGAAAGGAGACCCCTCTTGGCACACA TTTATGGAGGTTGTCCCTGAAGAGAAAGGCGAGGTGGGAGAGGTTCCCTGTACTTAAGAGAAGGC ACCAGTGGGCAAGAGACAAATGAAGAGGATGATGATAAAAACAATCACGGCA
WI-8314b	85 G C ---			GAGGGAAATGACATCTGGAGATCTAGGTATGGGCCATTGCAATTGAGCACATTTCTGGGTCTGT TTCTCTATCTAAGGG/CJAGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTGCTCTGTAGTCTTATGATGATCTAGAAGAGCACTGTCCAATAGAATTC TGTGATGATGAAAAGATTCTACTTCTGACCTATTCATAGGGTAACCACT
WI-8314	78 C G ---			GAGGGAAATGACATCTGGAGATCTAGGTATGGGCCATTGCAATTGAGCACATTTCTGGGTCTGT TTCTCTATCT/CJGJTAAGGGGAGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTGCTCTGTAGTCTTATGATGATCTAGAAGAGCACTGTCCAATAGAATTC TGTGATGATGAAAAGATTCTACTTCTGACCTATTCATAGGGTAACCACT

WI-8321	178 GA ---	---	---	TTTTAAATATGCCCCGTTTAGAGCAGACACAGTCACAATAAAAGTTAAAAGTTACAATGTGTCCAG TGTATATACCCAGGNAATCCATTCTTGGTACTTTCAAGAGCTGCTGTATATAGTACTGTCTGAGAAG TCCCCTTAGATAATAGCTGCCACTTTTCAGTATGGTTGAGAAATG/AJAGTATCTTAGTATCTTCTTA TTTGTCTATGGTTCTAGTTTATCAACCTACTTTATAGCTGAACGTGTGGC
WI-8321	178 GA ---	---	---	TTTTAAATATGCCCCGTTTAGAGCAGACACAGTCACAATAAAAGTTAAAAGTTACAATGTGTCCAG TGTATATACCCAGGNAATCCATTCTTGGTACTTTCAAGAGCTGCTGTATATAGTACTGTCTGAGAAG TCCCCTTAGATAATAGCTGCCACTTTTCAGTATGGTTGAGAAATG/AJAGTATCTTAGTATCTTCTTA TTTGTCTATGGTTCTAGTTTATCAACCTACTTTATAGCTGAACGTGTGGC
WI-8332b	123 AC ---	---	---	TATGTACTCACTTTCAGTTACCCCGTGCCTCCAGAAATCGCATGTGTCTCCACCTGGGGCGGATATA AATTACCTCTAGATTGTCCAAAGCCCAAGTCTTCCCTTCCCTGTGC/AJGCTTAGAACTAAGTAG CAGTACTGTTGGTGTGTTTGTTCCTCCAGCAATGCCTACTGCGAGTACTTAGTAACAACACTAG AGGTGGAGGGTNTCCGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8332	114 AC ---	---	---	TATGTACTCACTTTCAGTTACCCCGTGCCTCCAGAAATCGCATGTGTCTCCACCTGGGGCGGATATA AATTACCTCTAGATTGTCCAAAGCCCAAGTCTTCCCTTCCCTGTGC/AJGCTTAGAACTAAGTAG CAGTACTGTTGGTGTGTTTGTTCCTCCAGCAATGCCTACTGCGAGTACTTAGTAACAACACTAG AGGTGGAGGGTNTCCGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8378b	311 TC ---	---	---	TGCGGGCTTAACAGGAAGCATGACTGGAGGCCCTCAGGAAGCTTATAATCATGGCAGAAAGCGAAGG GGAAGCAAGGACCTTCTTCACATGGCAGCAGGAGAAAGAGAAAGGAGAGTCTACACACTTTT AAACAACCCAGATCTCATGAGANTTCCATCGGGAGACAGCACTAGGGGATGGCACTAAACCATAGA AACTGCCCCCATGATCCAAATCACCTNTCACAGGCCCTCCTCCAAACACGTTGGG
WI-8378	308 TC ---	---	---	TGCGGGCTTAACAGGAAGCATGACTGGAGGCCCTCAGGAAGCTTATAATCATGGCAGAAAGCGAAGG GGAAGCAAGGACCTTCTTCACATGGCAGCAGGAGAAAGAGAAAGGAGAGTCTACACACTTTT AAACAACCCAGATCTCATGAGANTTCCATCGGGAGACAGCACTAGGGGATGGCACTAAACCATAGA AACTGCCCCCATGATCCAAATCACCTNTCACAGGCCCTCCTCCAAACACGTTGGG
WI-8426	184 TG ---	---	---	TTTAGCACATATTTAGCATTAAGCCTCAAAGATACAGCAATATGTTACATCTCTTGTGAAAAACAG TTGTTGTAGACTGTTAANNNNNNNAAATGTAACTCCGACTTGTGCCTAATAGGATTTGACCNITAA GAGGNTCTTTTGTGTGGANGGGTGGCTTTGCTTGAACCTCCATCTGT/GJGCTTGTAGCTGGTG AGGCTGGGAGTATGGANGGNCGGGGGCTTGGCNATGNATCAGTGAG
WI-8450h	61 CA ---	---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTCTACATACACTC/AJCA TCTTCTATCTTAGTCCAAAGTTTGTAGTTTCAATCCCAATATACCAATTCATTTTAAAGA AAAAACCTCCAGTTATTGTCAAGAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTCAT

WI-8450g	55 T C ---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATTC/CJACACTCCAT CTTCTCTATCTTAGTTCCAAGTTTGTAGTTTCAATCCCAATATACCAATTCCTATTGTTATTTTAAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGTTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450f	108 T A ---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAGTTTGTAGTTTCAATCCCAATATACCAATTCCTATTGTTATTC/JTTTAAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGTTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450e	125 T C ---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAGTTTGTAGTTTCAATCCCAATATACCAATTCCTATTGTTATTC/JTTTAAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGTTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450d	125 T C ---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAGTTTGTAGTTTCAATCCCAATATACCAATTCCTATTGTTATTC/JTTTAAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGTTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450c	108 T A ---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAGTTTGTAGTTTCAATCCCAATATACCAATTCCTATTGTTATTTTAAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGTTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450b	61 C A ---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTC/AJCA TCTTCTATCTTAGTTCCAAGTTTGTAGTTTCAATCCCAATATACCAATTCCTATTGTTATTTTAAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGTTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450a	55 T C ---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATTC/JACACTCCAT CTTCTATCTTAGTTCCAAGTTTGTAGTTTCAATCCCAATATACCAATTCCTATTGTTATTTTAAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGTTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8458b	60 A/G ---	---	CAAGGAAAGCTGTCAGTCTTCATAAATTTCAAGAGTTACAAAAATACGTTATTTTAA/JGJCTA CAATTCAAGATTAGCATCCAAACCTCAAAACATGATGATACATTCGTACACACCATACAACTTCAC ACCTGGCTACAGCAATGTTGACTTACATCACCATTGTTTACTTGTGAAAACTTTATTGTCACAGT GACATCCATTCGCCAGACTTAATGTTATAAGCAGCTGAGCAGAGTTCTCA

WI-8461c	105 A T ---				CTTCTCCTCCAAAATCTACATGAATACCTGAAGACAAATATACTACAACCTTACAAAATGCCAATTA GACAAAGAGANTAAATGATATAATATAATCATTTT[AT]NNNNNNNNCCCTTGCTTATTACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAAACAACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAANTCAAGGATTTCGAAAAAGGGGG
WI-8461b	38 T C ---				CTTCTCCTCCAAAATCTACATGAATACCTGAAGACAA[AT]CJATAACTACAACCTTACAAATGCCAA TTAGACAAAGAGANTAAATGATATAATATAATCATTTTNNNNNNNNCCCTTGCTTATTACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAAACAACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAANTCAAGGATTTCGAAAAAGGGGG
WI-8461	38 T C ---				CTTCTCCTCCAAAATCTACATGAATACCTGAAGACAA[AT]CJATAACTACAACCTTACAAATGCCAA TTAGACAAAGAGANTAAATGATATAATATAATCATTTTNNNNNNNNCCCTTGCTTATTACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAAACAACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAANTCAAGGATTTCGAAAAAGGGGG
WI-8461	105 A T ---				CTTCTCCTCCAAAATCTACATGAATACCTGAAGACAAATATACTACAACCTTACAAATGCCAATTA GACAAAGAGANTAAATGATATAATATAATCATTTT[AT]NNNNNNNNCCCTTGCTTATTACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAAACAACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAANTCAAGGATTTCGAAAAAGGGGG
WI-9438	77 A G ---				AATAACATGTTATGAACAAGCTGGTTACAAGTAGGTAGATGACTTAATTTTGATAAAAAAT TAAAAAGCAT[AT]G/AACATGCATATAAAAAATTAGATTATGTACAAAATACCAACAGTATTTACTTC TGCTCAGTAATTAATAATCTTCCCTTGTGTTTGTCTTTTAAAAACATTATTTCTGAAAAAAA ATCAGAAAAACATGATCGTGGAGAAATTATTA
WI-9439b	101 C T ---				ACAGAAATTGACCTTTATTTGTGTACTAAAGCCTGTTTAACTTTTGATACAAAAGTAACATTTTAGTA CAGAAAATCCCAGTCTGCAGCTCAGTACCTGT[AT]GTGACACTGTACCATCTCAGTCCCACCTCT GCCTGTAACCTAGAAAACAGCCCTACCCCGAGGGGTCTGCGAGTTAATACCTTGAGAAATAGTCTA CAGTTTTTCATAGTTGTCTGAGCTAGAAAACCTGTACCTGTAAAAACAAAG
WI-9439a	76 C T ---				ACAGAAATTGACCTTTATTTGTGTACTAAAGCCTGTTTAACTTTTGATACAAAAGTAACATTTTAGTA CAGAAAAT[AT]TCCAGTCTGCAGCTCAGTACCTGTCTGTGACACTGTACCATCTCAGTCCCACCTCT GCCTGTAACCTAGAAAACAGCCCTACCCCGAGGGGTCTGCGAGTTAATACCTTGAGAAATAGTCTA CAGTTTTTCATAGTTGTCTGAGCTAGAAAACCTGTACCTGTAAAAACAAAG
WI-9446b	75 T C ---				GAAGGCTTGATTAAAGGAGGNTTTATTTGATGTAACCTTACCATTCCATAGACTATAAAGANCATTA TAAAAAA[AT]C/CCTCTAAAGNGACACATGCCCCAAATGACCANGNCATAAGCAAAACCTTTTAAAT TACTCATCTTCATATGTGTGTTGTGTCCTACTNTTATCACTGTGCTCTGCTGCTTTGCTGCTACCTA TGNGAACTGCACACTATCTGTGGCAATATGT

WI-9446	75	T C ---	---	GAAGCTTGATTAAAGGGAGGNTTATTGATGTNAACCTTACCATTCCATAGACTATAAAGANCATTA TAAAAAAATTCJCCCTCTAAAGNACACATGCCCAAATGACCANGNCATAAGCAAAACCTTTTAAAT TACTCATCTTTTCATATGTGTGTTGTNCCCCTACTNTTATCAGCTGTCTCTGCTCTTTGCTACCTTA TGNGAACTGCACACTATCTGTGGCAATATTGT
WI-9497b	185	A ---	---	ATTAAATGTCAAGGTTTCATGTTTACATTTTCTTATATCAAGTACAATGGTATATATACTTTTTTT GAGATAATTATTTCTAGATTCAGGCTTCTCTAGATGTAAGTNCCTAAAGCTTATAGTTTACATTGA TATCTAGACATATATCTTAAACAGCTCCAAATTTNCTTTAATTAATCAAAAGTATGTTAATGTCACTT GGAATTTACATGGAAAGGCCAACAAATAAATACTAAAGCTTGACTAATGSAAG
WI-9497	185	A ---	---	ATTAAATGTCAAGGTTTCATGTTTACATTTTCTTATATCAAGTACAATGGTATATATACTTTTTTT GAGATAATTATTTCTAGATTCAGGCTTCTCTAGATGTAAGTNCCTAAAGCTTATAGTTTACATTGA TATCTAGACATATATCTTAAACAGCTCCAAATTTNCTTTAATTAATCAAAAGTATGTTAATGTCACTT GGAATTTACATGGAAAGGCCAACAAATAAATACTAAAGCTTGACTAATGSAAG
WI-9523b	193	C A ---	---	GTGAAAAAGTTTCTATTCCATCCATACATAAGATTGTGCTAAGGATCATTTTGGAGAAGTGTG CAGCATTCAGAAAGTTGTATCTCATCATGCAGTCACTCAGCAGCATTTTATCTAAAGTACGTGCACA GACTCAGACAAATTACAAACTATTTAGCCCATGATCTATGGTGATTTTCCACACATTTGTA[C/A]AGTG AAAGCTCTTCAGCTTGGAAACAACCTTGTCAGGCGAGCTGCATGCACATATAT
WI-9523a	47	G A ---	---	GTGAAAAAGTTTCTATTCCATCCATACATAAGATTGTGCTAAG[G/A]ATCATTTTGGAGAAGT GTGCGCATTCAGAAAGTTGTATCTCATCATGCAGTCACTCAGCAGCATTTTATCTAAAGTACGTGCA CAGACTCAGACAAATTACAAACTATTTAGCCCATGATCTATGGTGATTTTCCACACATTTGTACAGTGA AAGCTCTTCAGCTTGGAAACAACCTTGTCAGGCGAGCTGCATGCACATATAT
WI-9554	202	T C ---	---	AAAAACAAAGTTTCATACATCACAAAAACCTCCATTATAACACAGAAGTGATTATTACCAGAC AAGCATCAGTGATGATAGTACTGCTTNTAGTTGTTATTGTACAACTGCTGTAGATAATGCAGCCCCATG CAATACACCCCAAGAACACACTAGAGTCTACACCCCAAGTACATATGATAAAGCAGCCCTCTGCAAGTG GTT[C/GCTGGTATACCCTAAGAAAGTCTACTGCAGCCATGTTGGTTATGATTTT
WI-9555	97	G A ---	---	CCAAAGGCCAAACCATTCATATGTATGGATTTCATAAACATTTATTGATCCTTTTGTGAGGTAAGTAT AAATACCTTTACATGGCTAACCTTCTAAC[G/A]CTTGAAAAATCAATTTCAAGGGGACTCTTTAATCA GTTAAATAATCTGCTTTAGAAAGGCCAACAAATGATCATACTTCAGATTAAATACAGGTAAGTATTGAG GGNTAAAATGGTACAAAAAAGGCTGTAACTCTTTNCTTCACATTGATCACA
WI-9625b	172	A T ---	---	TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAAACATAGCTACCATATATTTGTATCTNCTCCTTGGGAAAAACCTTTGGAAAAAATAACACGCACA TAAGTATCATAACTGAGGGTTGTGGACAAGTTACTTCTTA/TGTTTACCAATTTTATATTGACATAA AGTAGCACAGACTAGTTATTTCATTTAAAAAACAACACTGACAAATCTTTC

WI-9625	172 A T ---	---	TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAAACAATAGCTACCATATATTTGTATCTNCTCTTGGGAAAAACCTTGGAAAAAAAACACGCACA TAAGTATCAATAACTGAGGGTTGTGGACAAGTTACTTCTATGTTTACCAATTTTATATTGACATAA AGTGCACAGACIAGTTATTTCAATTTAAAAAACACACTGACAAATCTTTTC
WI-9647	144 C T ---	---	TTTTCTGAGATTCAAAGAGCTACATTTTGGTTAGTGTATGCTACTATACCTTTTTCATCCTTTCA ACATCTTTTGTACATTTTAGGTGATGCTCTTGTAAACAGTGTATTGCTAGACCTAAAAATCCAAGCT TACAACCT[C/T]GTCCCTTACCTGTATACATTTATTCATTTACTTTTCAATTTGGATTTTAAAAATGTTA ACTTAATACGTCCTTTTCAGATGTCCTGCTTTTGTAAATGTTGTTT
WI-9676n	114 A G ---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCA[AG]GATGTGGCTTTCCCTGCC CCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAACTCCTATGCATTGTTGTTT
WI-9676m	184 G T ---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCCCTGCC ATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGC[G/T]CATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAACTCCTATGCATTGTTGTTT
WI-9676l	84 A C ---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCCCTGCC CCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAACTCCTATGCATTGTTGTTT
WI-9676k	202 C T ---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCCCTGCC ATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGA C/T]CAGGGTCTCTCAGCTTTAAAGCCTTGGAACTCCTATGCATTGTTGTTT
WI-9676j	92 C T ---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCCCTGCC CCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAACTCCTATGCATTGTTGTTT
WI-9676i	173 T C ---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCCCTGCC ATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTT[C/C]CCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAACTCCTATGCATTGTTGTTT

WI-9676h	134	C A ---	---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGGCTTTCTGCCCCQ C/AJATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTG AGGCCAGGGTCTCTCAGCTTTAAGCCTTGGATCCTATGCATTGTTGTTT
WI-9676g	202	C T ---	---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGGCTTTCTGCCCCQ ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGAGG C/TJAGGGTCTCTCAGCTTTAAGCCTTGGATCCTATGCATTGTTGTTT
WI-9676f	184	G T ---	---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGGCTTTCTGCCCCQ ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAGCCTTGGATCCTATGCATTGTTGTTT
WI-9676e	173	T C ---	---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGGCTTTCTGCCCCQ ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAGCCTTGGATCCTATGCATTGTTGTTT
WI-9676d	134	C A ---	---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGGCTTTCTGCCCCQ C/AJATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTG AGGCCAGGGTCTCTCAGCTTTAAGCCTTGGATCCTATGCATTGTTGTTT
WI-9676c	114	A G ---	---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGGCTTTCTGCCCCQ CCCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAGCCTTGGATCCTATGCATTGTTGTTT
WI-9676b	92	C T ---	---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGGCTTTCTGCCCCQ CCCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAGCCTTGGATCCTATGCATTGTTGTTT
WI-9676a	84	A C ---	---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGGCTTTCTGCCCCQ CCCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAGCCTTGGATCCTATGCATTGTTGTTT

WI-9738b	40	C A ---	---	TGGACCAACACACAGACAGATGATTCCTGGTGCCTGTGTA[C/A]ATTACAACACTATTGATCACATGC AGCAACATCAACATCTCAAGGAGTCCATTGTTCAAAACACAGATAAATGACTCCACATTTTCCCTTT GAGTCAACAAAAGACTCTGCTTGACCTTGCTGGAGCGGGTGGTTTTTCACTATGTGAGTATCTA TCTTTTATTCTGTCCTTATGTTGGTGGCACATGICGTATGCTGICC
WI-9738	40	C A ---	---	TGGACCAACACACAGACAGATGATTCCTGGTGCCTGTGTA[C/A]ATTACAACACTATTGATCACATGC AGCAACATCAACATCTCAAGGAGTCCATTGTTCAAAACACAGATAAATGACTCCACATTTTCCCTTT GAGTCAACAAAAGACTCTGCTTGACCTTGCTGGAGCGGGTGGTTTTTCACTATGTGAGTATCTA TCTTTTATTCTGTCCTTATGTTGGTGGCACATGCTGTATGCTGCC
WI-9756	47	A ---	---	ACTGAAATGTAATGGCCAAAGGCCAGGACCTTAAATCATAGAAGTTAATCTGTGGGAAAA GAGTAACACAAAAGCATCTAACAGAGCAGGATGTGATGTAATGTGCCCTTATCATTAGTC AGTAAGATAAGAAAGCCCTGGTGAATCCACTCCACAAACACACAGATAATACACTTTTGGGAA ATTCCACTTAACCACTTGATCTTCTACTTTTTTATGATTTAAACTCTCCGTGG
WI-9758	135	A G ---	---	GATGGTCCCTTAAGGATTGCAATGGTTAATGGGCAGACTGGTGCAAAAGAGGCTGAATTGAATAAT TAGGAACTGGGAGAAATCAATTCAAAAGAGAAATCTTGTTGCAAGGTCAATTTTATATACTATTA A[A/G]TAAAAATAACTCTGGTAGGTTCTATAGCAAAATGCTAAGTAAAGTAACCGCTGGTTCTAAAT ATTACG
WI-9778	127	G A ---	---	ATTAAATCCAGGCAGCGGGGAAAAATGGATACTTTCATATGCTCTGACCCAACTATAAACTTTTG GTTCTCATGCACCAATTTTCAATTTTGCCTTCTCACTCCAAAGTACCAGTATTTACCAATTTG[A/CTCTC ATAATTGACTTTTGTACTGGAAGAACTCTTAGAATGTTGGAATTTCTCTATTACACACTTTTGCCTCA AAGAAATGTCAGTCAGGACTAAGGCAATAGTCTCAGGGCAGACAGCC
WI-9832	116	C A ---	---	TCTCCCTTTTGGCTCTCATGCGCACTCCCTCAGCTGCACAGAGCGTTTCTCCAGTGTAGTCTCTGGT CCATCTGCATCAAAATCACCTGCAGGACTTGCTGACAAATGCAGTTT[C/A]TGGATCCCACCCAGGA CTCAAAAAAAGTAAAGTGGGAGAGAGGACCTGGAATCGGTGTTGCTAGCAAGCCCCCAGGTGG TTTGTAAAGTGGACTAAAGTTTGAGGACCAAGACATGGAAGTTGGCTTTGGC
WI-9841	101	A G ---	---	TGGAAAAATAGCTTTTATCAATCTCTGATATGCTACATATGTCATGGAGAAATGCAGAATGGCATGA TATGAAATCCATTTTGAATGAATAAAATATAC[A/G]TGTGTATGTATATATACTATTAAACACTT AGGATTATATACACACAATAAAACGCTCTGTAGGATAAACTAAGGTTCTATCAGTGGGAAATGAGA TTGAAAAGAGGGGATGTTACTTGATGCTGTTG
WI-9880c	222	G A ---	---	GAACATAACACTTCTTGCATGGATTTTCTTGATTATGGCAGTTAAACAATAAATGTTATTAGATC ACTGGTCTCTGTGGGTTGAGTTTTTATGATATCTCTGTAGACCCATAAGGGAGGCTGTGA GTTGTTTCTACATCCTTGGACTATATAAGATCCTCTTTTAAATATATTTTATAAGCACATGAA AATGGAATGAAATAATGA[G/A]TTGACATAGGAATTACCTACATATTTTG

WI-9880b	157	C A	---			GAACCTAACACCTTCTTGCATGGATTTTCTTGATTATGGCAGTTAACAAATAAAATGTTATTAGATC ACTGGTCTCTGTGGGTTGAGTTTATGATATCTCTGTTAGACCCATAAGGGAGGCTGTGA GTTGTTTCTACATCCTTGGAC/C/A/JATATATAAGATCCTCTTTTAAATATATTTTATATAAGCACAT GAAATGGAATGAAATAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-9880a	108	C T	---			GAACCTAACACCTTCTTGCATGGATTTTCTTGATTATGGCAGTTAACAAATAAAATGTTATTAGATC ACTGGTCTCTGTGGGTTGAGTTTATGATATCTCTGTTAGACCCATAAGGGAGGCTG TGAGTTGTTTCTACATCCTTGGACTATATAAGATCCTCTTTTAAATATATTTTATATAAGCACAT GAAATGGAATGAAATAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-10183	127	C T	---			ACACTGCAGGCACCTCCAAATCCTNACAGACATATGCACCTTGGAAATCAACTCAGGCATGCACAGCAT CCCTGTGCTGGAGTTTATTTTAAAAACAACGCCCCAGTTATCACAGTTCTNTTTTGT[C/T]CACC ATTTCCATAACAAAAGAGCTACACAAAATTTGGGGGAGANACTCTCTTTGGAGACTGACACATT TGCAGAGGGGTCATGAATAATGATTCCAAA
FB25G10b	109	A G	---			TCCTCAATGACAGATGAACATAATTTCTCTTGGGTAGAAATACCTTTATGTCCATTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAGAAATGGAA/JGJGATTTTAGATCCTCCCCCAG TGACAAAGTAACTGAACCTGACCATAATTTATACATAAAATGGAATGTAAGAACCCTATTTTGGATATCC GGAC
FB25G10	109	A G	---			TCCTCAATGACAGATGAACATAATTTCTCTTGGGTAGAAATACCTTTATGTCCATTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAGAAATGGAA/JGJGATTTTAGATCCTCCCCCAG TGACAAAGTAACTGAACCTGACCATAATTTATACATAAAATGGAATGTAAGAACCCTATTTTGGATATCC GGAC
IB3071	102	C A	---			ACAACGCTGAACCTTCCATAACAGTCAATGGTACAGTCAAAACATCACATGTACAGAACACACAATTTA GATGAAC TGAAATTAAGNTAAATAAAATAAAAT[C/A]CAATTTTCAGNAAACAAAAATCAAAAC ATTAAGGNTCCCTGNNATATCTTAAACCCTAATGAGATTTCACCTGGNCTCAAGTCATTTTGTAGTGA GGCATTCACAATATGACCCCTATTAAACCCAGTCTAGGGATTCTG
NIB551	161	C T	---			CGTCTTTCTCTTTTGAGATTGCAATTAAGTAGATAATATGAGAGAGAACTGACAAATGGGTTGTCCC TACTGAGCTTGGGCCCAGGTGTACTTAGGAACCCATCCACCAGAGAGACTCATCTATGTTA ACACTAAGGATGCCCTGGAGGAGT[C/J]TGACCACATACATGCGGCCATTGGTTGATTTCAGCTTT GCAAGCAGCGTAGTGAGAAACCAAAAGCTTGTC
S72904	51	G T	---			AGCATAGAAAGTGATTATATTTTAAATGGTTTCAAGTGGAAAGTTCCCTTT[G/J]AATTTGTCAGTTT ATTCCTGGAAATCTTTTGAGTTAAATAAGGATCCTAGGACAGACACCTCGAACTACAGGCCCTAAA GAGAAATTGCTCAAAACCAAGCTGTAACCTCTCCCTTTCTGCAATTGGTTGCTTTTAAATA TTGCAAAAGTCTGTGATGCTAAACAGTATTGGAGTGTTCAGTGTCTGTA

UTR-00481	115	CT	---	---	TATCTTTTATCCTGGGGCCACAGTCTTGATTATCTCTTGTTAAAGACTGAATTTGTAACCCATTAGATAAATGGCAGTACTTTAGGACACACACAAACACACAGATCTJACACCTTTTGATATGTAAGCTTGACCTAAAGTCAAAGGGACCTGTTAGCATTTCAGATTGAGC
ESTC1	33	---	---	---	CCCTGTAGCAGTCTTCAGCCTCCTCTACCCCTACNAGATCTGGAGCAACAGCTAGGAAA
ESTC102	37	---	---	---	GCTACTACCACGGCTGCTTGGTGGACAAAAATAACNAGGAGGCATCCACGGGATTAGTTA
ESTC103	21	---	---	---	GCCATCAAAATTTCCCTCACANTCAATACTGTTGAACAACAAGATAACACATCTTCTTGCTCATCCC ACTTGAA
ESTC107	20	---	---	---	TGCTGGCTCACTTCTCACANGCTGTATTACCTTTTCAGAGCTGAGTGAGGCTGTGCT
ESTC109	35	---	---	---	AAACCAGGAAGGCCCTGCCCGCAGAGGCACATGNACAGGGCAGTGCACAGTGACC
ESTC110	23	---	---	---	AAACCTCACACAGAAAAAGAGGANAACACTCAGAAATGTGATTACAGATTAGGCA
ESTC113	37	---	---	---	AAGGGACACAGTGTGCTGACAAGGTGACACTGAACANACAGTTTTCCTTTAATTGTAAAGCGGG CATCG
ESTC117	24	---	---	---	AATTGGCTCTTCCACATGATACNTAAGTTCAAGGTCCAAAGTTCCCTATCACAATTTACAAAAAGC CTCCA
ESTC119	24	---	---	---	TGTCAGCAGATCTTGAGGGTTATNGTTAAGCCTGATAACAGCCCTCTTT
ESTC122	34	---	---	---	GACAATAAACAGCTAAGCTACTGACATAAAATATNCAATAAATTTATGAGATATAAGGTACAGATG AGAAAAATCTGAAA
ESTC123	21	---	---	---	GAAGCCAGTATGTTGTGGCAANATTGAGAAAAACACACTGAAAA
ESTC128	42	---	---	---	GCAGAGGCATCAGATAAGGCCCTCAGAAAGCCCCAGGCCATCATNTCCATGGGACCAGGCTGGCTCAA TGTTGGAACCTGG
ESTC129	20	---	---	---	AGTCACCATGCCCAGCCTAGNATGAGTTTAGTAAGATTTGGTTAIGCTGGGGAG
ESTC13	46	---	---	---	GTGTATCTGGGCTTCATGGATGCATAAAATTTTCCAGTTGGTAAGNAGCAGGTGCCGAGGGTCTGGA TCAGAAAA
ESTC130	49	---	---	---	GCCTGCTCAACAAGGTAGACAAAAACATAAAATCTTCAGGAAAATGAAACANGAGAAGCTGAAACAAT CTACACCTGAATG

ESTC132	30	---	---	---	---	GGTAAAGTCTAAATTACTGCCTTAGCAACNCATGTGTGTCAGGTTTTCTGCTGCA
ESTC137	21	---	---	---	---	CCAGTTGGCTTCTGTCCTCANAGTCTCTCTCCATGTGGCAACA
ESTC139	45	---	---	---	---	AGGACACAGCCTAAGGACATGAAGTCAGAGTTTCTCAGAGAGNGGGCTGGTCCCTGAGCTAG GAGGAGG
ESTC14	20	---	---	---	---	CCCATTGTGTCACAGGAAGNAGAGGAGGCCACGTTCTTACTAGTTTCCCTTGCATGGTTAGAAAGC TTGCCCTGGTG
ESTC142	72	---	---	---	---	CCTAGGCTCATAACAATACAGTCTCAATACAAAAGACGTAATAATCTATTTTATTTCATTTTAAATC AAAGANACCATTCCATTTCCTAACAAACA
ESTC143	29	---	---	---	---	GTTTACGAAAAGTACTGAAATGCTATTANTAGCTGAATTTGTGATTTCCCTTTTG
ESTC144	26	---	---	---	---	AAATCCATATTTTCTTGACATGAGGNGCTTTTTAGCAGCATTTCCG
ESTC146	20	---	---	---	---	CATGTCAGGATAAGGAGCANACACAGGATTTATACACGGTGGCAGCG
ESTC148	42	---	---	---	---	TCCTTGGTTGTTACACAGACACTTAAGTACTGTATGCTGTATGACGGCCTGTGGAGGCCCTG GGGTGGCTGGGCTGTGCTCTGAG
ESTC149	28	---	---	---	---	TCAGTTCAATTTATTGCTTTAAGAGTTANATACCATGAGACACACAGTTCTGG
ESTC15	28	---	---	---	---	GGATTGTAATATTGCCAGCTTTGTAAAGNCATTAAAGCAGAAGTTCTTCAGTGATCTT
ESTC150	20	---	---	---	---	CCAGGAAAACAAGCAGACACANACTTATAGAATCTTTGGTTTAAAAATTATTCATAATCAATATT AAACCTGATGTTTAAAGAACCTAATGAGA
ESTC151	49	---	---	---	---	GAAGCTAAGGCCCATTTTCTTTTAAATACAAATCTACTGGTGTNAAAACCTCAGAGCTTAGGA AACACAGCC
ESTC155	37	---	---	---	---	TTTTAATTGACAACTCAATCTCTACATACATACAGTNTTGCACGAATTATAAGTGGATCAACAATT ATATTATTGATACAAACTCATGAGCAATTTACA
ESTC156	32	---	---	---	---	GCAGCATTTGTGACAGGAGCGCAAAACAAANNCCTGGCTGCCGATGGAGCGGGGGGGCCTCA CCACCACCTGCAT
ESTC158	35	---	---	---	---	ACCAAGCCCTGGGATTTACTGTCTTGATGACTACANGGCTTTGCACAGCTGAGATGCTCAGTGTGC AA
ESTC159	31	---	---	---	---	AGCTGGCAAGAGACTTCTCGAGGCACATCAGTACGTTGGTCAATTTAGGCACGCTGCTGTTCTGCA GCITTTGAAAGG

ESTC16	23	---	---	---	---	CACTGAATGCTCTGCCATGAGCCNCAAGCAGCACAGTGATCATCACCACAAGGACAGGTT
ESTC160	38	---	---	---	---	TTCTAGCATGCTGGTGCACTGGGGGCGCTGAGCTGGGNGCAGTGGCAGTGTCACCTGGGCCCGTTTG GGACTGGGTGA
ESTC162	36	---	---	---	---	CTCTTCGTCGGTTTGCAGTTGCTGTTTGTTCAGNTACACCAGTCAGAGCTCCACAG
ESTC164	31	---	---	---	---	TCATTCTCCATAGAAATATGGTTTTGTAAACNCGAATACAATCCAATATATAACATTAACAAATCC GATACATACCA
ESTC169	22	---	---	---	---	GTCCTGGTGTGACGGGAATCANITTTGCTGGATTAGAGGAAGGTGCCGCGTCTGTTCCATGACTT
ESTC176	23	---	---	---	---	CACTCCTCCCTGAGCTACCCANGTAGTGTCTGGGAGCTGGCA
ESTC177	42	---	---	---	---	TGGGTGGCTCTTTAAATACCTTCCATTATATTTCAAATTTTNCITTTATTTCTATTAAATACCTTTTAT TCTCTTTATCCCATAAAGGCAACCAA
ESTC18	29	---	---	---	---	TCAGACACTGGCGACATCAGCATTGTCTCNLTGTACAGTCCCTCCCTGCAGGGGCCCTGGGAGAC AACTGGACAAGA
ESTC181	21	---	---	---	---	TAGGGATTCCAAGTTGCCTGGNTTAAATATAATACATATTCACAAAATTTACACAGCTCATGCATAC CA
ESTC186	43	---	---	---	---	GCTTGACTAGCGAGGCTACATCACAAATTTATAAAGTGCCAGATNAGTGCTAATTTGTCATTCAGCTTG ATTTTTCACCTCA
ESTC187	24	---	---	---	---	ACCATGATTGCCCTCACACAAGCATNATCAATCGCCACGAGAGACTGGATGCCAAAGAGATGGCTGG
ESTC188	25	---	---	---	---	TCTATTAAACAGGGTTATGTCACACCNTGTCAACCTCAAAACAGATGATCATCAGTCTGTCTCCAT CTTGC
ESTC189	27	---	---	---	---	AAAGTACAATCCAGTATATGCAGAAAGNTACTCAGCATCACACTCGTGATCA
ESTC196	42	---	---	---	---	TCCTCAAATACCACTTTCCCTAACTTATCAGTCTAGTAAGCNTTTCAAAGGAGGAAAATGGGTTAC CTTCAAGGG
ESTC197	26	---	---	---	---	ATCTCCAGTGTCTGCTGCCTCCTCCNCGCAAAGTCTCCACAAGCACA
ESTC20	33	---	---	---	---	AAGATTAGACAGACCGGTATAGTAAGCTCTGNGGAACTCCAAGATCTAGAGGGGCTGTGGGAA CGCTGCTTAGATC
ESTC200	44	---	---	---	---	TTTGGTGAAAAATCCCAATATATGAGTTTAAAAAATAATCATTANCATCATTAACAGTACTTTAAAT CAATTACTCCTTTTGCCTGCAACAG

ESTC201	35	---	---	---	TCTTACTTGGGTAGTTTAGCAAAACATTTTTAAANCCACATCCACAGATTGGTT
ESTC202	22	---	---	---	CTGCTGGAGGGAGGACAGACGGNCAGGGCGCTGGGTGGCGCCCCAGAAAGCGTGGCGTGATGTT CGAGATGAGGC
ESTC203	27	---	---	---	ACACTTAACAGGTTAAATATCCAAATNAAATTTACTGCAACTTTTGTAGAAATTTTATTGTGCTAC AAGACACGTTGCA
ESTC208	43	---	---	---	TATAGCCCCATCGCTCTCAGTTATTAGAATCTGAGAGGGGATAANAGCAATAACTATTGTTTAAAGC CTAAGAGTGA AAA
ESTC210	29	---	---	---	GATGAAGTGGCTTCCTTTGGCGAAAGGATNAGAAGTGAGTGACGGTGACCTGTG
ESTC212	27	---	---	---	GGGTAACCTGATGAGGAAGCTCTAGTGNAGAAATTCAGGACGCGGTCTTCAGAGCAGAGGGCTTGGT TCAAGTC
ESTC214	21	---	---	---	CTCCAGAGTCCCTCCTCTCANACCGGGCAGGAGGAGTTAGGGAAT
ESTC216	49	---	---	---	TGGCAAGAAATTTATTTACACTAACAAATTAATTTAATCACAGGTATTNTTAGATTGGTCAGAAAA CAAAAGACCA
ESTC217	28	---	---	---	TTTTGTCAATAATGAGCAATACACTGANTGGAATCTGCATGATTAAATAACATTAACAAGTTTCA AAACACACCCCA
ESTC219	32	---	---	---	GTACACATCCTGGGGTGAGCACACAGCAAAANGGGTGGGACGTGCAGAGAGGTATAGGGTAAAG GCAAGGAAGC
ESTC22	41	---	---	---	TCATTGAAGAAAAATTATGGGTTTTATTCTTATTCTAATTNGAGAAATGCTTAATGTCACAGGCTACA TAAGGGCC
ESTC223	27	---	---	---	CTTCTGAAGCCCAAGAGAGGGGCAGAANGTAGTTCTTGATTTAAAAAACAGAAAGGGAGGAGGA
ESTC224	37	---	---	---	CGAAGGTAGATTTCCTCACATATTACAAAAATACACANAAACACACACACACACACACA
ESTC225	20	---	---	---	TGCACGTACTCCCCAGACNGAGAGCTTACATACCATATAGAAAGAGCATAAGTGTTCAGAAGGA ATGTGTAGGATCG
ESTC23	27	---	---	---	TTCACTTTATTTCATATTCACCACNATAACGACTCCTTTAATTTAACTAAAAACCATACAGGGT TCCTGAAGGG
ESTC230	43	---	---	---	GCCTCCACGAAATTTGAAAGACATATTGGCTGACCTGATACNTAAGGAGAGGCCAGAAATTAAGA
ESTC231	24	---	---	---	CAAAAGGGTTAGTCATATTCCTCCCANCAACAGCATGATAAAATAATTC AAC

ESTC28	23	---	---	---	GAAGAGCTGGGCACGCATCTGACNTTCTCTCTATTCCTATAAAAAATAAAGGAGGAGAAATCTGC
ESTC3	20	---	---	---	CAGACATGACCTACCGTCCCGCCCTCAATTCATATTTATCTTGAGCCGCTTGTCAGGTTTGATTCGCACACTCC
ESTC31	32	---	---	---	ACAGCCCCACAGAACTATTGTAACAATATNTCAGTCGGTGATCATTTGTAATATACAATACAAAGCAATTTCTCAGA
ESTC33	25	---	---	---	AGCACTCCAGCTCCTGACGTTGNGGACCAGGGAACCTCCGGAA
ESTC39	26	---	---	---	AAGGAAAGGGAACCCACCTGGGCTTNGGTCACAGAACTCAGAGCCTGGGCATTA
ESTC4	23	---	---	---	CCACTGAATCACACAACATGGACNAATCTCAAAATCATTATGCTGATGGAAAGAAACCAATT
ESTC40	22	---	---	---	GGCATGCTAGACAGAGGCATTANTTTGAAGATCTTTTAAAAATATTTTGACTTGTTCCTCCCTTCAC
ESTC45	37	---	---	---	TTTGAGGTTTGTCGAGTTTGTCTTTGTAACNCTCTCATCGAGGCTATATATAA
ESTC50	56	---	---	---	CTGTCCGTGTGAGCCCTGCCGCTGCCATGGGCCAGGAGCACCCTGGTGGGANCCGGGCGAGATGTTTACCCTGT
ESTC56	45	---	---	---	GTGCCCTGAAGATTAGCAGCAGCAGCAGCAGGTGGCAGGAAGNAGTGGAGGGAAGGACACCAAGT
ESTC57	20	---	---	---	AAGTGGCCCTCCAGTCCNCTCTCTGGGCACAGATCCCACCACTGCTGCTC
ESTC59	38	---	---	---	GAAACACAAAAGTGTGAGAAAAAACTTCTCAAAATTTGTTCCAGACTTCAGGAAAAATGATTTCCACATGGTAAGGCC
ESTC6	27	---	---	---	TCTGCAGCACTTCACTACCAATGAGCNTTAGCTACTTTTCAGAAATTGAAGGAGAAAAATGCATTATGTGGACTGAACCG
ESTC61	57	---	---	---	AGTGATTTGGCTAGGCGTGGTTCTCATCTGTGAAATTCACAGCGCAATGACAGCANCCTCTCTCCCACCCACTCAAG
ESTC63	20	---	---	---	ACAGACACAGCATCACACCCNAGGGCCACGGGAGGGTGGGGAGACGACACTTTTCCCTGGGAAAAGGCAGCTCTAATC
ESTC69	20	---	---	---	GAGAGGCTAGTCAGGAGGGANACCCTCAAGTTTAAATCCCCACACTTACTTACTGCTCATCCGTCACITTCGGCTAA
ESTC7	45	---	---	---	AGTTTCCCTAGAGCTGTGGGCCAGATAGCTGTTCTGAGTTGCANGCAGATGGAGATTTGGACACTG

<u>ESTC72</u>	37	---	---	---	GGGCTCCAAATGGGTATTGGGCCAGGAGGCTGGCNITTTGGCGTGACGCCTAAAAAGTGTGACC AACAAATTCACAGCTACAGGAAATCTAGAACAAAATCAAATAATTCATCACNITGGGTGA AAAAGTTG GAAGA
<u>ESTC74</u>	49	---	---	---	ATGACTTTCCTGTCCTCATCGAAACCAAGAGTTTCCCAGNGAGCCCTCCTATCTGCGGTTA
<u>ESTC77</u>	40	---	---	---	GGCTCAGCACAGGGATAAGANCCCCACTCCGCATGTCCCAGAGGGCAGCACTCCAG TTTCAGATGATGGGGTCTGAGATGNTCCCTCAGGCTGCATCAGCTGCTTCAGICTCCAGAACAGAAA GAGCCTGACCCA
<u>ESTC81</u>	20	---	---	---	CAAAATCAAATACACAGATCCAGATATGTGAACCATATATACATATCTATACANCCATTATTTAGAC TTTCACAAACCT
<u>ESTC82</u>	25	---	---	---	TTTAGCTGCTATACCAAGTTTCCATAAANCCTGCTGCTGGTGGGAGGCTACAGCCTGACCACATTC TTTGC
<u>ESTC83</u>	53	---	---	---	ATTGCAAGGAAGTGAACGTGNTCAAACAGAAATGGTGACAATGA
<u>ESTC85</u>	28	---	---	---	CTGGTTCCTTCGTCTGGCATTCTGCTCCTCCTNGCCAGTGTCCACCAAGTGTCTTCCCGATGAT
<u>ESTC89</u>	22	---	---	---	CTCCCCCTCTCAGTTCACAGTGGAGACTANGGAGATTGAGGGCAGGATCC
<u>ESTC90</u>	33	---	---	---	GCACGTCTTTGTTCTCTCTCCAGAAAGTTGNAGACGCTAATTAGTTGATTATCIGTCG
<u>ESTC93</u>	29	---	---	---	AAATGACTTGACGAAGCTCATAGAAGATTAGCAGGTAGTAGAATAATGACTGTGACTCTTAATTCA GTGGATCTCCCTGGCCACCGTTTTGATTGAGCTGCAATGCTTCCCTTGACTGTTCTCCA/C/TGCCAG ATCTTATCAATGATCTTTCACCTAAGAAACAGCAAAAGATTCTGGCAAGCACACGATCTAGAGATAC ATCTTATTGCGATTTTTCACAAAAATCAAAGAAGAAAGAGGCTTAGCTG
DWU-100	127	C T	---	---	TTCATCCTAGATATCTACTCAAATAAATTGAGACAAGTGTCAAACAGAAAGACGCTTGTGCTGAA TGTTATGGC/GJGCCCTATTACAGTAGCCAAACGATGAAAACACCCCAAGCTATATATTACCA GATGAAAGGATAAACAAATGTGGTCCATCCATACAATGGAGTATTACACAGCCATAAAAAGGAAT GAAGCAGTGATCCCTACTACACTGTGGAT
DWU-177	77	A G	---	---	CAAAATACCTGGACTATCAACCTTGTGCTTAATCCCTGCAGCATTC AAGGTTAATCCATCTAAGTGAC ATTTTGAATTCAGCGGTGCCACCCAAATCATGCCAGCTTCTGTCATATGAATGAGATATACATTT ATGCTGACCTTCCCTCAAGACTGATTTTTCATGCTGGGACTTACAATATCTCAAGGAACAGCAATG TCAACAGGJA/CTGGGAACACCGCCCTATCTGAGCTTCGGCTCCCTCC
DWU-286	213	A C	---	---	

EST10398	147	C T	---			TGCTGGGGTGGCAAGGCTGCAAAACAAGGAGGCAACCCAGGAGGCTTTTATGAAGGGGCCATGGTA
2a	14	G C	---		---	AGATGCTGCCACCTCTTATCTACTTATGATGTTTCACTTTGGGGCTTGACATTTCCAAACACGGAGAAG
ESTD-C7	14	G C	---		---	CATTGTTTCTTTC/TGGGCCAAGAAGGTATCTACCAATAGTGTCTATTAGGCAATTTG
ESTD-	90	T C	---		---	ATATCGTGGCCTTA/G/C/TACCTAGAGCTGGACAATCCTGCTGGA
D4S95	90	T C	---		---	CTTTCATGCACGATAGGCTTCTCTACTAATCACAGAATTTTGAGAAGAGCAAAACAACCTTTCAAGG
ESTD-	38	G A	---		---	ATAATGGGGCAATCACCTTCTTTT/C/C/TCTCTTAGAGTCTACCGG
GPPK2L	38	G A	---		---	AGTCTTCATCTGCGGTGCCAGGTAGATCCCTTTTACC/G/A/CCGAGAACTGCTCGATATC
ESTD-	82	A G	---		---	CTGGGCTGCGCGCAGCAGCTGCTGGCACTGGACGGCGGGCGCAGGCTCAOCTCTATAGTGGGTCG
HRASb	82	A G	---		---	TATTCGTCCACAAA/A/G/TGCATCTGGATCAGCT
ESTD-	37	C T	---		---	CTGGGCTGCGCGCAGCAGCTGCTGGCACCTGGACGG/C/T/GGCGCCAGGCTCAOCTCTATAGTGGGG
HRASa	37	C T	---		---	TCGTATTCGTCCACAAAATGCATCTGGATCAGCT
ESTD-	81	A G	---		---	GGAGGCAGGAGGTGGGGAGGGGCTGCTGCTGCCAGGTCCACAGACCAGAGAAGGGCCCTCAGTG
NRAMP	81	A G	---		---	TATCCCAACCCCA/A/G/TGTGGCGCTGGGAGATGAAGAGAGGTTGATGCAGGT
ESTD-OTC	18	A G	---		---	GTGACCTTCTCAGTTTAA/G/AAACTTTACCGGAGAAGAAATTAATATATGCTATGGCTATCAGC
EST36751	36	C T	---		---	AGATCTGAAATTTAGGATAAAACAGAAAGGAGAGGTATGTAACA
7	36	C T	---		---	CCAAGTCGTTCAATTTAGCTTTGCAGGTTTAACT/C/T/GATTACTTTTCTATTCAAATCTCTGTA
					---	AAATTGAAATATGAACCTAGTTTCTGATCTATGGTTTCAAGTTAAACAG
					---	CACGTGGAAGGAGCTATTTTGGAGGCTTTAAGAGTAAAGAAATCTGCCCAAACTTGTGGCTGAC
					---	TTTATGGCTAAGAAAGTTTCACTGGATGCATTAAACAATAA/G/JTTTACCTTTTGAAAAATAA
					---	ATGAAGGATTTGACCTGCTTCGCTCTGGAAAGAGTATCCGTACCGTCTGACGTTTTTGAACAATACA
EST40562	109	A G	---		---	GATGCTTCCCTTGTAGCAGTTTTCAGCCTCTCTACCCCTA
					---	GCTCTATACCCCTGTGGTCTCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGCTGAGAA
EST18288	121	C T	---		---	GATTGACAGGTTTCATGCAGGCTGTGACAGGATGGAAGACTGGCTGCTCCCTGA/C/TGGGAGCCAGT
3	121	C T	---		---	GTGGACAGCACCCCTGGCTTCAACACCTACGTCCACTTCCAAGGTAAGGCCAAACCTCTCTGCTGGCTC
					---	TGGCCCTAGGACTTAGTATCC
ESTD-AK-168	31	C T	---		---	GGGAGTGACAGCTAGAGCAACCAAGGGGGGCT/C/T/TACAGCTGTGTCTCATGGAGGACAGGCTTCT
					---	GCTCATTTCTGG
					---	AATCCCAGCACTTTAGGAGGCTGAGGCAAGGCATATCACCAAGGTCAGGAGTTGAGACCAGTCTGA
					---	CCAACATGGTGAACCCCATCTCTACTAAAAATACAAAATAGCCAGGCAATGGTGGTGCATGCCTGT
ESTD-ALB	180	A G	---		---	AATCCCAGGAGGCTGAGGCAAGGAGATCGCTTGAACCTGGGAGGCG/A/GJAGGTTGTGGTGAGCCGA
					---	GATGGCACCATTTGCACTCCAGCCTGGGCAACAAGAGTAAAACTCTGCTCTC

EST70523 3	182 G T ---			TTCCGGCAGCCCCCATCTTGGCACCCCTGGTCCCTCCAGGGCCACCCCGGGCAGCTACCCGCTCTCGCTCGGTAAACATCCGGCCGGCGGCGTCTTGGACATAGCTGGACCGTTCCGTATAGGAGGACCGTGTAGGCTTCTGTCCGGGCTTCCAGGGCCAGCCCTG[7]CAGAGAGAGGGGTCCCTGTGGTGAGCTGAACACAGCTGTGGAGTGTCTCCACGTG
ESTD- APOA2	101 C T ---			CCAGGTGTTGTGGCACGTGCCTGTAATCCAGCTACTCTGGGAGAGCTGAGGCATGAGAATCTTTTGAACCGGGAGGCGGAGGTTGCAGTGAGCTGACATCG[7]GCCACTGCACCTCCAGCCTAGGTGACAGAGCAAGACTCC
EST58707 7	112 C T ---			CAGTGTATCTGGAAGCCCTACAGGACACCAAAATAACCTTAATCATCAATTGGTTACAGGAGGCTTTAAGTTCAGCATCTTTGGCTCACATGAAGGCCAAATCCGAGAGAC[7]CTAGAAAGATACACAGAGACGAATGTATCAAAATGGACATTCAGCAGGAACCTCAACGATACCTGTCTCTGGTAGGCCAGGTTTATAGCACATTTGTCACCTACATTTCTGATTGGTGGACTCTTGTCTGCTAAGAACCTT
EST74167 6	137 C ---			AGACCATGAAGGAGTTGAAGCCCTACAAATCGAACTGGAGAAACAACCTGACCCCGTGGGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGCGCGGCGAGGCCCGGCTGGCGCGGACATGGAGGACGTGCGCGCGGCTGGTGAGTACCGCGGAGGTGCAGGCCATGCTCGGCCAGAGCACCCGAGAGCGTGCGGGTGGGCTCGCTCCACCTGGCAAGCTGCGTAAGGGCTCCTC
EST43211 8	132 C ---			CGCCTGTTGCAGTACCGCGGCGAGGTGCAGGCCATGCTCGGCCAGAGCACCGGAGGCTGGGGTGGCCTCGCTCCACCTCGCAAGCTGCGTAAGCGGCTCTCCGCGATGCGGATGACCTGCAGAAAGCGCCTGGCAGTGTACAGGCGGGCGGCGAGGCGCGGAGCGGCTCAGCGCCATCCGCGAGCGGCTGGGCCCTGGTGGAACAGGGCGCGGTGCGGGCGCCACTGTGGGCTC
ESTD- APSB	126 A ---			GGAAATAATGGAGCCTGTGGGAAGGAGCGTCCGAGGGGTGGGCTTTGGCAAGCCCTTGCTGAGCAGAAAGGCGTGAAGACCCGGAGCTCATCACATCTCTGACTGGCTGCCAACACTCATGAAGCTGGCCAGGGACACACCAATGGCACAAAGCCTCTGGATGGCTCGACGCTGTGGAAACCATCAGTGAAAGAGCCCATCCCCAGAAATTGAGCTGCTGCATAATATTGACCCAAAC
EST36770 4	144 C ---			TGTAGCCAAAGTCACCTGCATCATCTTTGGCTGCTGGCAGGCTTGGCCAGTTTGGCAGCTATAATCCATCGAAATGTATTTTTCATTGAGAACACCAATATTACAGTTTGTGCTTCCATTATGAGTCCCAAATTCAACCTCCCGATAGGCTGGGCTGACCAAAAATATACTGGGTTTCCTGTTTCTTTCTGATCATCTTACAAGTTATACCTTATTGGAGGCCCTAAAGAGGCTTATG
EST26021 1	137 A ---			TAATGTAAGCTCATCCCAAGAGCCTGCACCATGTTTGGGTTGAGTGAGTGTTCGAAACCTGTCCATAAAGTAATTTTGTGAAGAGGAGCAAGAGAACATTCTCTGACGACTTCACTACCAATGAACATTAGCTACTTTTCAGAAATTGAAGGAGAAAATGCATTATGTGGACTGAACCGACTTTTCTAAAGCTCTGAACAAAAGCTTTCTTCTTTTGAACAAGACAAAAGCAAGGCC
ESTD- BA511	29 A G ---			GGGCAACATAGTGAAACCCCATCTCTACA[AVG]AAAAATACAAAAATTAGCCAGGTGTGGTAGCAAGTGCCCTAGTCCCGAGCTACTTGGAGGCTGAAGTGGGAGGATCCCTTAAGCCTGGGAGGTGGAGGCTGCAGTGAGCCAAGATGGTGCCACTGCA

ESTD- CB22	119 C T ---	---	GGCAAGTTTTATTGATAGAGAGGAATCAATAATGGCAATGAGGAGACATCACCTGGAAATGTTAG GCAGTGCCTAACTGGGGATGGACAGACAATGGCAGTGGCAACCCATAGGGCTGGATACAAAAG ACAGGCAAGGAGGTAGAACCATCAAGAGAAATAGGCTGGTACCCCAAGCAAGGAGGACCT AGTAACATAATTGTGCTTATTATGGTCTTCCCGGCTTCTCTCACACAC
ESTD- CB23	136 C ---	---	TAGAACCATCAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCTAGTAACATAATTGTGC TTCATTATGGTCTTCCCGGCTTCTCTCACACATACAGAGCCCTACAGGACACAGAGCT CTCAGAGAACCTAGCCCCATTACCTTCCCTTCCAGAGGACCTGAAAAACGTTCCCAACCCGA GGTCGCTGTTTGAGCCATCAGAAGCAGAGATCTCCACACCCAAA
ESTD- CB24	145 A ---	---	ACCAGGACAGACAGCTCTCAGAGCAACCTAGCCCCATTACCTTCCCTTCCAGAGGACCTGAA AAACGTGCCACCCAGGTGCTGTGTTGAGCCATCAGAGCAGAGATCTCCACACCCAAAAG GCCACTGGTATGCTGGCCACAGGCTTACCCCGACACGTGGAGCTGAGCTGGTGGTGAATGG GAAGGAGTGACAGTGGGTGAGCAGACAGACCCGACGCCCTCAAGGAG
ESTD- CB25	146 A G ---	---	GTTTCTTTCAGACTGGCTTCACTCCGGTAAGTGAGTCTCTCTTCTCTCTATCTTCCGCGTG TCTGCTTCGAACCCAGGCGATGGAGATCCACGGACACAGGGCGTGAGGGAGCCAGAGCCACCTG TGCACAGGTAGCTACATGCTGCTTGTGTCACAGAGCTTACCAGCAAGGGTCTCTGCTGCC ACCATCCTATGAGATCTGCTAGGGAAGGCCACCTTGTATGCGGTG
ESTD- CB27	125 C T ---	---	TTTTCTGTTCCCTGAAGATTGAGTCCCAACCCCAAGTACGAATAGGCTAAACCAATAAAAAAT TGIGTGTGGGCTGGTGCATTTCAGGAGTGTCTGGAGTTCTGCTCATCTACCTGACCTGATCTTC TGATTAGGGAAGCAGCATTCCTTGGACATCTGAAGTACAGAGCCCTTCTCTCCACCCCAATGCT GCTTCTCCTGTTCACTGATGGAAGTCTCAACACCATTTCCATACC
ESTD- D4S338	59 A T ---	---	TTTTCTGTTTACCTTGTTCAGATCCTTCAGAGGAATCCCTATATGCGAGGTATATGAATATGTA TTTCTTAAACAATAAACTTGAAAGTCCAAAATTAGCTTGCATCCATGGACTGCAGAAATAAATGTTA TTTTAGCTGTCAGAAAAACAATACTAATCTTGCATATGTTTCATCAGAGCCCTTGGGTGACCAGGTGA TTGCCAATAAGCAGTAATTTTGAGAGGAATCTTGTTCATGCACTAG
ESTD- CYP2D6	61 A G ---	---	CAGGCCAGCGTGGTGGAGGTGTCACCATCCCGGACAGAACAGGTACGCCACCACTATGCAAGJCA GGTCTCATATTGAAGCTGCTCAGGGTCCCTTGGCTGAGCAGGGCCGAGAGCACTACTCGG
ESTD- D11S1873	40 A C ---	---	AAAAAACATTTAACACCTTTCAATCATATACACCATA/CJATTTCATTTTTCACATAAGTCA GTTTGAGCTGAGTTTCCAACTTACCTGCAATCTAAAATGTCATAACTGATTAAATGCAAGTTCAACAG ACAACCTTCCCAAGCATCTACGATCAGAAAGGTCAAAATATTACATATCTGGATTAAATATGCCCCA TATCTGCATGTC
ESTD- D17S33b	169 C T ---	---	CATCCCCAAGCCCATCTTAGCCACTGGCATTTTGGCCCTCTGACAGATACACTCAGGGCCGT CATGCTGCACACATCCAGGGGGCCCTACCTTGTAGTCCATGGAAAGGCTCCTCTGGGGGGGTG GGGTGTGTGGCTATGGTGGTCTGTGTAGACCTGGGGGCTTGGTTTCAGTTGCACTATTGCGTT ATTGCAGATTGCTTGTCTTCCACCTGAGCGAGCCCTC

ESTD- D17S33a	75 C T ---	---	CATCCCCAAGCCCATCCTTAGCCACTGGCATTCTTTTGGCGCCTCTGACAGATACACTCAGGGCCGT CATGCTGCTACACATCCAGGGGGCCCTACCCCTTTGTAGTCCATGGGAAGGCTCCTCTGGGGCG GTGGGTTGTGTGGCTATGTGGTGTCTTGTTAGACGGGGCTTTGGTTTCAGTTGCACATATTGCGTT ATTGCAGATTGCTTTGTCTTTCCACCTGAGCGAGCCTC
ESTD- D18S8	133 A G ---	---	TTTGAGACCACCCCTGGCCCAACATGGCGAAATCACATCTCTACAAAAATTACAAAAATTAGCTGGGTGT GGTGGTACATGCTATCGTAATCCAGCTACATCGGAGGCTGAGGCAGGAGATTGCTTGAACCC[A /GJGGAGGCAGAGCTTGACGTGAGCCCAAGATCACACCACCTGCACCTACAGCCTGGGTGACACAGTGA GACTCTGCTCAA
ESTD- D3S11	44 G ---	---	AACTGATTAGAACCTGAAAATACATAATTTATCTGAAAAAAGTCGAGTTATTGGCTCATCACATTGG AATTTTGCATCATTAATAAATCCAAATAAGTACACTGTATAAAGAAATTAACAGAAATATCATTTGT TTATTCAAACTATTTATCAGTTATTTATTGGTAAGCCATACATAATCTAAAGCATGTTCTGAAAG TTTA
ESTD- D3S12	37 A G ---	---	AGGTTCCACATATTGCTGATGTTGCTGATGTTTCCJAGJGGAGCCTTGATGTGATCTCTCTCT CAGGTATCCACCTTGAGACGTACTTTTCAAAACTCTCTACAGCCGTTGTTGTTATTAAATCAAGGT TGAACATAAAGTA
ESTD- D3S2b	247 C T ---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCTGCTG TGAGTCTTATTCAAACTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGATTCCC AGAAGTGAACATACCTGCTCTAGAACCCAGAGTCATGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAATATAATAATCTGCTCTTTATTGGAAGGATGCCTJGGT
ESTD- D3S2a	248 G ---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCTGCTG TGAGTCTTATTCAAACTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGATTCCC AGAAGTGAACATACCTGCTCTAGAACCCAGAGTCATGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAATATAATAATCTGCTCTTTATTGGAAGGATGCCGGTATGT
ESTD- D7S399	83 A G ---	---	TGAATCTTAATTGCTATCTACAAAATGTATAATCCTGAATCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCJAGJGTCTCTCTACATCATCTTTCACAAACATTTTCATCCATGGACTCCATAC TAGAATATTTGAAGAAACAAACATGACAAACATTTTC
ESTD-DMb	146 A C ---	---	GTGGGGACACCGAGGGCTCCAGGCTGGGGCTTTGCACGTGTGGCTCAAGCAGCTGCTCGGCTCCACT TCCATGGGTGTGGGGCTGGGACCTCACTGTCCTGGGAGAGGAGGAGGGAGTGGGAGGGAGACA GAATGCTGATTJACJCTGTGGTGAGAACCAAGTCTGTCCTGTGGGTAGGGGAGCTGCTTCCAAAG ACCTCCTGATTGAGGAAGGGGAGCAGCAGAGCCGAAGAGAACAGAGT
ESTD-DMa	66 C G ---	---	GTGGGGACACCGAGGGCTCCAGGCTGGGGCTTTGCACGTGTGGCTCAAGCAGCTGCTCGGCTCCACJ GJTTCCATGGGTGTGGGGCTGGGACCTCACTGTCCCTGGGAGAGGAGGAGGGAGTGGGAGGGGAGA CAGAATGCTGATTATCTGGTGGAGAACCAAGTCTTCTGCTGTGGGTAGGGGAGCTGCTTCCAAAG CCTCCTGATTGAGGAAGGGGAGCAGCAGAGCCGAAGAGAACAGAGT

ESTD- DRD1	154 C T ---	---	TCCCCAGCCCTATCGGTCTATTTGGACTATGACACTGACGTCTCTCTGGAGAAGATCCAAACCCATCAC ACAAAACGGTCAGACACCCAAACCTGAACCTCGCAGATGAATCTCTGCCACACATGCTCATCCCCAAAAGCT AGAGGAGATTGCTCTGGGGC/TTCGCTATTAGAAACTAAGGTAC
ESTD- DRD2	144 C ---	---	TCTGCCCTTGGTGCAGGAGCTGCCGGGAGGCCAGGAGCTGGAGATGGAGATGCTCTCCAGCACCA GCCACCCGAGAGACCCGGTACAGCCCATCCACCCAGCCACCCAGCTGACTCTCCCCGACCCCG TCCACACAGGTCTCCACAGCACTCCCGACAGCCCGCCCAACACAGAGAAGATGGGCATGCCAAAG ACCACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD- DRD3	109 C T ---	---	AAGACGATGGCCAGGATAGCGCGCAGTAGGAGAGGGCAGTAGTAGGATGTGGGGGGCTGGCTGG CACCTGTGGAGTTCTCTGCCCCACAGGTGTAGTTACAGTGGC/TACTCAGCTGGCTCAGAGATGCC ATAGCCACAGAGGGAGGTGCGTGATGCCAAGGGGCTTCCTGTAGGAGA
ESTD- ERBB2	93 C T ---	---	TCTTCAGGATCCGCATCTGCCCTGGTTGGGCATCGCTCCGCTAGGTGTACGCGCTCCACAGCTGG GGTAGGGGGTGGTGGTCACTGCTGCTGGGGGCGGTGCAGACCCACCGCGGGCTGGGAGGACTTCA CCCCGCTCACCCTCGTTTCTCGCAGCAGTCTCCGCTCGTACT
ESTD- ETS2	43 A G ---	---	ACTCACAGTGCCTTTAAGTGAAATGGTCGAGAAAGAGGACCC/A/GJGGAAGCCGCTCTCGCGCTG GCAGTCCGTGGGACGGGATGGTCTGGCTGTTGAGATTCTCAAAGAGCGAGCATGCTGGACACA CACAGACTATTTTAGATTTCTTTTGGCCTTTTGCACCCAGGAACAGCAATGCAAAAACCTCTTTGAG AGGGTAGGAGGGTGGGAAGGAACAACCATGTCTTTTTCAGAACTTAGTTG
ESTD-F9	111 A G ---	---	AGATCCTGATGATTTTTTCTCTATTTTTTCTAAATGTTTTACAGTTTGAAGTTTAGATTTATGCCCA TGCTCCATTTTGAAGTTAATATTTGTGTAAGATGATGTTTA/A/GJGTCAAACCTTCATTTTTTTTCC ATAGGTATGTCCAAATTTATCCAGCACAAATTTGTTAAAACAAAAAC
EST68787 5	144 A ---	---	CTTCTATGGGATTTGACTTTATTTTCTCCATTTGCTTACCTTTTACAGGTGTTAATATAGTGAAGAAG GAAGCTTGACGCTCATGACAAATTTGAAGCTGACAAATACACAAGAAGGAATAAATTCACAGTCAA AGAATCAAGCACTTTTGAACATTTGAAGTTGTTTTTGAAGTTGTTGTCACCTTTAATACAACTAG CAGACGGAACTGAACCTCAGGGTAAGAAT
ESTD- GCDH	200 C G ---	---	CGCAGACCCGGTCAGTGTGGGGTGGGAGTGTGGAGGGAAGGAGGAACTGGGGGTTTAGGGACT TTCCGGGGTGACTTTCCCGTTCTGTGCTTGACAGAGAAAGCGGGAGAACACAGAGCCAACTGGCTAA GTGTAAGGGACCTCTGGTGGCACCCTGTGTTCTGCTGCCCTGTTCAGCTGTCTGTCTGCCGAGTTC/ GJGACTCTGTCCCGGAAATTCGAGAGCT
ESTD-GCK	88 A G ---	---	GTTTTATGCATGGCAGCTCTAATGACAGGATGTTGACGCCCTGCTGAGGCCACTCCTGGTCACCATGAC AACCACAGGCCCTCTCAGGA/A/GJACAGTAAGCCCTGGCAGGAGAAATCCCCACCCACACCTGGC TGGAGCAGGAAATGCCAGCGGGCCCTGAGCCCCAGGGAAGCAGGCTAGGATGTGAGAGACACAGTC ACCTGCAGCCTAATTACTCAAAGCTGTCCCCCAGGTACAG

[illegible]

EST45311	151	C T	---			GCCCTCCTCTCTCCAAATCTGTCCCTATAGTTTTTCCTCTATTAAAGTGAACATACATGCAATCTTTTAGT GGATAGATGCACACAAACACAAAGCCATTATGGGGAAGGATCCACGTGTGTGGCCATATTGTAACA CATTTTCTGCAAAATC/TACCTCTTTCATTTAACAGCCCTTATCAATGGCCTTTTCTTTTTCAGTA GTACATACACATCTGTGTCATTTGTTGAAT
EST65258	80	A G	---			TGCCCCATCAGCGCGGAGACATGGCTTGCCACAGCTCTTGAGGATGTCACCAATTAACCAGAAAT CCAGTTATTTTCGAG/CCTCAAAATGACAGCCATGGCGCGGGGTCTTCTGGGGCTCGTCGGG GGGACAGCTCCACTCTGACTGGCAGCTTTGCATGAGACTTGAGGAGGGGCTTGAGGTTGGT GAGGTTAGGTGCGTGTCTCTGTGCAAGTCAGGACATCAGTCTGATTAA
EST38216	26	A T	---			ATGCAGGATGAAGGTGGACAGGGAGG/TGAGGGCCCAACCTGTCTCCAGGGCCTGCAGATGTCG CTGGACTATGGGTTGTGACCCCACTGACCTCCATGAGCATCAGGG
EST62782	149	G T	---			ATACTAGTACAAGTGGTAATTTTGTACATTACACTAAATATTAGCATTTGTTTAGCATTAACCTAA TTTTTTCCTGCTCCATGCAGACTGTTAGCTTTTACCTTAAATGCTTATTTTAAATGACAGTGAAG TTTTTTTTCTCTG/TAGTCCAGTATCCAGAGTTTGGTTTTTGAACCTAGCAATGCCTGTGAA AAAGAACTGAATACCTAAGATTTCTGTCTGGGGTTTTTGGTGCATGCA
ESTD- KRT10b	183	C T	---			CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTCCATGTGAGTGTACCTTTTGGCAATATT AAAGGAAGAAATGCAATTTTAAAGTAACTGCTAAGGTTTTTCCATTAAACCACATATTACTTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAG/C/TGTGCTTTTAAATAGT CTCTGCCCAGATACATCTCCCTATATAAGTTATAACCAGTATTGATA
ESTD- KRT10a	133	A G	---			CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTCCATGTGAGTGTACCTTTTGGCAATATT AAAGGAAGAAATGCAATTTTAAAGTAACTGCTAAGGTTTTTCCATTAAACCACATATTACTTCTAAG G/GAGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGCTCTTTTAAATAGTC TCTGCCCAGATACATCTCCCTATATAAGTTATAACCAGTATTGATA
ESTD- KRT8b	231	C T	---			ACCTCACCCCTCCCTTAGCCGTGGGAAGCAGGAAATCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGGCCTGACATGAGACCTCAGACAGAACTTTCTAGAGTT TGCTAGAGGTCAAGGGTCAAGACTAAAGAGGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCATAG GCTGCCCTATCTCTCCCGTCTCAGGTTTACCA/C/TGTCAACATTGACACA
ESTD- KRT8a	21	C T	---			ACCTCACCCCTCCCTTAGCC/C/TGTGGGAAGCAGGAAATCTCTCCAAATCCATGAATACACATC GGATTGGACACCTTGAGAGTCTTAACAGCAGGGCCTGACATGAGACCTCAGACAGAACTTTCTAGAG TTTGCTAGAGGTCAAGGGTCAAGACTAAAGAGGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCAT GGCTGCCTATCTCTCCCGTCTCAGGTTTACCACGTCAACATTGACACA
EST75099	82	C T	---			CACTTGTGTGTAGATCTCTCAGTGGCGCTCTACTGGTTGACTCCAACTTCACTCCATCTCA AGCATCGATGTCAA/C/TGGGGGCAACCGGAAGACCATCTTGGAGGATGAAAAGAGGCTGGCCCCACC CCTTCTCCTTGGCGCTCTTGGAGGTGTGG

ESTD-LF79	142 A G ...	---	GGGTGATTTGAGGCTCAGTTAATATTTCAAAATGTAAACCGTAGCAAAACGTCATTGGTATTAGA AAATATAAAATTTCCAATATGTAGTGTGTTATACCTGCCTCTGCCATGCAGCATCATAGCCTGT GGGAACCIAGGGAGGGCTTCCCTTACCACCCAGA
EST35879 9	142 A C ...	---	GAGATCGGTGTGTGAGTTATTAGGCATGGTTACCTGTGATTCCTCCCAATCTTGTGCGTTCCACCGATG GAACTGCCGGCAAATCCTGACACGTGTGCACCCAGGCTGTACCCAAATAGGTGAACATGGCTTCGAG AGAGTTGAGCAGATTCTTGAAGACAGCAGCGGGATGGGGGAGGAGAGAGCTGCCTGGATGA
ESTD-LMP2	35 C G ...	---	A TACACATTTCTTACCCATTCACTGAAACGACTCAGGCAAACTGGAGCCTTGTAGGAATGGAGT TGACCTTCCCCAAAGCCACTATGATAAGCTATTTGGTG
ESTD-LPL	113 C T ...	---	TGTCAGTGTCCCTAGGGGCACCTCACCCTCCAGCTCTTCAGCTCTGCCCTGCTGCTGCCCTGCA AGGGTTTGGCTTAATCTCAATTCATGCTCTTCATCTTTTAGC/TTAGCTGTGGGGTTTGTGTTG TTCTCTGTTTTTGGCTTAGTATCTGACTACTTTTAAATATAAAAGAGATGTATCTAAACAAAATAG AGATTGTTATCAGAAAGTTCAACAACATTTTAAAAAATTTTTCACCTG
ESTD-MCC	45 C T ...	---	TTGTGAGGAGTGTGCTGATGCTGCCTCCCTCCAGCTCTGCCCTAGC/CTGAACTTCAGGACAACGTGC AG
ESTD-METH	118 C T ...	---	CATCCATGTAGGAGAGCCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAAACAGCATGCATCCCCGAA TCTCAGGAAGTCTCTGCTTCCCAAGGGTTTGGTCTAAGTTGCTGATTACC/CTGGATTTTCTGACG ATCTTCAACTGCTAGAGCATCTGGTTCTCTGTTTAGCATGG
ESTD-NF1	25 A G ...	---	ATTATCCAGATGAATTTACAAAACCTAGTACCAGATCCACAGACTGATATGGCTGGT
ESTD-NFKB1	107 A G ...	---	AACATGGACTTGATATTTGTACAAAAAAGTTTATTTTCTAAAAAAGAAAAAGAGAAA AAATTTAAAGGGTGTACTTATATCCACACTGCACACTGCCTT/AGGCCAAACGCTTATTGTGGT AGGATCAGCCCTCATTTTGTGTTGTGAACTTTTGTAGGGGACGAGAAAGATCATTTGAAATTC GAGAAACTTCTTTAAACCTCACCTTTGTTGGGGTTTGGAGAGGTTATCA
ESTD-NPPA	45 A G ...	---	TGTCCCTAGGCCCCAGCCCTGCTTGTCTCCCTGGCTGTATCTTCA/GGTACTGCAAGAGAACACA GACAT
ESTD-NRAS	202 C T ...	---	GTGTTTCTTAATCTTTCCAGGAACACAGTGACCATAATTTCTTTCTGCAGGCATATAGAATTTGGT GGGTTTCTTTTATGTAGGGTGATATTGGACTTTTGTGTGATTATATATAGCAATTTGAGGG ACAAACAGATAGGCAGAAATGGGCTTGAATAGTAGATGCTTATTTAACCTTGGCAATAGCATTG CTTATCCCTGTGGTTTAAATAAAAT
ESTD-PAI1	100 A G ...	---	GCCACCAACACCCACCCAGCACACTCCAACTCAGCCAGACAAGTTGTTGACACAAGAGAGCCC TCAGGGGCACAGAGAGAGTCTGGACACGTGGGG/AGTCAAGCCGTGTATCATCGGAGGGCGCGGG CACATGGCAGGGATGAGGGAAGACCAAGAGTCTCTGTTGGGCCCAAGTCTCTAGACAGACAAAACC TAGACAATCACGTGGCTGGCT

ESTD-PAR	120	A	---	---	CTCTTCAGGAACCAACAGCTCTTCTTACCAAAACAGGACTTATTGCTGTCCGAGAGGTACAACCCGTAGA ACTTCTTCTCTAACTGTAATTTAGTTAAAGGAATCGAACTGGCTCTGAAGACATGGAGATACTGCCT AATCGACTGGCTTTCATTAGCTCTGTGAGTGTCTTCTTACCTTTCTGTGTTCTAGAACGTTTTCTTAG GACTGGCAGTTTAAAGCTTTCACCTTAGGCTTCTGTATACCCATGCCG	
ESTD- Per/RDS	74	A	G	---	ACCTACAGACGTGCTGGATGGTGTGTCCAAACCCGAGGAATCTGAGAGCGAGACGAGGCTGGCTGCTG CTGGAGA/GJGAGCGTGCCGGAGACCTGGAAGGCGCT	
EST68308	5	29	C	T	---	GGAAAGAGATTAAAGAGCTTGATTGGAC/CTJAATCTGGTCTTTGAGTGTGGAAGAGAGTTTCATGTC TCTGCCCTGAGTTACAACAGAATCCTTTAGTACAGCGAGTAATAGATATATTCGACACAGATGGGAAT GGAGAAGTAGACTTTAAAGGTAAGAAAGTAGTATTATTTTA
EST54045	6	39	A	G	---	GGAAATTAATAAATATTTAAATACCTCCATTTGCTTJA/GJTCCTTTTAGTGAAGATGATACCTGCTG AAAGACATGGCTAAAGTTATGATTGTCATGTTGGCAATTTGTTCTTACAAAATCGGATGGGAAA TCTGTTAAGTAAGTACTGTTTTGCCCTTGGAAATGGATTTTAAATGTTGACTTTATCAT
ESTD- PXMP1	88	A	G	---	---	ATGAACATGGTCTTAAATTTATGATATGTTTGTATAGCTATCTTAAAGGGCTCTTTTTTTTTTA ATGCAGAAAGAGGGGAAAAAA/GJGAGCGAGCTGTGGTGACAAAGGTGTTTTTCTCAAGGCTCATAC AGATTCTGAAATCATGGTCCCTAGAACATTTTGTAAAGAGGTAAAGTCTTATGAAATTAATACTT
ESTD-RDS	127	A	---	---	---	CCCGAGGAATCTGAGAGCGAGAGCGAGGCTGGCTGTGAGAGAGAGCGTGCOCGAGACCTTGAAGG CCTTCTGGAGAGTGTGAAGAAGCTGGGCAAGGGCAACAGGTGGAAGCCGAGGGCGCAGACGCGAGG CCAGCCCCAGAGGCTGGCTGAGGGCCCTGGGGCCCTCCCTCCCGAACACTGAGAAATAGTGCACCT CCAAGAAACGTGGATCTCCCCCTCATCCAACTCCGAAAGTCTGAA
ESTD- s14544	94	G	T	---	---	TTGGGAAGTTAGAGCCTATATTAAATTACGGAATTACTAAGGCAGGACACAGAGGCTTAAATTGAAAA TATCCCAAAGTTGAAATGCTCAGTTG/CTGTGTGGGTTAGATGCAGGATTTATATGATCCGTTA ACCTCT
EST52908	0	45	A	C	---	ATCACAGGTCTCTGGTCTCTGGCCATCATTTCTCTGGGAGAGATGG/ACTJGGTGGTCTGCAAGCCCTT TGGCAATGTGAGATTTGATG
EST19590	55	C	T	---	---	AGGAGAAGCTGAGGAGGGGAAGAGAGACAAGAATGACATTGATGAGTGAAGATGTJCTJGGCTCAG GATGCCGGAAAAATGAC
EST76136	39	C	T	---	---	TGAAGCTTCTGCCACGCTTGCAATGTTTCTAGGAGAACCTJCTJGGCTCATACCTTTATCTATAGCCTT CCCCTAGGCTT
ESTD- SPTB	176	C	T	---	---	TGAACACCCCTGTGTCCGGAGCCAGGTGTGTTTCTCTCTGGAGCCCTGAGGAGTTTGTGTCTGTGTG CAGTCCCCCGGCCAACCTGTGTTGAGCCTGGACATACACCTTCACTCTTGGCCCCGGAGAAAGAC ATTTACCCCACTGGCCATGTCCCTGGCCTGTGTGTGCACA/CJTCCTCTGTGAAGACCCCAACCCCTGC CTCCCCAACCCAAAGCCAGTTTCTAGCAAGGCGAGGAC

ESTD-IAT	224 C	---	---	AAATGGTCAGGACCCCTGATCCACAAGAAGTGGTACCATTTTCATCAGGGCCATCAGTTTCATTTCAGCTC CCATGACTGGGATGCTAAGTCAGCAAACTGAGTTTCATTCATCTTAAATGACTTTGTGGACAGGATCA ATTTCTCTCACCTAGAACGTTTGTTTACAACCTTTTCTCCAGTATGGATGGGATTATGATGGGGG GAGAAAGCAAAATTTTAAATAGGACCCCATGAGACACATCA
ESTD- THFB	125 A C	---	---	TGCGGCTTTCCTCGGAGGTAGACTTCTTACTTGGCTGTGATTTTCCAAAGAGAAGAGTCCCAAG CACACGAANAACAGAAAGTTGCAGATCCCATGAGGCCAGTCTCAATCACACAGGATC/A/C/CTTCAT CCACACTGGATTGGCCCAACAAGTCTGAGTGCAGCCAGGACTCAACGGTCCCTGTAGATGGG TAGTGAAGTTTTCATCTCCTGTGAGCTTCTGGATTCTTGTTCCACCGCAACAAGAGAGTCTATGC CAAGGCAGAAAAGCTGGTCTTCATGGGCAAAATCAATGTCTCTCCAGATTTCAG/TATCCCCCAA GCAGTGCATCCATTGACACATAATAATGCATCCAGACAAGAGGTCAATAATATGATGTCGTTAA CATGGGTGTGATCCATTTTTCATTTGGCCATAGTCCCTATGGGGATGACA
ESTD-TYR	122 GT	---	---	AGTAGTGGATGAAGCTAACAGCCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AACTCCAGAATCCTAATCAGTCTGGTCTAACAAATGCCCTACTCTTATGCATTAGTATCACAA AACCACCTGGTGAATATATAGATTGAGTTAATTAAGTATTTTCTTTCACITTTATACCTTCTTCT AATACAAGCATATGTTAG/A/C/ATTAAGTTCTAGGCATACTT
ESTD- TYRP1	222 A C	---	---	AGTAGTGGATGAAGCTAACAGCCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AAACTCCAGAATCCTAATCAGTCTGGTCTAACAAATGCCCTACTCTTATGCATTAGTATCACAA AACCACCTGGTGAATATATAGATTGAGTTAATTAAGTATTTTCTTTCACITTTATACCTTCTTCT AATACAAGCATATGTTAG/A/C/ATTAAGTTCTAGGCATACTT
ESTD- TYRP1	222 A C	---	---	TTCCCAAGGCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCAAGACACAAAGTCAAGAGACAGGAAACACAGTG ACTCTGAGATGTCA/C/T/CAGACTGAGAACCACCGTTATATGTACTGGTATCGACAAGACCCCGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12	148 CT	---	---	TTCCCAAGGCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCAAGACACAAAGTCAAGAGACAGGAAACACAGTG ACTCTGAGATGTCA/C/T/CAGACTGAGAACCACCGTTATATGTACTGGTATCGACAAGACCCCGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12b	148 CT	---	---	TTCCCAAGGCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACAC/A/G/TGGATGCTGGAATCACCCAGAGCCCAAGACACAAAGTCAAGAGACAGGAAACACCA GTACTCTGAGATGTCAAGACTGAGAACCACCGTTATATGTACTGGTATCGACAAGACCCCGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12a	74 A G	---	---	ATGGGCTGAGGCTGATCCATTACTCATAT

EST58607 0	105 A G ---	---	CTCTGGATGGGTTACAGGTGGCAGGCACAAAGCCAGTCCATCCTGTAGTCATCATAGTTGTTGGCTCC CAAGTTGCTCTCCTCACTGGAGAACAAAGGACAGCCAC[A/G]GGCGGGGATGGCGGGGAGTTG TGGTTGGCGCCACGGCTGTGGCTCGTTGTGAACGGTAGCCTTTGGGTTGCGATGCGCTAAACCTTTGT TTCTGGCCAAAGGAGGGGGTGCCTGCTGAGATGATAGATGGGOC
ESTD-VWF	36 G ---	---	AGGTAGGAAAGCAAGAGTTGATTAGTGAAGGAGAGATGGACCTACCTTCCACACTGTCTCTTTGG TCCCCTAGAGTCTG
EST71770 6	189 C G ---	---	AGCACACCTCTACGTCAAGCCTCAGCACCATGCTGTTCTATAAGGATGACGTGCTGTTTACAA CATCTCTCCATGAAGAGCACAGAGATTATTTATCTGAAGTCGGATCTATGACTCAGGGACAT ATAATGTACTGTGATTGTGAACAACAAGAGAAAACCACTGCAGATACCAG[C/G]TGTGGTGGGA AGGAGTGCCAGTCCAGGGTGACACTGGACAAGAAAGAGGCCATCCAAAG
ESTD- TNFAb	152 A G ---	---	TTCTGCATCCTGCTGGAAGTTAGAAGGAAACAGACCACAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGGTTTGGGGGCATGAGGACGGGTTACGCTCCAGGGTCTACACACAAATCAGTCAGTG GCCAGAAAGACCCCTC[A/G]GAATCGGAGCAGGGAGGATGGGGAGTGTGAGGGGTATCCTTTGATG CTGTGTGCCCAACTTCCAAATCCCGCCCCCGGATGG
ESTD- TNFAa	88 A ---	---	TTCTGCATCCTGCTGGAAGTTAGAAGGAAACAGACCACAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGGTTTGGGGGCATGAGGACGGGTTACGCTCCAGGGTCTACACACAAATCAGTCAGTG GCCAGAAAGACCCCTCAGAAATCGGAGCAGGGAGGATGGGGAGTGTGAGGGGTATCCTTTGATGCTT GTGTGCCCAACTTCCAAATCCCGCCCCCGGATGG
EST52418 6	113 A G ---	---	CAATACAGGGTCAACTGCTATGATGTTTGGAGCCCACTACCCCTTTGGTGGCTACAAGATGTGG GGGAGTGGCGGGAGTTGGCGGAGTACGGGCTGCAGGCATACACT[A/G]AAGTGAAAACTGTGAGTG TGG
EST13586 3	89 A G ---	---	CCCACTCTATTTGCCAGCCCCAGGGACAGAGCTGATCCTTGAACCTTAAGTTCCACATTGCCAGGA CCAGTGAGCAGCAACAGGGCC[A/G]GGGCTGGCTTATAGCCTCCAGCCAGCCAGCCCTGGCTGCAGA CATAAATAGGCCCTGCAAGAGCTGGCTGCTTAGAGACTGCGAGAAGGAGGTGCGTCTGCTGCTGCC CCGGTCACTC
EST51976 7	123 A T ---	---	AGGCAGAACTGGGGCCCCCATCGGGGGACGTGGAAGGCCACTTGAGCTTCTGGAGAAGGACCTGA GGGACAAAGTCAACTCTTCTTCAAGCACTTCAAGGAGAAAGAGAGCCAGGACAAAG[A/T]CTCTCTC CTCCCTGAGTGGAGCAACAGCAGGAAACAGCAGGAGGAGCAGCAGGAGGAGGTGCAGATGCTG GCCCTTTGGAGAGCTGAGCTGCCCTGGTGC
EST11458 6	140 A G ---	---	CCACTTTGGTAGTGCCAGTGTGACTCATCCAAATGATTTCACAGTGTCTATCTGTTCTCGAGTTT CTCTGCCATGTTGCTATTGCAGGACGGACCTGTCCCAAGCCAGATGATTACCAATTTCCACAGTGGT CCC[A/G]TTAAACATTTCTATGAGCCAGGAGAGATTACGTATTCCTGCAAGCCGGGCTATGTG TCCCAGGAGGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTGTGGCC

ESTD- AT3aa	60 C T ---	---	---	AGACCTCAGTTTCTCTCTGTAAAGGGAAGTTTGTCTTGATCTCCATGGGCCAGC[C/T]AGCA CTGGTCCCTGTGAGTCTATCAGGTAGAGGAGATGGGACCAGGTGGAGAGGAATTTGAAAGGGCA TTGGAATTCAGAGCAAGAGACAGATATTAAGAGCTGGGAAATGTGG
EST39852 8	106 C G ---	---	---	CGGTCTCCTTCCAGGTATTGTGCAAGGCCGAGATGACCTCTATGTCTCAGATGCATCCATTAAG GCATTCTTGAGGTGAGTACACCTTCCCACTCTT[C/G]GIGGTACAGAAAGGAGATGCATGAACA GCAGGAACACGTGGAAGGCCCTGTTCCAGTGTAAAGGCATGCAAAAGGCCCTCCACAGGCTGCTAT AATACAGCCCT
EST62448 0	112 A G ---	---	---	ACCTGGTGTGCTGGTGGTGAACCTGGTCTCTTGGCATGGCCGCCCTCTGCGGCCCTGGGCCCTGG TCCTCTGGTGTGGGTAGTCTCTGGAGTCAACGGTCTCTT[G/G]GTGAAGCTGGTCTGTGATGGCA ACCTGGGAACGATGGTCCCGCAGGTCCGATGGTCAACCCGGACACAAAGGAGAGCGCGGTTACCC TGGCAATAT
EST36027 2	120 A C ---	---	---	AGTGACTTCCAAGGAATGGCTACCCAACTGCCTTCATGCGCTGCTGGCCAACTATGCCTCTCAGA ACATCACCTACCCTGCAAGAACAGCATTCATACATGGATGAGGAGACTGG[C/A]AACCTGAAAA AGGCTGTCACTTACAGGGCTCTAATGATGTGAACCTTGTGCTGAGGGCAACAGCAGGTTCACTTAC ACTGTTCTGTAGATGGCTCTCTAAAGACAAATGAATGGGAAAGACAA
ESTD- COL2A1cc	112 A G ---	---	---	AGAAATGATATAGTCTCAAACTGGCCATCTCCATTTTCAGTCCAAAAGTTATACAGCTAGACAACA GTGGTGACATACGTTGCTATTATGCTCTCTTCCCTGCTACTT[C/A]GIGGGTGTCAAGGTGGAAAA GGTGAACAGGGTCCCGCTGGTCTCCAGGCTTCCAGGTAAGTCAACTCAAGCATATACAATACTGCCT TTGGTCAGCCTATTGAGCTGTAAATCACCATACCGTACCT
ESTD- COL2A1dd	97 C T ---	---	---	TGAGAGAACACCTAGTCTCCATCTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTTGGTGGGACCTGGAAACA[C/T]TGGACTCTTCTTACTGCAGCAGACAAGACTTA CCCAAGAGAGATTAAATGGCAAGATATACAATACAATTTTATTTGACCAAACTATCATGGAACA GCATT
ESTD- CPT2	150 A G ---	---	---	GCCGCAATGCCGGGAGTTTCTCCAATGTGTGGAGAAGCCCTTAGAAGACATGTTTGATGCCTTAGAA GGCAATCCATCAAAAGTTAACTTCTGGGCAGATGAAAAGCTACCATCCTTCCCTCATCATGAAAAC TGGGAGGCCGGGCAT[G/G]GTGCTCATGCTGTAAATCCAGCATTTTGAGAGGCTGAGCGGGTGGAT CACTTGAGGTGAGGAGTTTGAGACCAACCTGGCCAAACAT
EST12274 0	135 A G ---	---	---	CCCCAGTTGACAGCCACTGCTAGACTAAGTTTCTGCTTCCAATAGAGCCTTACCAAAGTGAT TACATAAAGAAGTCAAGTGGTTTACTCTCATGACCAAAATCTTCCCTCTTAGGATGAGGTG A/GTGTAAATGACCGATGGGGTCAGAACTGTCTCTGTCACCATGGAGGATATACTAAGTGAAGA TAAATCAAGCCACAGAGCTTGCAGATC
EST76807	91 G ---	---	---	ATGCTAAGGGGATCGGACATGAAGGACCCCTGTAGCCGATGTCTCTATCTCCAGCGGCCCTGTCATC CAGCTCACTCATCAATGGGCCAGTCAAGGCCAGGCACTGGGCTCCGGAGGACTCAACCACTGCCCCCT GCTGCCATGTGGACTGGTGCAAGTTGAGGACTTCTTG

ESTD-SSA1	111 C T ---	---	TTACATTTGTGGATTGTTCTTTTGTGCTGTCAGCACCTTTTCAACATGATGTGATGCCATTTGTCCAAAG TTTGCTTTGGCTGCCTGTGCTTGTGGGATATTTGAAAGAGATTC/TJTGGCCAGTCCAAATGTCCTAGA GAGTTTTCCCAATGTTTTCTTGTAAATAGTTTCATAGTTTGAGGCCCTTAGATTTAAGTCTTTAATCCATT TTGATTGTGATTTCTGTA
ESTD-FYR1	109 A G ---	---	CTTCGTACGGGAGGTCACGTCTCCGCTCTTTCATGGACATATGGATGAGTGTCTGACCATTTCCC CTGCTGACAGTGTACACGCGCAGACTTGTCTACTATGAG/GJGGGAGCTGTGTGCACATCATGCG CGTCCCTCTGGAGGCTGGAGCAGTGAATCAGCTGGAGTGGAGCCACCTGCGTGGGGCCAGCC ACTCCGAGTCCGGCATGTCACTACCGGGCAGTACCTAGCGCTACCCGAGG
ESTD-WT1	70 A G ---	---	AAGACCTAGTGAATGTTCAATGTGCTTAAAGCTCCCTTCTCTTACTCTCTGCTGCAGGATGTG CG/GJGTGTGCTGTGAGTAGCCCCGACTCTTGACGGTCGGCATCTGAGACCAGTGAGAAACGCCC CTTCATGTGTGCTTACCCAGGCTGCAA
ESTD-F2 EST44438 7	100 C ---	---	GATAAGTACACTGAGGCCCCAGGAGGTTATTGCCTAGTAGCCCAACTGTGCATGCAGCTTAACCTCT GCACCAATGGCTCCAAAGGCCGTAGGGGAAGTGGGGGATCTAGGGGATGGTGAGGAATGGCCC AGCCAGTCCCGGGGGTGGCTGGTCCCAACAGAGGAGGCGGTGGAGGAGGACAGGAGATGGGC TGGATGAG
ESTD-PBDA	103 A G ---	---	GCAGCCAGGAGCCGCTGCACCATGCCCGCATAGATGCGGACCTCAAGCTCGACTTCAAGGA/C/TJG TCCTGCTCGACCTAAGCGACAGCCTCAAGAGCGGAGCGGAGGTGGG
EST12839 3	122 A G ---	---	CCTTCATGCCAGATGGAATTCAGTCCCTTCCAGTATGCTGAGGAGCAGAAATATGGTCTCTTTGCT CTGAGCCGTGGCTGGGAAGGCGAGGACTAATCCAA/GJTCCTCTACCCGACCTTGTCTGTCATACAG ACGGACAGTGTGTGGCAACATTGAAAGCCTCGTACC
ESTD-CTLA-4	48 A G ---	---	TGCAAAACACACAAAATCTTCTCCAGATGCCCTATGGCTGTGGAGAGCAGAAATATGGTCTCTTTGCT CCTAACATCTATGTACTGGATTATCTAAATGAAACACAGCAGCTTACTCCAGAG/GJTCAGTCCA AGGCCATTGGCTATCTCAACACTGGTGAGTGATTACTTGAAGGGAACCTTGAATGTTATTCAAC TGGATTTCCAGTAGGTTTCAGTTACTTATGAATATTATGATACTTAGCTTAG
ESTD-ACE	96 C T ---	---	ATGGCTTGCCTTGGATTTCAGCGGCACAAGGCTCAGCTGAACCTGGCT/GJCCAGGACCTGGCCCTG CACTCTCCTGTTTTTCTCTCTTCTCATCCCTGTCTCTGCAAGCAATGCACGTGGCCCGAGCCTGTGT GGTACTGGCCAGCAGCGGAGGATCGCCAGCTTGTGTGAGTATGCATCTCCAGGCAAGGCCAC
EST54419 8	88 A G ---	---	GATCAAGCAGTGCACACGGGTACGATGGACAGCTCTCCACAGTGCACCATGAGATGGGCCATATA CAGTACTAAGTGCAGTACAAGGATCTGCC/C/TJGTCTCCTGCGTGGGGGGCCAAACCCCGCTTCCA TGAGGCCATTGGGAGCTGTGGCGCTCTCGGCTCTCCAGTCTGAACATCTGCACAAAATCGGCCCTGC CTTCTGCCTAATTGAATGATATTGTGCTGTGGGACCTGAGCAGCTTTATGGCACAATGATCACTA TTTTCTTGACCCCTACTTAC/GJATCTCTGGGAGATGATTTGGGTTAGCGTGGTCTGATGTTGCTA CTATAGTCCCAAGTGAA

WI-2625	98 G A ---	---	---	GGGAGTCTGGCTGTAGTGGTAGACAGCACTGAAGATGGAGGAAGAGAGAAGAAACAGGCGAGAA GCACGTGGTAGTTAAAGGGCTATTTAGGA/GA/CAAAATTGATGATCTCCCTGAGGACTCGCAG AAATTACAGCAGTGGACAGGGTTATCTGTGGTGAATTCAGTTATCCACTTGCAGGAGGAAAGCCCA GCCAGCAAAAG
WI-2924	54 G A TAGG	TGACCTTCCTA GTCTCTCTTA	GCCTAAGTGT AATCACAGGG	TCGTGTGCATATTTCCCTCTTTGACTCTGACCTTCCTAGTCTTCTCTTATAGG/GA/ACCCTGTGATT ACACTTAGGGCCCTACCTGGATTATTTAGAACAAATC
WI-2939	72 G T GTGCCITT	GGCTTGCTCA	CTTGTTGAGGG AAGGTCTTG	CCATTGTTGAGGTGGTGGGTCACCTGTCATTCCTCGCACTCAACAAAGTGGCTTGCTCAGTGC CTTTG/JCAAGACCTCCCTCAACAAGAATGCTTTCCATGCTCCCGTGTCTTTGAAAAATTCGACT TTATCCTGAAAACTCAGCTGCAGTGTATCTCCGGTATAAGCCACTCCIG
WI-3203	99 G A AGACGAG	GGTTATGCCGC	TCAAGTATTGC CTTGTTGG	CTTGCTACCATGCAATTCACAGCATACAAACCTCAGTGAAATGCCGTAAACCCCATTTATAAACAT CTTGCCATCGAAGGGTTATGCCGACAGCAGG/GA/CCACACAAGGCAATACCTGAAGTGACTTGGA GAATAAGATTGTTGGATGGATGAAAGCAGAGAAGGAGATGCTAAAAAGTGA
WI-3473	101 A G GCCCTAGGGA	AAGCATTTTA GCCCTAGGGA	CCTGATGTCAC CAACATTTCT	GGAAAAAGAAACCTGAAGGATGAGTAGAAGTTAATGGGAGATAGTTGGTGATAGGCCCTGTTTGGGA GATTGCAGAGAAGGAAGCATTTTAGCCCTAGGGA/GA/GTAGAAAAATGTTGGTGACATCAGGGCT ACACACTTTCTGTATGCTCTTCATCAAA/GA/GTCAGGGCGTCATTTCTGCACATGGTGATATTTAAG CAGGAGAGCATTTGCTTGGCTCCCC
WI-1796b	29 A G ---	---	---	ACACACTTTCTGTATGCTCTTCATCAAA/GA/GTCAGGGCGTCATTTCTGCACATGGTGATATTTAAG CAGGAGAGCATTTGCTTGGCTCCCC
WI-1796	29 A G ---	---	---	AGTCGTCATCTTCAGGGTCTAACTCTGGATCTGGCTGCAGAGTAGGAAAGAAAGATGGGTGAGT AGTCACATTAGGTATTTTCCAAATAA/C/TJAAAATGCCCTCTGAAAAATATCTCTCCCATGTCCCTGTC TAAATATAACATTTTCCC
WI-4360	93 C T AAATAA	GTAGTCACATT AGGTATTTTCC	GAGAGATATTT TTCAGAGGCAT TTT	GCTGAGCTTTGTGGCAGAGCCAGGACAAATCAGCTGCCGGATTTTAAATAGATTTCTGCAGCACTGCAA CAGGAACCAAAAATCAGTC/C/TJGGGTAACAGAGAGTGGTTTTCACACCCAAA
WI-1959b	87 C T ---	---	---	GTTGTGCTGTAGCAGACACAGAGGCA/GA/GAGAGGAAAGCCCTTTTGGTCCAGGGGCTTACAC TGAATCCCTCAACAATGCAAGATGAGCTAATGGTCTTAGAGGTATACTAAGTGTGAGAAAAACA AAGGTATAGGGTTTG
WI-1973b	28 A G ---	---	---	CTTGAGTATGCGTGGATTTGGTATACAGAAATGGGAGAGCTGGAACATAATCCCCCATATACCA AGGGACAAATGTATCTGTTCTACAATTATACAGTAGGAGACATTTATGTTCCATGACAATGGTAAT TTTTAA/C/TJGACAGTTTTTAATTGAGTGAATACCATAAAAAATAATAATAGTAGCAGCTAATATT TACTGAGCTGTTACTAGGTGCCTATAAATAGC
WI-1980b	140 C T ---	---	---	

WI-2015b	190 A G ---				TGTCAGATAGTCGGTCTCTACCTAGGTGCAGTAGCATGCTAGAGCTATTAAAGTACACAAATTATGCT ATATATTTATACAAATATACAAATTACTTGCAGATAGCATGACCATGCTAGTGAAACCCACACAACTAT GTGTGAATCGTCTATTAGGGTTTGTCTATAAACTCTACATGGTGTCTTTTCCAACTTAA/GJCATATACTT CTAATACCATAGAG
WI-754b	49 C T ---				GAAGGCACAGGGAGAAGATGGCTGTCTATCCAGCCAGGGAGAGAAGC/TACATTTATTGGTAA TCCTATAAGTGCATCTTTAAATTTGATTTACTTTAGA
WI-754	22 T C ---				GAAGGCACAGGGAGAAGATGGCT/GJGTCTATCCAGCCAGGGAGAGAAGCCACATTTATTGGTAA TCCTATAAGTGCATCTTTAAATTTGATTTACTTTAGA
WIR-1b	56 A G ---				AGGCAATCAGACCTACAGAAAGGAACCCCAATAAAACTCTGATGATCGTACATCC/A/GJTGCGCTG GAGGGTGATGCTCTCTGAGGACATGGAGCTTCATGTTGGAGCCCTCCCTG
WIR-1	56 A G ---				AGGCAATCAGACCTACAGAAAGGAACCCCAATAAAACTCTGATGATCGTACATCC/A/GJTGCGCTG GAGGGTGATGCTCTCTGAGGACATGGAGCTTCATGTTGGAGCCCTCCCTG
WIR-3b	72 A G ---				TAATTTAAATGGGGCCAATAACACAGTACTTATCTCACAGCATTTCTCTAAAGGCTAAATAAGAA GAAGT/GJGTCTAAAGTTATTAGCTCAGAGCCTCACACATCTCAGTACTGATAAACAATAAGCA AAGCTGGGTGCTGAGATAAGA
WIR-3a	69 A T ---				TAATTTAAATGGGGCCAATAACACAGTACTTATCTCACAGCATTTCTCTAAAGGCTAAATAAGAA GA/TJGTATCTAAAGTTATTAGCTCAGAGCCTCACACATCTCAGTACTGATAAACAATAAGCA AAGCTGGGTGCTGAGATAAGA
WIR-4	47 T ---				GAGCCTTTCTAAAAATAAGGATTGTGACTAGCAACCTCCTGTACAGATTCCCTGCTCACACATGTGCA AGGCAGCAGCAAAATTTGCCAGCTGCC
WIR-5g	209 C ---				CGGGACAGAGAGACAGAGAGAGAGATTCTGCAGCATTACAAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG
WIR-5f	196 C ---				CGGGACAGAGAGACAGAGAGAGATTCTGCAGCATTACAAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG
WIR-5e	194 C ---				CGGGACAGAGAGACAGAGAGAGATTCTGCAGCATTACAAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG

WIR-5d	191 A ---	---	CGGGACAGAGACAGAGAGAGAGTTCTGCAGCATTCACAAGAGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGTCCGTGGCTCTATGGAACACACAGG TTTTACGTCCAG
WIR-5c	177 C ---	---	CGGGACAGAGACAGAGAGAGAGTTCTGCAGCATTCACAAGAGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCCGTGGCTCTATGGAACACACAGG TTTTACGTCCAG
WIR-5b	159 A ---	---	CGGGACAGAGACAGAGAGAGAGTTCTGCAGCATTCACAAGAGTTATTAGGACTCAGTTCTGCTG CTGTGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTT AGGTTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCCGTGGCTCTATGGAACACAC AGTTTTACGTCCAG
WIR-5a	37 A G ---	---	TAACCTGAAACTTTGCTTCTCTCATCTCAGGGAGAACACAGACTTCATGTTAAGACCCAGAA[A/C] CGCAGTCTGGGGTTGGGCGAG
WIR-6	63 A C ---	---	TTTCGTGACTATT[C]/AAGCATCTGTAGAATATTGAATACATAGCTTGAGATTGATC
WIR-7	12 C T ---	---	GGCGTCCTATGACTATCCTGGTCATTGATTGACTAATGATTCCTG[C]/TGCCCTTG
WIR-8	46 C T ---	---	AAACAGAAAAATAGAGGTTAT AAGGATGGAACATAAAAGTTGTCAGAAGAGGATGA[C]/GJCTGAAG AAAGAAATTACTCCTCTTTTGACCAATAAATACAATTGGGAAACACTGGAACCAATGGCTTGATTACT GACAAAC
WIR-2	56 C G ---	---	TGTCCTTGCTTATGCCTGCCTCTTTCGCTTGGCAGGATGATGCTGCTATTAGTATTTACAAGAAAGTA GCTTCAGAGGGTAACCTTAACAGAGT[G]/ATCAGATCTATCTTGTCATCCCAACGTTTTACATAAAA TAAGAGATCCTTTAGTGCACCCAGTGAATGACATTAAGCAGCATCTTTAACACAGCCGCTGTGTTCAAAAT GTACAGTGGTCTCTTTTCAGAGTTGGACTTCTAGACTCACTGTTCTCAGTCTC
WI-7069	93 G A ---	---	GGTCATTTCTCTTTTATCTGTCAGGCAGCCAGCTGACTT[A]/TCTCTCTGTTTCTGCTATCTCTCCC CCACATACCAACTTCTCACCATGATGATTATACCAATAATACAGTTCTTATATGAGGGGCTCTGGA AAATTAGACAGTGAAG
WI-18694	41 A T ---	---	CACACTGTTACACACCTATATTTCAAGTTTGGAAATGC[A]/GJTATTTGCAAGCAGCAATACAAAAAGTA TTCATGAAGAATGCATAATCTCTGAAATATGAAACATCCCT
WI-18612	37 A G TGC	CCTATATTTCA AGTTTGGAAA CTTGCAAT	TTGTATTGCTG CTTGCAAT

WI-18517	87	C T	CAGGAATCAG GTGCAACA	TGTTTGGACAA GTGCAACA	TTAAAAATCAACTAGGGCTCACCCCTCAACACCCCCCTCCATTGTCAACCTCTACAGCCTGCATGCC ACAGGAATCAGCAGCCTGAC/TTTGTTGCACCTTGTCACCAACAACACTGACTGC
WI-18668	76	C T	GGCGAAAAAC TAGGCAAAAA GC	GCTAAATTAAA CTGCACITTTT GC	CGATTGACAACCTTTTATTTCACCTAGGTAAACAGTCCAAATCAGTGTAGATTGGCGAAAAACT AGGCAAAA/C/TTAGCAAAAAGTGCAGTTTAAATTTAGCAAAAGGCTCAAGACAGTATGTGGAAAGGAA GGTGAGATTTCCTCCTACT
WI-18680	75	T C A	GCTGTCACCTCT AGCATCTGGA T C A	CCTCCTGAATA TACAACGGAGC TGAAGGCCCTG CTGG	TAAACATACGAGTACTGTACACGCAAGCATGCATCCCTGAGTCTGAGTGAGGCTGTCACTTAGC ATCTGGAAT/C/GCTCCGTTGTATATCAGGAGGGGA CACCCAGGCTGTACCCAGGCTTCTTGTGCGAGCACACCAAGGGCAGGTTGGGCTTGAAGGAGCC CTTGAGGAACACGGGTTCTCCGAGGGGTAC/C/CCAGCAGGGCTTCAGCTTAAAGTCG
WI-18704	99	A C	GGTTCCTCGA GGGTAC	---	TGTGGGCAACCTTGTTTTAAATTGCAAAAC/A/GJACTTAAATTTACAGCACATTCAATAATGAACCAAC AGGAGAGTTGCTGACTTGTAAACATATGAATATATAAAAATCCCTTGCAATTCAGGTAGTCAAGGTA AAAAGCGCATACAAGGAAG
WI-18673	29	A G	---	---	ACCAGTCATGTTTATTGGAGGTTAATTCCTATTAGGATATGAAAGGATTTCAGCAACGATTGAGATT GTGTTCTCACGGAGGGGCTCGGGCCAAGTCTGTTGGGGTGGGGGTGCAGAGT/C/GTGTCTCTTTC AGTGGTATTTGGGAC
WI-18640	121	T C	GTOGTGGGTG GGG	GCAAATACCAC TGAAGAGGAC A	GGGGAGGAGGAGTAGATTGCCAAATGAGGCAATTTTTTAAACTCCCCGAGATTTCTTCTTATTT TATATTTTCATTTTTCATCTAAT/C/TTACTGAAGCCATTTCTTTGGTTAACTTAGA GGGAGAGGAGGAGTAGATTGCCAAATGAGGCAATTTTTTAACTCCCCGAGATTTCTT/GJCTTA TTTTATTTTCATTTTCATCTAATTTACTGAAGCCATTTCTTTGGTTAACTTAGA
D11734	83	A C	TCATCTGATAC CTTGTTTCAGAT TTC	AACCAGGATA AGGCTACAAC ATTT	GAGCATATGCTGCATGAGGAGCCTTTCTATCTTACATTATGGCTGGGAATCTTACTCTTTCTGATA CCTTGTTTCAGATTT/C/A/AAATAGTTGTAGCCTTATCCTGGTTTACAGATGTGAAACTTT CAGGACTTGTGGTGACGCTGCAGACACAGAGCACAGCTCATGGCAACATCACTGGGGCCAGAGAG AGCTGTCCGCCAGTGCATCATTAGGGGCTTTTCATTGCTAGTACTAGCCCCCTTAAATGCCAGCCTG AGTACCTGAAGGAATCTGGGAATTA/TTGGCCTGGCCTGAAAGTGGCCCATCATACCCACTGTT CT
D49493	159	A T	CCTGAAGGAA TCTGGGAATT	ACTTTCAGGOC AGGC	TAITTCATAGAGGAGACCTAGGAGGAGTTGACACAGCACACTGCTCAGCAGATGACTTAAATTTT CCCTTAGCCATTTTGTCTCTCAAGTCCCTT/C/TCATCCATACCACTGCTGATTG
EST10030 7	98	T C	CATTTTGTTC TCTCAAGTCCC	GCAGTGGTGGT ATGGATGA	TAITTTGGCTCACTCTGGAGGCTG/A/GAAGTCTAAGATTGAGGTTCCACATCTTGTGAGGGCCTTC CTGTTGAGTCAATAACCTGGTGGAGTGCATCATGTGGCAAGAGAGAGGGCTACAGAGAGCAAGAGAA A
EST10052 2	24	G A	GCTCACTTCTG GAGGCTG	TC	---

EST10605 2	118 C G ...			CTCTCAAGTAG ATAAGAGCA TAATCT	---	CTCTCAATTTTC AGAAAGAATT TTGTTT	CTTGGTAATACAGTTCTGTATTATACAAAAAAGCTTTGTTTCTCTGACAAAGCTGTACACATAGA AACAAATTTCCAAATGGACAGGAAGCTTAAATTTGTGGAGATGCCCATGT[C/G]TTGTGAGACTTAA AAAAAGAAAAAGATCCC
EST11048 0	61 T G			CTCTCAAGTAG ATAAGAGCA TAATCT	---	CTCTCAATTTTC AGAAAGAATT TTGTTT	CATGTGTCATCCCATGATTGAAAAGACATGTTGCTCTCAAGTAGATAAGAGGCATAATCTT[G/JAA ACAAAATCTTTCTGAAAATTTAGCTTATGAACCTATTACACTGCAACCCAGAGAGGAGCAC
EST11260 8	101 G T				---		TATGGAGCCAGAGGAAGTGACACTATATGTGGAAGTCTGAAAGAAATGAAGTGTCAACACAAAA TTCTATATCCAGCTAAATATCATTTAAGAAATGAAG[G/T]GGAAATGAAGGCAATATCAGATAAA
EST11349 9	109 C T				---		TTTGATGGAGAAATCCGAGGCCCTGCCAGCATCCCAACAGTAGATTCTTTGGACGAAGAAATCCT TCTGTGGAATTCAGCTTACCGCCCTTCCCTCATCTGCTGGTG[C/T]TTCCCTCAGAGCTTTAATGTCCGT CCTGCTCTCCGAGTCAG
WI- 16632a	71 A G			CCAACCTACTT TGGAGCCCT	---	TCCAGCTTTCT CTAAAACTCC T	GAATCTGGGTATTAAATAGCGGGTGCCACAGGACACATAGGAAGAGCATCCCAACCTACTTTGGAG CCCT[AG/JAGGAGTTT]TAGAGAAAGCTGGAGCCCGAAGACCAGTAGTAGGAGGTAGCCAGACCAA AAGGGAGGAAGGAGTGGAA
EST11772 6	74 A G				---		CCAGGAATAAAGAAAAAGAGTCAGAGGAACAGCTTTTGATGTTATGAGGCTGAGACACTACTC TTCTTCA[AG/JGACTATTTTCACTCTGACTATAAGTGAATAAATACATTGAAGACTTCAGGAGCTCA
EST11795 3	82 G A				---		CTTGCCATTTATTTTGTGCATGTGTTCTTAAAGGCTGTGAAAGGATAACTTGGAAATGTGGGAAAC ACATAGATCCCAGA[G/A]TATTAAAGGGCTGGAAAAGTAGCCTTAAGAC
WI-16644	42 G A			CAATAAGCAG CTCATTTTGAT TAC	---	ACTTCATGAAT TTTACTTCATG TATACC	AGAGCAATGGTGGCATCTCAATAAGCAGCTCATTTTGATTAC[G/A]GGTATACATGAAGTAAAAATTC ATGAAGTAAATTCATTATACCAAAAAAGCCCTCCACAGAACTTTTCATGCACCCCTGAGCTATGTGAAC TGAAAAGTAACAGTGGGAT
EST12005 9	56 A G			TTGTATAATA ACACTCAGTA CAAAGTCTGT	---	GGCTGGTCACT TOCTGGAT	GCCTAGTAATCCAAAAGGAACATGTTTGATAATAAACAACCTCAGTACAAAAGTCGT[G/JATCCAGG AAGTGACCAGCCCGACGTGTGCTATGACCCCTCTGAACCTCCCATTTCCATAGTTTTTGAATC
EST12055 9	32 T C				---		GTGGAAAATTTTATCTGTACGTCTTTCCIT/CJATTATAATTATCTTGTCCCTTGATTTCAGCACCC CACCGAATTTGCAGGCAGTGCTTTCTAAACTGTGCCCTGTGAGCTGTAAAAGTCTTCT
EST12492 1b	95 A G				---		CCCCAGCAATGACTTGGAGTTGTGTCCTCAATTACCAAGTTACATACTGTGCCAAAATTAAGCTCTC TTCCCCAGAGGCATTAACTGAGATTAT[G/JGGAAACGCACAGCAAAATTGACGATGCAGCTTTTAA CCTTTTTA
EST12492 4	25 A G				---		ATCTTGAGGTTTCTGGCCCTGTCAG[G/JAAGTGACATCTTTTACTTACCAGGTCAGGAACCCCTAT AAAGAACTGTGTAGAAAAGATATCAGGTCAGACTTTTAAAGGGCTCTTATCAGCTCAATAAA

EST12502 2	52 C G ---			ATAACTAGGGAGAAACCAAACTGGAGGCAAGTCCACAGGTCACACTTGTCA[C/G]CAGCAAGTAT AAACAAAGTGGTTTCGATGAAGAGAAATGCTCAGGGGAAATGACCATTTTTTAAGGGCCATGTG GTGTCGAGGCAGTTAGAGG
EST12619 8	105 T C ---			CCAGAGAAAAATTAGAAATGATCGGTAAAGAAATAGGAATGCATATTTCAACTCACTGTACAAAA CAGGTGTTTATTATCCCAATGACAGTGTGCCTGAGAT[C/G]ATGCATGTGGCAGACGAG
EST12620 0	67 A G ---			TTTTCTCTCTCCTTCATTATTATTTGTTCAAAACACTGTCTAGTACCAACATTGTCCACCGGGC[A /G]TTGAGAATACAATAATTGAAGAAGAGTCACTGCCTGCCCTCTGGAAAAATCAGAGTATTTGA
EST12817 9a	22 C A ---			TTGGGGTTCTCCAGGATCCAG[C/A]CTCGTAGCTGATGTGCATGAGGTTCTCATCCATGCTCCACGG GTCTTGGGAGTGACCGGATGGGAATCCATGTTCCTTTCGTAAGTCCATCAGGTCATTGGG
EST12941 8	23 T A ---			TCTCAGCTTCCACCTGACCTGCA[T/A]CAACAGCCAGTTATTTCCACCAGAAATTTGTTGCGTTTCA ATGTAGTGTATTAGCTTTAATACACTGCACCTGTTTTTG
EST12949 2a	52 A G ATACTGTT	GGCTTTAATCA TAACCTAATA	TGTGTCCCTGT GGGTCTC	AGGATTTTCATGAGGCTTTAATCATAAOCCTAATAACTGTGTTAAAAACAACAC[A/G]TCTGTCACCTTG CAGAGACCCACAGGGACACACATTTCTCTCCTCTCACATAGACTCTGAGGTAGGAGGTACACTGGCT AAGGAATAA
EST13067 4	104 C T ---			ATTTTTGTTTTCTTAAATGAAGCATAATAAACAGTTAAAAATCTCAGAAAAATCATCTATAGTTGA GTGTAACAACTCCCTAAATCAGTCTTCTAGGGCCAC[A/C]TGGAGCAGAAAGCAGCTTCCCACCCAAAG CACCTCTGAACCT
EST13117 6	66 A G ---			TGCTGTCTGCATCAGTCCCTTTAAAAATTTAATCGCTTTTATACAAATTGACACCAATAAAATGCAC[A /G]TATTTAAAGTTTACAAATTTGAGAAGCTGACACGTTGCCATACAGACACACCTCAITTTTACTGTGC TTTACTG
EST13121 6	44 C T ---			TCTGCTTTAAAGATTCTTCATAGCTGCTTAGGTTTGTCTTCC[C/T]AGCATATTCAGCTATAATCA CCTACATTCCTCCACAATAATTTCTGTGTGCGCCAGGCCAGTCTCCTCACTGTCCCATGAATAGCC AGCTTATTCCACTCT
EST13226 6	74 T G ---			AACTGTTTACTAACAAAGGTGCTTTAATTTGAAAAGCATTGAGGAAATAAATTAATGAAATAGTCT GGCCATT[T/G]GACTAACCAAGTTCTACAAATTTACATAATCCGTCACTCAGATGAGCATATACCAAG TCAGAGGAAACAAAAACATG
EST13230 6	72 G A AGAGAGC	GCTCAGATGTG ACAGAGC	CCGGCTCCTGT ACAGAGA	GCATCATCAGCGGCTTTTACTGAACCTACAACCAACTTGCCTCAATATGCAGCTCAGATGTGAGAG ACGC[G/A]TCTCTGTACAGGAGCCGGTACTGTCTTCAATCCCTTGCATGCAGGTGTTTACCACAGGCA AACAGTTTACTCCACAT
EST13236 9a	70 T C TCTCAGGCT	AACCAAGATTT TCTCAGGCT	ACAAGAGGGTT TGACAAAAGA G	AAAGATATAAAACAACCTCCCATCAGTAGCAATACAAGGTATACATTTTAACCAGATTTTCTCAGG CCTT[C]TTTTTGATACCTTTAGTAGTTAACTCTCTTTTGTCAAAACCTCTTGTATATAACCA

EST13278 2a	51	A G	CITTCACGAA CAATATTTTAG	CATATCTGG GTGGTGAGAA	TTGCGAGAACGTTTTACAGCTCCAAACCTTTCCACGAAACAATATTTTGGGAGATTTTGAATTTAT TTCTGTAGTTCTCACCACCCCAAGATATGACAGCTTG
EST13282 0	99	A T	CCACACATTTTC AGTCCAGA	GATGGAAATTT TGAGGAAGGTT	GCTCACTAGATGAGCATTGACCAAAATATTAGATAATACCTGTTGGGAAAGTGCTGAATTTACTAGCC TGCCTGAGAAATCCACACATTTTCAGTCCAAAGATTAACCTTCCCTCAAAATTTTCCATCTCCCATCAGA GG
EST13290 9	39	A G CTT	CAATTTT TAGA AGTTGGGTTT	AAATCACTTCA TGGAAATTTCA	AGCTCATCTGCAAGCAAATTTTAGAAGTTTGGGTTCTT[AG]CTGAAATTTCCATGAAGTGATTTT TTTTCTGTGCTTAACCTTACGTTACTTAAGACCTAAAGACAAAGTGGTATCACATCACATATTTTGT ATGTGTGGGCTTTTIG
EST13518 2	45	C G	---	---	GAAACATCCTCCAGTAGATTGAGGTTAAAAATGATTCAGCATTTA[C/G]ACTTTAAAAATTTACCTCA ATGTTCTCGGAGTCGTCATAGTTTAAATGACTTCTGCACCTTCCCTTATAACCTTGATTG
EST13522 8a	66	A G	---	---	CAGGTTGGTGATTTCTCAACTAGGAGCTATTTGCCCCCATCCCCCAGCCGCGAGTGCTGGAGAC[A/ G]GTTTGTATTGTCACAACCTCGGAGAGGTGGGTGCTACTGGAATCACTGGGTAGAGGCCA
EST13568 6	69	T C	---	---	CTTAAGGAAGTGAGCCAGATGAATCCATGACCAACCTGGTTGAGAGGCCATTGGTCTAGGAGTAGA AA[T/C]GCACACAAGGAATAAGGGAGAGGAGGTTGCGTTAGTTGAGGGAGAGAAAGTTGGGAAGCA TTTCAAGCTAAGTAAATGGT
EST13785 0	101	C G	---	---	AAGATTACGGGACCATAAGAACTGCCCGCCGACCCATACACACACAATTTATAGCAGGTAAACCAA CTGAAAGGAAACAAAGTAATGACTTTCTTTGAACAAA[C/G]TGAATTACGAAAGTGAAAGGCTACAGGG TGATTACTA
EST14038 1	25	A G	---	---	CCTCAACCATCTGTAAACCCGAGCC[C/G]CAGTGACCCGGGACTTGTGCTTCCCATCCAGCCCTCT CCTATCAGCATCCGCTAAGCGTCAGTCAGCAGGTG
EST14083 7	23	A G	---	---	CAATGGTGTCATGTGAACATA[T/G]ACCTATTCAATAAGTTAAAAATAATCCCTTCTTGCAATCA CAGTGCAAAAGGCATGAGGGTGAAAGTCATCTGCTAANAATGACCGAACAGGAGGGTAGGAGG
EST14221 5	42	T C	GCATGCTAGA CAGAGGCATT	GGAACAAGTC AAAATATTTT	AATATCAATGCATCTTGTGGCATGCTAGACAGAGGCATTAT[C/T]TTTTGAAGATCTTTTAAAAAT ATTTTGACTTGTTCCTCCCTTCACACTCATTTTAAATGT
EST14812 2	50	A G A T A	CAAGTCAGCTT CTACATCTGA	TAAAGATTAG TTAAATCCCAT TATGTACT	TTCACTTAGTACCAAGGATGCCCTTCAAGTCAGCTTCTACATTCTGAATA[AG]AGTACATAATGGG ATTTAAGTAAATCTTTAGAAGTCCGGAGTTGCCCTTTCTAACAATTTTCATATCAGGTGAAACAAAT TTTTTCATATGGGTGATT
EST14815 3	128	A T A T A C T G G T T	CATCACCCACC ATACTGGTT	CGGGAACA GTACCGAA	TTTGGCTCGGCAATACATAGTGGCAATGCAGCGTGAGTTCGGCCGCTCCCCACTGAACCAGTAAT TCACCAGACATGGCGCACTTAAATAAAGTTGCCGTCATACCCCACTACTGGTT[AT]TTCC GGTACTGTTTCCCGTA

EST15420 6	109 C A	TTTAAACCCCAAGACTTGTAGATGTCAGGACTCCGATCATTTTCTCGCTATAGCTTGGATATCTTA ATCTCCCCCTTTGTCATATAATCATATAGCAAGGGACTC/AJGGAAATTTTGGCTGCTTCAAGTCA TTCCAAAACCTCTCAGG
EST15700 6	48 G C GGA	GAATAGCTGA AACAGAGATA TTATTCTC	GTCAACAGCACCTTTTATTAGACGTGAAAGACAAAGACAAACAGAGGA/GC/JAGCAGAGAAATAA TCTCTGTTTCAGCTATCCAGGATGTTATGCCAATTATCCAGAGTCTTGATCTGATGTAGTA
WI-16739	57 G A CACAAGC	GATAGTTGATG TTCAATTATCC CTATAA	AAGGATTGAAAACATACCTAGATCATATAAATTTGTGAAGGTTTTGCCATCACAAAGC/G/AJTTATAG GGAATAATGAAACATCAACTATCCTACAGCTAAACCTAATGAAGACCAAATGGCTCCAAAGGT
WI-16782	96 C T CACTGTAAGG	CTTCTATCTTT CTGTTCTCTCCA TC	CTTCTCTCTTCCCTAGACGTGGAATACACACGGATACAGTATCTGGAGATGTAGCAGCTGGCTCTTGAC CATAATGGTGGGAGTCTCACTGTAAGGA/C/TJGATGGAGGAACAGAAAGATAGAAGAAGTTTGGGGT GCTGATGAAATTGIGGGG
WI-16783	64 A G G	TCCTGAGATGT CTTTTACCTGA G	AAAAATGTAAACCTTAGAGGTGGCTCTTTTGTGTCACCTTTTCTGAGATGCTTTTACCTGAG/A/GJ CTAATAAGGATTGAACCAAGCAGTATTTTTTAATGGCAAAAGTCCAGATGTAACCTCGAGT
EST15948 2	58 T C	CAGGACTTAAGGTCAATTTTGCCTGGAAGACTTTAACTAAAGTCAAGGCAACATAGGA/T/CJTGTA CAGCACCACTCGGACCAGGAAGTCTGAAATCGTCACACTAGCTGCCAGCCCTTTTTCCTGGC TGCTCTGCTCCAGAGC
EST16088 8	89 G C	GGTTTGAAGACGCAGCTTTATCTCCACCTGCCACTGGGATCTCATTTTGAAGAGCTGTTTGTGACGCC TTTTCCAGAAAAGGCCGCTC/GC/JGGGTTTTCTGAACCCCTCTATGGCATTTTAGAAT
EST16089 9	96 C T	CGTCTGAAGTTTTCTTTATCACAAATGTCACATCAATCCCTCGGGCCCTGCTCAAAATGCCACCTCTTC CTGAAAGCCATCCCTAAGTAGTCTCTC/C/JAAGAGGCCATCCCTGCCCTTTCTTTGCT
EST16100 1	24 C G	ATCCAGCTGTGAAGGACAGAGGAG/C/GJTAACACACAGTCCATTATAAGGGGTGTGCACATTCCCA GGGGCTCCAAATAATGCAACATTGTTTCACTCGTCCATGCTGCTGATAGTTTCATAGTAAAAAAGTC ACTCCAGACAGGTTGGCTC
EST16104 9a	83 A G	TTCTTTTAAATAACCCACAGACACCCATGACACTTCCAAATTTACAGAGCAAAAAGTGATTTGCAG CTGGTTCTCTCCAGGGA/JGTTGGCCCGAAGCTGGCTCAGTTCACCTCCAGGACCTCAGTC
EST16118 0b	119 T C	ATGGTATAACAAAATCAGTTCAGGTTTTTTTCTGAACAAATGATCCTTTGGCTTTCCCGTGGCATG CTCCTAAACAACTAAACAACCCCTCTACGCTCTAATCAGTCACCTAAGATA/CJCGAGTGGCAAGT CTTTCACA
EST16118 0a	32 C G	ATGGTATAACAAAATCAGTTCAGGTTTTTTTCTGAACAAATGATCCTTTGGCTTTCCCGTGGC ATGCTCTAAACAACTAAACAACCCCTCTACGCTCTAATCAGTCACCTAAGATATCGAGTGGCAAGT CTTTCACA

EST16151 2	53 C T ...			AGCCAATTCAAACGAACTCTATCAAAACACACAAAGGCCTAGAGGAGATT[C/T]AATGAACGT AAATAATTCAAGGCAATTTTGATCTAAAGCATTTTGTCTAGCTCTACAAAGGCATGAATGAGGTGT GGTCACGTTTGTATAGGA
EST16182 6	54 G A ...			CATTGGTTGGGTAGGGAAGATAGTAGTGCAAAATAAATGGTAAACAGCAG[G/A]AAATGGAA TTATAGCTTTCTTTTCATATAGGGAATTGAAATTTATTTACTAGGGTGATAGGCAGAAAGTAGTA
EST16183 2b	59 A G ...			GCAGGTAACACTGTGGTTCAACAACGTATTGTTCTTTTCATAAAAGAAAGAAATATCTAGTTG[A/G]GTAG AGGAAGGCACGTCTTCCTGGCCCTTCCTCGTTTCATATTTTATGTCACTGTCTAACGTGGGCCGTGT GCAAGAGATCTTTGAGA
EST16198 4a	28 G A ...			AATCTTAGGCTCTGGCTTTCAAAATCA[G/A]TACAGACAGATAAGAGCTTTAAGTATTTTCGCATTT CCCCAGAGGAAAAGTCAGCATCATAAACCACATGGGTGCATGCTCACGCACATGGGTGC
EST16229 2c	52 T C ...			TGTGAACCTCGAATTGCTGTGCCAAGTCTGAGTCACAGTTTCATTTGGGAG[T/C]CCCTGTGCAGCC CTTGCCAGTTTCCACGAGGAGGATACCTCCACTAGCTGATTCAGACAGGAGGCTGCA
EST16229 2b	45 T C ...			TGTGAACCTCGAATTGCTGTGCCAAGTCTGAGTCACAGTTTCATTTGGGAGTCCCTGTGCAGCC CTTGCCAGTTTCCACGAGGAGGATACCTCCACTAGCTGATTCAGACAGGAGGCTGCA
WI-16816	124 A G TGGGTTA	GGAGCCATTGT	GCCTAGATTTT	CAGACTTTTCTCACACCTCATTTGGCTGGAACTGGGTGCACATGCACATCCTTGAACATCATTTGGCAA AGGGAATGGGTGCATCAAAATTTGCTTAAGGCCAAGCAGGAGCCATTGTTGGGTTA[A/G]ACTGTCC TGAACAAATCTAGGCTC
EST16269 5b	49 G A ...			GCCACTCTCTGTGGCTTGTCTCTGTCCAGCTGCTGCCAGTGCCAC[A/G]TGGTCTAGCCCTCATGG CAGAAGCATTTTAGCCAACTCCTGGTGTCTCCACTCTCTCTCTTCCGCGCTGGGGCTCACCACC TCTTCTCTCTCAATC
WI-16824b	83 G A ...			GTCAACCCAGCCAAATGCTTCAGGAATAAATGATGGTGTGCAGCTGTTGTTCTTATGAAGAAGTCAG AAGCTGATAAACGTGG[G/A]CTTACACCTTAGCACGGATAGTTTCTGGTCCCAAGTGGGTGTGGA GCCTTCCATTATGGGAATA
WI-16824a	47 T C CAGCTGT	TGATGGTGTG	TTCTTCATAAG	GTCAACCCAGCCAAATGCTTCAGGAATAAATGATGGTGTGCAGCTGTT[C/G]TTCATTATGAAGAAGTC AGAAGCTGATAAACGTGGGCTTACACCTTAGCACGGATAGTTTCTGGTCCCAAGTGGGTGTGAGC CTTCCATTATGGGAATA
EST16445 3	96 T C ...			TTGCTTTTATTATCCAGAACGGCATGCTACAGATACITGIACAGCATGAACATTTTATTATTACAAA AATGGCTTCCAAACCATTAAAATGAACCTT[C/G]GAATAAGAGCATAAAACGGAAACAGTAACATCA
WI-16857	47 G A A	CAAATAAGCA GCTAATGGCA	TGTGAATTGGG AAGACCACT	TATAATCCATCCTCCAACACACACACAAATAAGCAGCTAATGGCAAT[G/A]CTAGTGGTCTTCCCAA TTCACAAGACCTGTGCTTCAAAATTGTTTTCCTGATAATGTGGAGAAATCTGCTCTTTATGTA

-201-

WI-16879	79 C T	GATACAGGCC ATATTCCCA	CAAGGCTTTCT AGAACTAGAGT CC	AGACAGGTCAACAACTCTCTAGGGATAAAGATATAATCCAGCACAGCATTATTTCCAGATACAG GCCATATTTCCCACTTATAGGACTCTAGTTCTAGAAAGCCTTTGGGAGAACAGGCACCCAG
WI-16882	99 A G	GAAATGCCA CGTCTCTGAC	GACACATGTCA GGTAAATCGC AATGTTCTGAA	ACATGAATGGCAACCTCTTAGGTGGGAGAACAAATCTCCCCCTTACCCCAAAGGTACTCTGAC AAGGCTATGAATGAATGCCACGCTCTGACAGCGGATTTACCTGACATGTGTCATCTCCCT
WI-16888	70 G A	GCTAACTTTGG GCAGGTTTC	TTGACCAAATT TAA	GTAGTAATGTTTCACTACCCGGGGAGAGCAAGAACCACTGGAACGGTAGCTAACTTTGGGCAGG TTCG/AJTAAATTTGGTCAATTCAGAACATCCAAAT
WI-16905	75 C T	ACTTGGCCTGT TTGTTTCA	GTCATACTCT TCTAGGCAGTG GG	TTTGTGTTTGTATTGCTCCCAACATCAGAACATAAGTTCCATGAAACAGGAACCTTGGCCTGTG TTGTTCA/C/TCCCACTGCCCTAGAAAGATATAGACA
WI-16910	74 G A A	AAGAGTAAAG ATGGCGCTAG	CAAAATGAAG TATCGTTTCTA TAACAGA	AGTTTTCAGTATGTGCTTAAGGAGGTTATATTCGCTATGACTTTTCATCTCAGAAGAGTAAAGATGGCG CTAGAA/G/AGTATCTGTTATAGAAACGATACITTCATTTTGGGCTGAACCAAGTGAAGGT
WI-16918	93 C T	CAGCCATTAA CACCAGCAC	TCCTGATACAG AAGTGGCATC	GGAAAGAAAAATAAATACTACCACCTTCTCTGCTACCACAGAGCCTAAATCTAGGAATTTGAC TTTACTGCAGCCATTAAACACCAGCAC/C/TGATGCCACTTCTGTATCAGGAACCTTAACGTGACAACC ATGAAAGGTCTCTGAAAG
WI-16947b	127 A C	GGAAAGCAGA CCTGGGG	ATGTGATTGCC CGTGG	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTTCTCATGGAATAGGCCTGGAGCAGCAGGATT TGGCTGAGGCTTTCAACTGACATCAGACAAGACTGCAATCAAGGGAAGCAGACCTGGGG/A/C/JCCA CGGGCAATCACATGAGATG
WI-16947a	58 C G	CATGGAATA GGCCTGGAG	GCCTCAGCCAA ATCCTGT	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTTCTCATGGAATAGGCCTGGAG/C/G/JACAGG ATTTGGCTGAGGCTTTCAACTGACATCAGACAAGACTGCAATCAAGGGAAGCAGACCTGGGGACCA CGGGCAATCACATGAGATG
WI-16966	43 T C	AAATGCACAC TACATAACAA CCTAA	TGCAAGTTATC AGTATAAAAA CTCATATT	CATTGTTTTACTTTAAATGCACACTACATAAACCACTAATAT/C/JCTTAACTTGGTCCAACATATTT AGTATACTAATATGAGTTTTTATAGTAACTTGCAATGCCATTAAA
WI-16995	55 T C	GAGCAGTAGA GACTGAGGTA AATAGTATT	CATGTTGATTT CCAGGCGT	TTGAGTGCCAGACATCAAGCATAGAAGAGCAGTAGAGACTGAGGTAATAGTATTT/C/JACGGCTGG AAATCAACATGCCCTCTCTTCTGTGAAGTTGTACGATGGAGCTGAGAAGGCTGAGTCAATCT
WI-16992b	60 T G	AAATACATGGTGTCAACCTCAGCTAAGCACCAGAGTACACTGTGCGCCCTCATCTGAGATT/GJGTG TAGGACTGTAAAGGAATGTGTTTGGGGTTTAGGAA
WI-16992a	46 G A TC	AAGCACCCAG AAGTACACTG	CACATTCCTT ACAGTCTTACA C	AAATACATGGTGTCAACCTCAGCTAAGCACCAGAGTACACTGTG/A/JCCCTCATCTGAGATGTG TAGGACTGTAAAGGAATGTGTTTGGGGTTTAGGAA

WI-17010	23 T C	TTCACAGGA	AATAATACGGT	ATGTTTCAACAGGAAAGCCATGTCATGACATTCAAAACACCGGTATTATTAGAAGCTCATTTAAT
EST17127		CA	GGTTTGAATGT	TGTTTAATGCAGACAAAAATCAAGGCTAACTAAAGCAGATCCAATGACCCAGTGATCAACCTAGA
9b	74 C T	CACTCGGCAC	GGGAGGGCAGG	GGTCCACG
		AGACAGAGT	GGTG	ATTCCGCTCCAAACAGCATCCAGGCCGGGCATCTCCCCACGATTTTATAATACACTCGGCACAGA
		AATCTCTTAT	GGACTATGGCT	CAGAGTCCTGGGAGCCATGGGGCACCCCTGCCCTCCCCAGGCTTCTTAAGTAACAAC
WI-17040	94 T C A	CATCTCAAGOC	TATTCAGTGAT	CACGCGTTTCATTAATTTGGTACAAAGCATGAACACTCAGGACAGATTGGCACAATACATGCAGTTC
		G	G	GAGAAATCTCTTATCATCTCAAGCCAGTCATCATCACTGAATAAGCCATAGTCCCAGTCTCGTTTTC
		GCCAAGGGAT		AAATCTTCTCATATTGT
		TAACGTATAG	GGGGATCCOCT	TTGTTTGTGTTTGTCTCTCTCTGCGCAAGGATTAACGTATAGGTCCTTAAACAAGGGGATC
WI-17044	47 G T G	TG	TGTTTAAGA	CCCCACTTATAGCTGACAGCAGCAGCTGCAACCAGCTGACTCTCTCGCAGAAATGGCAGGGAATCGAAT
		TGGACTTGTCA		CAAAAAGAAAAGCAAGTG
		GCCTATAACT	TGTAGAGTTAG	GCATGTGTTGGAGCAGATCTCCATGGTAAGCCAAAAGTGGAAGTGTGTCAGCCTATAACTACTCTTAAAG
WI-17021	62 T A ACTC	ACTC	TGGCAGCTGC	CAGCTGCCACTAACTCTACAGGCACAGTAACACTTATACAGGAGCAGCATGCCAAAAGTGCCCTGG
		CCAGAAAGGA		GAGGTGCCAATAAATCAA
WI-17065	90 T C CTT	AAAGCATAAA	CCCAAGAGAC	TGTAAAAAATGTAGACATGGGGGAAAAAACATTCGTATCAACATGTGCTGTTTCTACTTCCGGTA
		TGTACAGCCA	AATGAAATCCT	CCAGAAAGGAAAGCATAAACTTTCAGGATTCATTGTCTCTTGGGT
WI-17066	32 A C T	ACATCACTGT	AATGTTCTGGA	TTCATAAGGTTGTACAGCCCAACATCACTGTTTCATCCAGAACATTTTCAACATCTCAAAAAGA
			A	AACTCTGCACCCATTAGCAGTCACTCCCTGTAGTTCCTCATAGGCAATGGCAACTGCTGATC
				TGCTGACTGTGATGACTTAGTAAGGCCATCACAGGTTGCCAGAACATCTACTCAACTGTTCCAGCAT
WI-17074	86 T G ---	---	---	AACTCTCTACACAGGCCCTTTCATACATAGGAGTATATTTGGCCCAAGACTCACCAGTAGAAGTATT
WI-17104b	108 T C ---	---	---	CAGATGAGAACTCATGCTGGCTCATCTGCAAGCTTCTGATGCTTTGCGAGCTTTCCCATTCATTCCA
				AATCAGAAAGCAGTCAGTGGCCCGGTGTTTCCAGACGGCTTTCCTCTTTGTTAAGAAATTA
WI-17114a	37 T C GACTTGTGTTT	TTCCATCAAG	TTGTATTATAA	AGCGTCCAACAGAGATGTTCCATCAAGGACTTTGTTTTCCTCTCTCTCACTCTGCTATTATAATAC
		GATGAAATTC	ATAGCAGAGTG	AAGCTACCTCCCAAGGCCAGATGCTTAAGTGCTAAAAGAAAGACTGCAGCCACAATCAGAGTTACAT
		AGATAGTCTTC	AAGAGAC	GGGA
WI-17150	76 T G CTCCT	CTGGAAGATAT	TTCCTCAGATC	CGTGGCTGGACTAAGTGCTCTTTCCATGTGGACACATCTCCACTGAACAGGATGAATTCAGATAGTC
		CATTTCTTTGT	G	TTCCTCTTTTTCATATCTCCAGGATTCAGAAAGGGCTCTCTTTGTCTGCTCTAATTT
		AAAATAACAA	CAGAATCTTGC	GAAATCGAATACGTCCTCTTTTGTAAAAATAACAATAACGTTTTCAGGCAAAAGCAAGATTCTG
WI-17163	43 A G TAACGTT	TAACGTT	TTTGGCCT	TAAACCAACATTTGGAAGGGGACACAGGGAGGGGAGGGAAGGGCCAGATTTTCAACGGTTT
				CCTCCACATCTGCAGACAAA

WI-17178	127 T C	GGACTCCTCA	CCCTCAATTTT	AGCAATGTCCCTCCCAATTTTCATTAGCTATGATGGAGTTATCAGTTTCATTTCAGAGCGAATTACTGG
WI-17180b	81 C G	---	CAACTGCTTC	GGCAGGGGGTTTAAATATCCTGATGGGTTTAAATCAGTGAGGACTCCCTCATGAGGAGCTTC/JAGAA
WI-17180a	47 T C	CACAAAATA TAGAGAATCC	---	GCAGTTGAAATGAGGG
WI-17180a	47 T C	TGCA	TGCGACGAGAC	TCATGGACATCCTGAAGCAGACACACAAAATATAGAGATCCTGCACATTCCTCCAGTCTCGTCGACAG
WI-17156	54 G C	TGTTCTCTAAA CTTTAGATATC	TTGGG	GCTTCAACAAATTACIC/GAACATCTTGCCCATTTTGTTTCATTATCCGCACCCACACTGACAGATGAG
WI-17149b	79 T C	---	CAAGAAATAT	GGAGTC
WI-17149a	48 C G	CAAGTTTGA AGGAGGAACA	ATATTTGATTC	TCATGGACATCCTGAAGCAGACACACAAAATATAGAGATCCTGCACATTCCTCCAGTCTCGTCGCA
WI-17197	67 G A	CTGGGGTAC	TGTGGAA	CAGGCTTCAACAATACCAACATCTTGCCCATTTTGTTTCATTATCCGCACCCACACTGACAGATGAG
WI-17198	38 A C	GCAGAAAGTAG	---	GGAGTC
EST18753	27 C T	CTACCCAGGCT	OCACGCACGTG	TGAGGTAGCAGGGCATTCCTTAAGAAATGTTCTCTAAACTTTTAGATATCTCCCATTCCTCCACAGA
WI-17108b	74 C T	GGTCTCAT	CATGA	ATCAATATATATTTCTTGGTTGGAAATTTTAAATGTTCTTAACATCTGCCTACCATCCACCTCAAT
EST19067	41 A G	GGTCTCAT	GGTGAGGTGGT	TAATATCTTG
EST19067	41 A G	GGTCTCAT	GCATACC	CAGGCAGTTAATGTGCTGACATAGTAACAAGGTTTGAAGGAGGAAACATCTCATGCGCGTGGAA
EST19125	28 A G	GGTCTCAT	GCATACC	ACCCAAATTTGTCATTC/GTGTATGAACACTACAAAGGATGGGGAAAGAACACATTTCTCTCACA
EST19125	28 A G	GGTCTCAT	GCATACC	ATTTTGTCTATGTTCCCTGGGCTGGACTCCAGCAATCTCTCTGCCTCAGCAGAAAGTAGCTGGGGTACICG
EST19125	28 A G	GGTCTCAT	GCATACC	/AIGGTATGCACCACCTCACCCTGCTTATCAGTTTCGTTTAAATAGAAATATTTGACTTTTAGATGCGCA
EST19125	28 A G	GGTCTCAT	GCATACC	TGATTTTCAGTACTTTTCTCCCTGCTGCTAGTTTACATTTTCTAGTGGGACAAATGGACAA
EST19125	28 A G	GGTCTCAT	GCATACC	ACCATCTCTGTTTGAATTTGAATACACAGATACATGCAAGATATCTTACAAGAAACAATGACACATCC
EST19125	28 A G	GGTCTCAT	GCATACC	TTC
EST19125	28 A G	GGTCTCAT	GCATACC	TCGCTATGCTACCCAGGCTGGTCTCATTC/JTCAGGCTCATGCGATCCTCTGCTCTGCAGTGGCTGG
EST19125	28 A G	GGTCTCAT	GCATACC	GATAAGACACAACTGCCACCAGGCTGCCCTAGGAGTAGTCTTAATGCTGATGGTGGG
EST19125	28 A G	GGTCTCAT	GCATACC	TTATTTTAAACATAACCAGATGCACCTTGGTTTTTACATTTCTCTGGTTGCCATTCAGTCTCAAAGT
EST19125	28 A G	GGTCTCAT	GCATACC	AAACAC/CITGGGAGCATATGATAAATCGTAGTTTAAAGGAAGCCATAGCACCTTACAGAGT
EST19125	28 A G	GGTCTCAT	GCATACC	ACACAAAATTTACCATCGTGACCAATTTAAGGGTATAGTTCA/GJGTGGCATTAGTACATTTCAACT
EST19125	28 A G	GGTCTCAT	GCATACC	TTTTGAGCAACCCGCCATCACCATTTCATCATCCATCTCCGTT
EST19125	28 A G	GGTCTCAT	GCATACC	ACACAAAATTTACCATCGTGACCAATTTAAGGGTATAGTTCA/JAGTGGCATTAGTACATTTCAACT
EST19125	28 A G	GGTCTCAT	GCATACC	TTTTGAGCAACCCGCCATCACCATTTCATCATCCATCTCCGTT
EST19125	28 A G	GGTCTCAT	GCATACC	CTGTTTCTCAGAGATGACACTGCCAACAC/GJTCACAGATTTTGACATACAAATACAGTTATGTTATGGC
EST19125	28 A G	GGTCTCAT	GCATACC	TATTCACAAATTTACAGTAGTGTTTTTTCTCTGAAAAA

EST20824 8	115 T G	AGTCGGGAGT GCTGATTG	AAGATTTTATC TTGGACCCGA	GTGTGAAGCCGGAGTTTATTATTATTTCAAATCAGTCTCTGTGAAAACTCAGGGATTGAGGTTTTTA AGGATAACTTGGTGAGTAGAGGGCCAGTAAGTCGGGAGTGCTGATTGT/GTTCGGGTCCAAGATAAA ATCTTAGG
WI-17347	50 A G	ATCCTCAGAA CTTCTCAGCCT	TCAAGCATCCA CTTGCTA	TTGGTTAAATGATGCCAGATGGGTACATCCTCAGAACTTCTCAGCCT/GAGGTAGCACAAAGTGG ATGCTTGAAGAAACTCAGTCTTGGAACTCAGACAGCAATGGAGACGGGATGTGAGTGGGACCA
EST21904 b	128 G A	TTCATATGGCC ATTTTAATAA GTG	GGCAGGTGTC AGAAAGCAT	TGATTGGGCTCTGGGAGCAGGTGGGCAGTTCAGTGGAGGACAGAGGAAAGTAGACGAGTAGAAAT GAGACTGGAATCAATAGAACAGAAAATGTACTAGGCTTTCATATGGCCATTTTAAATAAGTG[G/A]TA TGCTTTCTGAACACCTGCC
EST22111 3	82 T C	GAAGATCTGT CTGGCATTCTT	TGGA AAAACA GCCCCAC	CAAACAATGTAGACATAAGGGAACAAAATTCAGAGAGCTCAAGTCAACCATGTTTGCTAAGAGAAGAT CTGTCTGGCATCTTTT/CIGTGGGGCTGTTTTTCCAAGGCACA
EST22197 2	78 T C	AATTATTCTGC TATTCTGCCA	ACCATGAAGG ATGCGGT	GTTTAATGATCACTCAACAAAATCCACAGGAGAACTCTTAAATGTTTACAAGCACCAATATTCTGCT ATTCTCGCCAT/CJACCGCATCCTTCATGGTAGAGTATCACAAAGTAAAGTTTTCTGGTTGTTTCATC TACTTAAACCA
EST22311 9c	92 T C	---	---	TTTTCCATGGATTAGATCATCTTTTTATTGAGTTATAATATACATAAAAAATCCACCACTGTAAACAG TAGCATTCAATGGTTTTTACTCTA/T/CJGTCAAAGCTGGGCAACTATCACTACTATCTAATTTCAGAA CACTTTCATCATCCAG
EST22311 9b	54 A G	---	---	TTTTCCATGGATTAGATCATCTTTTTATTGAGTTATAATATACATAAAAAATCC/A/GJCCACTGTAAA CAGTAGCATTCAATGGTTTTTACTCTATTGTCAAAGCTGGGCAACTATCACTACTATCTAATTTCAGAA CACTTTCATCATCCAG
EST22311 9a	41 T C	GGATTAGATC ATCTTTTATT GAGTTATAA	TTGAATGCTAC TGTTTACAGTG G	TTTTCCATGGATTAGATCATCTTTTTATTGAGTTATAAT/T/CJACATAAAAAATCCACCACTGTAAA CAGTAGCATTCAATGGTTTTTACTCTATTGTCAAAGCTGGGCAACTATCACTACTATCTAATTTCAGAA CACTTTCATCATCCAG
EST22319	19 A C	---	---	TCGAGGAGCTCTGAGGAGC/A/CJACCAAGGGACGTGTGCCAGGGCCACCGTGCAGGCAAGTG GTCCAACTCCTTCCTCCCTTACAAAACTCCAGCCTCACCCACACAAACACTGGCTGACAGGCTTCT TAAGCCTTTTTTAACGTG
EST22433 c	103 A G	AAGACATGTT CACCAAGTGA	CAGCTTCAGCT TAAGTGACAGA	GATGTTAATGACTTTCCTTTGAGATATGATGGAAAAATATTCAGGTACACATGGAAAAAGACATGTT CACCAAGTGAACCAATCTAACCCAGAAAGCTTTACC/A/GJCTGTGTCAGTTAAGCTGAAGCTGAAAT CTGGGAGCTTGACATGCTG
EST22657 9	71 A G	AAATGGATCC TTATCTGCACA	AGTTTCAGTTT GCATGAATTTT	TATCCATTTCAGAAAAAAAATGACTTAAAAAATACAATTTCTATCCAGAAAATGGATCCTTATCTG CACA/A/GJCCATTGAAGAAAAAAAATTCATGCAAACTGAAACTATGCTTT

EST22993 5b	71 T C	ATCCTTTTGT TCTACCCC	TGCTGTAA TTGACTGTAA TG	GCCTTTTATTGCTCCTTTTAAACATCAAAATGTTTATAACACACTTGATCCTTTTGTCTACCCCA ATT/CJ/CATTACAGTCAAAATTAAACAGGCAATATAATAGGCTAACAGAATGCTTGCAATTT
EST23021 0	108 T A	---	---	TTATTTCTCAGCTTACCATTGTTGACTTATCTCTGTACAAGGTGTTTTTCTCCATGGAGAAATG TTAAATCTTTGTGAGGTTAATTTTATTAAATCTTTGCCTTT/AJAAGTTTTGACAGTTTGTGCTTTCT T
WI-17387	55 C G	CCTTGCAGAT TGAAGAAAA	GCCTTTGCTA AGATTAATAGT AACTACT	ACAGAAATTTAAACATGCAAGTTTCATTTACATTACCTTTGCAGATTGAAGAAAAA/C/GJAATATTAG TAGTTACTATTAACTCTTAGGCAAAAGCCATTTCTTTG
EST23669 1	101 A C	AATGTAAGCT CCAGAGGCAG	CCTTCCCCTOC TGTAAGC	TTTTTGGCTTGTCTGCAGAAATAGATGAAAAGAGAAAAATATACCCAGATACTTTTGTCTCACTCTCCCA AGTGCACACTAGGCAATGTAAGCTCCAGAGGCAG/CJ/GCTTACAGGAGGGAAGGACGCTGAGGC CAAGAGTGTGGCTCACTG
EST23733 9	31 T G TT	GGCTGTTAGTT TTGTTTGT	TGCACCTTAAA TCCCATCAAT	AAAGGCTGTTAGTTTTGTTTTTCCCTT/GJ/ATTGATGGGATTTAAAGTGCATATAACTGAAG GCAAAGTCCAAGGCTAGAGAAAGATATAGGCCCCGAGAGAGAGGCTCAGAGATTCTAGAGGGCGC TGAAGAATACCCACCTAAA
WI-17470	83 A G	GTCCGTCOCG CCAG	CCAGTGACGAG GOOGA	CTGACACGTCCTGTGTGCGGGGTGCCATGTGGCGTGTGTGTGAGTGAGACTTTTTTACTGCGTCCC GTCCCGCCAGCCCTA/GJ/TCGGCCTCGTCACTGGCCCTTGGTCACTTTGTATTTCTGCTTGGTTGGAAA TACCATCAGCCTTCC
WI-17519	55 T C A	GTGTCTAGC TAATGAATGC	AATTATTATT TGCAGGCAATA CTC	TTTTTAACGAAATCTCACTACTGCAATGCATTGTTGCTCCTAGCTAATGAATGCAT/CJAGAGTATTG CCTGCAAAATAATAATTGAGATTCTATTTTAAAGAGCTTAGAACAGTACATGGTGCCATAG
EST25356 3b	95 C G	---	---	TCCTTGATACAGGTAACCCAGTTTTGTAAACATTATTCAGAACTTCACTGTATCTTCAAGTTTTGATAT CAGCATCTCTGTGGAGAAAGCAGTGTG/CJ/ATAATGTCAACATCAGGATTTCTTTTT
EST25356 3a	26 A C	---	---	TCCTTGATACAGGTAACCCAGTTTTGTG/CJ/ACATTATTCAGAACTTCACTGTATCTTCAAGTTTTTGA TATCAGCATCTCTGTGGAGAAAGCAGTGTGCTATAATGTCAACATCAGGATTTCTTTTT
WI-17581c	99 C T	---	---	GGGTGACGCTCCAGAAATGGGAGACAAGCCAAATTTGGGAGCAGATTGGATCCAGCTTCATTCACCAATT ACTACCAGTTATTGATAATGATAGAACCCAA/CJ/TTAGGCGCAATTTACATTGACGGTCAATGC
WI-17581b	86 T C	ATTCAACATT ACTACCAGTT ATTGATAA	CGTCAATGTAA ATTGCGCT	GGGTGACGCTCCAGAAATGGGAGACAAGCCAAATTTGGGAGCAGATTGGATCCAGCTTCATTCACCAATT ACTACCAGTTATTGATAA/TG/GATAGAACCCAACTAGGCGCAATTTACATTGACGGTCAATGC
WI-17596	86 A G C	ACTTCCCTGTG TAAACACTCC	CATTCTTATAG CTAGAAATCGA CAATAT	GTGTGCTGTTAAATGGATAATAGCAGTCTCTCATCTCTGAAGGGTGGGAAGTAGGAGAAGGCCCTACT TCCTTGTTGTAACACTCCCG/GJ/ATAATTGTGCTGATTCTAGCTATAAGAAATGGGGCCACTAAGTGGGTC

WI-17623	46 T C ---		---	TGTGTTTTAAATTTCCATATAATTAATGTTGGGCACATTTC/GCATGTGCTTACTGGGTC ATTACATATATCTTTTGTGAAGCATCTGCTCCAAATCTTTTGGCTGACTTTGGAGTTTTTGGT
EST26419 1b	46 T C ---	ATACAAAGGC	---	ATTTACATACAGAGATACAAAGGCAACTATGTGACGCAACAATCTGATTC/GGGCAGTCCAAACTTCT TGGGAGGAAGTAAATTCATGTTAAATGTCATGATGGCTGTTGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGACAGAGAAATG
EST26419 1a	35 C A AG	AACTATGTGC	CAAGAAGTTTG GACTGCC	ATTTACATACAGAGATACAAAGGCAACTATGTGACGCAACAATCTGATGGCAGTCCAAACTTCT TGGGAGGAAGTAAATTCATGTTAAATGTCATGATGGCTGTTGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGACAGAGAAATG
EST26780 5	69 G C ---		---	TCAGCTTTAATTTAAGGACATGTAATAAAGATGCAATTTGACAGGACAGCAGACTAGTTCAAGC AG/GC/JAGGTTAGACCAGTAACAACAACCAAGAAAGCAAGTCTGTTCCATCTTGGCTTTACCA CACTTACAAACTGATACCC
EST26900 7	39 A G ---		---	TACTTCAGTTTAAGGCAATTTCCACACAGAGACTGTCTC/JAG/GAGACGGGCACAGAACCCAGACACC GTAGAAACACACCACCACCATGTCATGACGGGGAAGCAGAG
EST27152 1	101 C T ---		---	CAAAGGATTTTATTTTGTCCCTAAAAGTAAATCTAGAAAATAGCAACCCACTGCAAGAAGAGTT CTATACTAAACATTTTCAATCATCTCTCTCTC/JTTTACATGGTGTACTCTTTTCATGTACACAT CATCGGAAACAGACTGA
EST27504 0a	33 G A ATTT	GCACTTTGCA CAATTTAATA	GCTGGTGTGAT GCTACTGTAAT G	TTTTTGACATTTTGCAACAATTTAATAATTTATC/GA/JCATTACAGTAGCATCACACCAGCAGTCAAT AATGCCACTTTAGGCAAAAGTCTTTCAGTATTTCTGTTACACATCTGTTAAACAAGAACCCATACATT GGTAAATTCATTTCT
EST27662 4	51 C T C	CACATTCTGTT CTCCAGTCTTG C	TTATGGAATG GCTTATGTAAC C	ATCTTAAAGGACCATTAGAAAAGGCCAGTCACATTTCTTCTCCAGTCTTG/C/JAGGTTACATAAG CCATTTCCATAAATCTATAGCCTTCTCTTAGAGTAACACACACACTCTTTTGGAAATGTTT
EST27788 3	100 A G ---		---	ATTTTATTAGGCGGTACAATTTCCAAAGGTGTAAGGTGAAGGAAAGGCGAAGGCGCAATACAT TATTGAGCTGAAAACAACATTTACATTTCAAGGAC/JAG/GCTTCCAGACAAGCCATGTAGAACCAGCAT GCCTTGGGACTGTGTGGAT
EST27828 4	58 G A AGAACCCAC	GGAAGTCATC AGAATCCAC	GTGCAGAGAGG TACTCCAAGTA C	TCTTCTAAACTTTCTTCTGTTGGATCCAGTGACGTGGAAGTCATCAGAACCCCAQ/GA/JGTACTT GGAGTACCTCTCTGCAACCAAGATAGCTGGCTGATTTCTGCTCAGTCACAATTTTACTTGAA
WI-18369	58 G A ACAATC	AATAAATTC AATCTGTCAC	TCAGAAGGCC TTATCCATT	TAAAAATTTGAGATACATTTCCCAATGTAAACAATAAATTTCAATCTGTACACAATC/GA/JAAATG GATAAGGCTTCTTGACAAATTTCTGCCACCTCCGTTTAAACGCATCAGAACTCAATCTTATCTC
EST28036 4	37 T C ---		---	TCCCGCTTCCAAAGCTTTATTGGCAATATGCTCTATTC/JAAGAAGATGATCAATCCTGTTGCCTCT AAGTCAATGGAATGAAGAGCTGTGTCAGGGACACACACCCGCTGCTGAAGGAGAGACTGCTGTTGTG TCCACCTCTTATTCATAG

EST28483 7	31 T A	GGAGTAAAG GTGTTCTTCT TTAAA	TTCTCGCATT TATTTTATAC CA	CATTTGGAGTAAAGGTTTCTTCTTTAAATATATGGTATATAAATAAATGCGAGAAACATTAAAC GGAGAAATGTACAGACACAGACAGAAAGACATGAGTTTCTGACTGTGACACATTTGGTGAAA
WI-17724	50 T C	TGGGCGCTCC TGTC	TGGTTGGCAG TGTC	AGAAITGGTCTAGTAATCGTTACAGGATTCGGTGATGGGCCCTCCCTGTCTC/JGACACTGCGCAACC CACAGCTGGAGGGGCACCTTAAGGCACGTCATTTTGATTAGA
WI-17730b	68 T C	TGAGCCTGGGGAGAAAGACCACAGAAAGTGAAGTGCTATTAGTTACATACACCAAGTGATACACTG TTT/CACATGATTTATGGCTGTTGATGTTGACCTCAATAACCTGGCTGATGATGATGTGTC
WI-17730a	39 A C	GACCACAGAA GTGAAGTGCT CATT	TCAACAGCCAT AAATCATGTG	TGAGCCTGGGGAGAAAGACCACAGAAAGTGAAGTGCTATT/CJGTTACATCATACCAAGTGATACATA CTGTTACATGATTTATGGCTGTTGATGTTGACCTCAATAACCTGGCTGATGATGATGTGTC
EST29041 5b	53 G A	GGAACAAACA CATTAAAGCAT CA	GGTATTGTTGA TTTGAGGAGTT AGC	TACTCAGAAATGTGAGTTCATGAGGAACAACACACATTAAGCATCATTTGTCACTG/AJGCTAACTCCT CAAATCAACAATACCCCTTTATTTTAGCCATGAAAAC
EST29128 4	58 A G	CTTTAGAGGACACCACTGTTGTTGGACTTAGGGCCTACCCCTATCCAGCAGGTGCC/JGTTATTT TCACTTGGTACGTCGTGAAGGACCGTTTCCAAATGAGTTACAGTCACAGGTTCTGAGCAGACATGA GTTTGTCTGGGACACT
EST29912 3	103 C T	TCTGCCAGCTT ACAGGCT	GCGTAAGTGTC TCATCTCTCTG T	ATTTATTAGGTATCTGCTGTTGGGGTGGGGAGATTGTTTGAGATACTGCAACAGACACACAA AGCAAAGAAAGAAACATTTCTGCCAGCTTACAGGCTC/JACAGAAGAATGAGACACTTACGCGATG GCCATGATACACAGCAGTGA
EST29936 8	121 G C	TATTGGTATGCTTAGGGAAGATTCTGATTTAGAGATATTAAATCTTAAAGTTAACTCACCATGAAA TTTAACCTTCTGTACTGGCTTCACTGATGAGGCGAGTAACTACATAGGGATAAA/JG/JAGCTCAGTA TCTGGAATCATGCTTCTCTG
EST30223 2	99 A G	AAATAATACATCATGGGAATGGGATATCCATCCCTCAAGCATTTATTTCTTTGAGTTACAAGCAA TCCAAATTACACTCTAAGTTATTTTAAATATATCC/JAGGATTTAAATTTCTCTTAGTTCAATCTTGGGA GG
WI-16260b	86 G A	CTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAGAAAAGACCCAGA GTTTCACAATATAGGTAGC/JA/ATAACCAGGCTCACTTTCCCTTCCGTGAGAACTTCGTGGGAC
WI-16260a	59 G T	TGAGGTGGATT CAAGAAGAAA A	CTACCTATATT GTGAAACTCTG GGT	CTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAGAAAAG/JTACCC AGAGTTTCACATATAGGTAGCGATACAGGCTCACTTTCCCTTCCGTGAGAACTTCGTGGGAC
WI-17835	30 G A	ACAGGAAATA TTGTGCTTTCT TG	TGGGGTATAGG AACAGGC	AAGAGAACAGGAAATAATTGTGCTTTCTTG/JAGGCTGTTTCCCTATACCCCAATATCATAAGAAATT GTTGTTGCTCTATATGTTACGTTCAAAATCTTTTGTCTTAATCAATCCAAATGAATTACCTGAATT TTCTCTCTTTGTTCAAAA

EST31951 4	87 C T	GGGTGTCCAG CCAACA	CCACCAAAAT CACCTCC	ACAGCCATTTATTATGTCTTACCTGGTAATATCAGAGACTGAAACATTTTCACTCTTTTAGCAATGACA TCGGGTGTCCAGCCCAACAC/CTGGAGGTGATTTGGTGGGAATTCCTATCACAATTTATCT
EST31968 8b	95 T G ...		---	CGAATTTGCTCTCTATTTTGTGATCTAGTAATCCTAAAGATTTGGGGGGGGTTACTATAAGT GCATTTTATAATGGGATTTTCTGCTT/GJAAGTGGGATTTTCTGCTTACATGGGAAAGGTGCAAAAG ACAGTGGTACTGCTGCC
EST31968 8a	75 T C T	GCGGGTTACTA TAAGTGCAATTT	TGTAAGAATCA GTGGGCAGTT	CGAATTTGCTCTCTATTTTGTGATCTAGTAATCCTAAAGATTTGGGGGGGGTTACTATAAGT GCATTTT/GJAATAATGGGATTTTCTGCTTAACGCCCACTGATTTCTTACATGGGAAAGGTGCAAAAG ACAGTGGTACTGCTGCC
EST32063 2	103 C T ...		---	TCCATGGATGAAGAGACGCTACCATGCCACATCCCCACTTCCCTCCGACCAGATGTCGTGGCCAGAGC TGGCTTCCCCTTCCAGACCTAGCTGGCTTTGTAGT/C/TTGTTCCAGGCCCATTTGAAATAGCAAAACGCAC AGTCATGTAGCACTCGG
WI-16303	65 A G ...		---	AAGGCTTTCGAAGCATTCAAGGCACCTTGGGTGTTGTGCTCTAAGTTTCTGGTCACTGCAGCCCCC/AG TTCTGTATTAGGGAGCACCCCCAAGCCAGTAACAATATGGTTCTTGGCAG
WI-17800	29 C G	GGGAGCACAA GAGAAACTCA	TTTCTACAAT TAATCCCAGTC TT	TGGACATGGGAGCACAAAGAGAAACTCAGT/C/GJAAGACTGGGATTAATTTGTAGGAAATATTTTCACAG TTTCCACAAGTCAGAGAGCTAATCCCAACCCCTGTATCTGGAACATACACTGCTGCCATTTTCTGTC CCATGAAGGGAAATACCC
WI-17857	34 T G C	CCTAAAGTCTG GGATGACTTTC	TTGGCTTAGGT TCTACTTGATG T	AAACTGTCAATCCTAAAGTCTGGGATGACTTTCC/T/GJATTTACATCAAGTAGAACCTAAGCCCAAT TCAGAAATCAGAAATCCTTTTGTCCATCAAAATCCAGCTAACCTCAAGCTGAATTAATTTGTTCAATCT GTATCTGATGTAGTTAAACCATGGCCTGTCATGATTATATTGCTATAAGGAAGGGAACAAATCTTTA TAGTGTCCTCAAGATAATTAATTTCTGGTTTAAATCTTTGCCAGCAAGCAAAATAT/AJCCGACTGAC TGCTCCTTAGTCTGTGATC
WI-17860	121 T A	TTTGCCAGCAA AGCAAATA	ACTAAGGAGC AGTCAGTCGG	
WI-17866	43 A T	TTTTATAGCCT ACTTCTCAAA	CCGTTGTCACT AATCACAACAA A	CAGCAACCTTTTGTGTTTATAGCCTACTTCTCAAAATTTGTT/A/TTTGTGTGATTAGTGACAACG GGGGAATCTACAATGCTCACATCACAGTAACCA
EST33301 4c	80 G A ...		---	GAAAAAAAGTCAAAATGTGTTCCCTTTATGGGTGATGCCACCATGATTGCCCTCACACAAGCATGATC AATCGCCACGAGAG/AJACTGGATGCCAAAGAGTATGG
EST33301 4b	63 G A ...		---	GAAAAAAAGTCAAAATGTGTTCCCTTTATGGGTGATGCCACCATGATTGCCCTCACACAAGCAT/G/A/ ATCAATCGCCACGAGAGACTGGATGCCAAAGAGTATGG
EST33460 1	44 G A CA	AGCGTGGTTTT CAATACTAAA	CTGTATTATT GTTAAATATTT GCATTGTT	CTATCCAAAGATATTTATTGCAAGCGTGGTTTCAATACTAAACA/G/A/JGTGAACAAATGCAAAATATT TAACAATAAATACAGTGATTAAATAAGCCATGGCATATCCAGTTGATGTAATACTTTTGCAA

WI-17904	50 A G	AAAGCATGAC AATAAAATGA ACAC	CGCTTATGTTA ATAGTAATTCC CG	CAAGTGAATATTGATACATGGCTGACAAAGCATGACAATAAAATGAACACAC[AG]TACGGGAATTAC TATTAAACATAAGCGATAACATCAAAACATCTGGTAAATGCAGTTAAACACAAACACACAAATGA
EST34149 5	69 A G	TGCCAAATAC TCAAGTGTGA GAT	AACTACTAGCG AGAACAACATA ATAAAATC	GTITTTCTTTGAGTGACACAAGCTTGTTCAATTTTGAGAAATGTGTGCCAAATACTCAAGTGTGAA T[AG]GATTTATTAGTTGTTCTCGTAGTAGTITTTGGTATTCTATGAAAAAAGCAGCTAGTTCAGC TTACAATCACACAAGT
EST34343 8	95 C A	---	---	TGGGAAAACATAAGTTAACTCAAGAAATATATCCAGTCTTTATGTTACTAAAAACATTTGTAATAGTGT TTTTATCAATGATGCCGAGGTCACTGCT[C]ATACAAAGATTAAAGAAACTTACCATCAAAACACTTC CAGTGCATCAA
WI-17982	98 C T	GGACCATATG ATATATAACT CCTAAAGC	CAGAAATTATG TGATAATAACT CCTTCC	GGTACACAATTTTAAATGGAAGGAACCAACAGGTATGTTGAAAGAACATCAGTACAGCTGGAGACAGG GAGGGACCATATGATATATAACTCCTAAAAGC[C]TGGGAAGGAGTTATTATCACATAATTTCTGGGC GCTACAGAAAGTTTTCATCA
WI-17993	118 A C	---	---	CTCAGTAACTCCGGTGTATAATCTGCCATTTATTGATTTATTTATGATAAAACACCTCTCATTTGTGA AAAAACAGCTAAGGGTGACATCTCCAGACCCCAACCACTGTCCCTGTAATGT[AC]CTGCTGAGAGTCC ACATTTTGGAAATCCAAT
WI-17996	84 A G	GTAGAGGCGA AGGGAACAG	AGGCACATGGG CAGC	CCCATCCAGAAACCCCGAGTGTGATGGTGAAGCAGCATGAAAACAACATCTCCCCAGGCCCTCGCAGT AGAGGCGAAGGGAACAG[AG]GCTGCCCATGTGCCTGTCTAAAGACGCCACCTCAGGTTGATGT CACCTGTGGGAGACCGGGT
WI-17136	33 C G	---	---	ATTCTTTATAAAACACCATGTCCCTAAAATGT[C]GATTCACATATATGCACACCTTCGATGTAT AGGACACTGATCAAAAAGACAGAGAAATGTGTCCCT
WI-18041	24 A C	---	---	GCCACTGAAAAAAGGTGCTCTTCC[C]GTTTCTAACTCCCTGGACTCCCTCATTTGGAACTGAAGCTC ACAGATGTTTCAGCTGGACTAGTTAGACTTTGCTGTATTTTAAAGGCAGTGTGATGCTCCAGGAT TCAAATACTTAATCA
EST35164 8a	57 A G	CACAGCCCTGC OCCC	CCCTCTGGATT CTGAATCTCAA	TTGAACCAAGGCCCTAACAGATGACTCAGCAGGGCCCTTCAAGCACAGCCCTGCCCCC[AG]TCTTGA GATTCAGAATCCAGAGGGTGCTCAGTCCCTGGTTTAGGTGCTTCTGTGACATTTCCCTCTTG
WI-18052b	67 A G	---	---	AGCGAATGAAATGCTACATAGGCTCCCTGAGTTCCTTTCATGTACGAATCT[CT]GGTTACACATCTT A/GIACAGCAGAGCTGCTGAGGGAGGGTGTGTTTAAATGCTGATGCATGCTCAGCACAGTGTCTGGC ATGGCCCATCCATGCTTT
WI-18052a	50 T C	CTGAGTTCCT TCATGTACGA ATC	CTCAGGCAGCT CTGCTGT	AGCGAATGAAATGCTACATAGGCTCCCTGAGTTCCTTTCATGTACGAATCT[CT]GGTTACACATCTT ATGGCCCATCCATGCTTT
WI-18054	46 G A	GGGAGTGGG GAGTAAA	CGTACCCCTGC TTCCA	CTGTTGTGCTGAGAACAGAGGGGTCAAGGGAGTGGGGAGTAAA[AG]ATGGAAGCAGGGGTGACG CATGCAGGAGTCCAGACAAAAGACGGGIGATTTCICAGGTTGGTAGCAACAGAGGTAATG

WI-18064	54	G A A G A	GTAGTGTGCTA AGTGTATTTC	CCAGTGGTATG ATTGTGACATT C	CAGCTGCCAATCATCTCTCAACCCGTGGGTAGCTGCTAAGCTGTATTTCAGAG/GA/GAATGTACAC AATCATACCACCTGGGAGAGAAAGAGTAAAGACACAGTCTTATTAGGTGCCAACTGGGGTACCTGGGAG GCAGAAA
EST35347 2	97	T C A A	GCATAAAATT TCCAGTTGGT	CCCTCGGCACC TGCT	TTTAGCACCATTCTTAGTGGAGCAGGATTCTTGATCATGGGTGGAATTTGTGTATCTGGGCTTCAT GGGATGCATAAAATTTCCAGTTGGTAAAGT/CJAGCAGGTGCCGAGGGTCTGGATCAGAAAAAAGG CAGGCA
WI-18070	28	A C G T A T	AACCCACTAC TACTCAGAGT	AAACTAATA AGAACTGGA GGTTTT	AAACCCACTACTTACTCAGAGTGTGTAT/CJATATTAACACATGAAAGATATAATCTTAGAAAAA ACCTCCAGTTCTTATTAGTTTGATATTTCTGTACTCAGAAGCATTTTAGGTTGCAAGGATATAA
WI-18080c	80	C T ---		---	TGGCATAAAGTTTGCAAAATCAATATCAAACTAGTCTCTCTTTGTAAATTAATACTACTATGCCGTG TTTGACITTTAT/CJTTCTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGTAT
WI-18080b	65	G A ---		---	TGGCATAAAGTTTGCAAAATCAATATCAAACTAGTCTCTCTTTGTAAATTAATACTACTATGCCGTG/ A/TGTTTGACITTTATCTCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGTAT
WI-18080a	41	T C A G T C T C	GCAAAATATCA ATATCAAACT	CAATTTACATA AGAGATAAAA GTCAAACA	TGGCATAAAGTTTGCAAAATCAATATCAAACTAGTCTCTCT/CJTGTAAATTAATACTACTATGC CGTGTGACITTTATCTCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGTAT
WI-18086	63	G A ---		---	GTGGGATCCTATAAAAGCAGCCATGTGTGAACAAATGATATGCACAGAAAGCATACTTCTG/A/ TGGCTTTGTACACGGGTTTCTTCAAGAGGAAGATGACTCAGCCCTCCAGCTTCTGCAGTCTAGC TTAGGAGAGGIGITTTGAA
WI-18115b	71	C T ---		---	AACTACATAGTATGGTGCCTGGCTTAGAATCAATGGGTAAAGCCCTTAGTGACCTTTGGTATCC TTC/CJTGTGTATGAAAGACAGACCTCTGCTGGAGGACTCATTACAATGTAAAGAAAGGGGTGAG TCAGT
WI-18115a	70	C T T T	TTAGTGACCT TTGGTATCCC	AGAGGTCTGTC TTTCATACCAA A	AACTACATAGTATGGTGCCTGGCTTAGAATCAATGGGTAAAGCCCTTAGTGACCTTTGGTATCC TTC/CJTGTGTATGAAAGACAGACCTCTGCTGGAGGACTCATTACAATGTAAAGAAAGGGGTGAG TCAGT
WI-18136	78	A G ---		---	TTTTGAGAAGCAGCTCTGTAAGGCAAGGATGCATTCAAAAATGGCTTTGAGGATTAACTCTCTCTTA GGTAATTTGC/GJTAAGAACAAATAAAGCATTTTAAAGTCCACTGCCGCCCTTAGAAACT
WI-18169	115	A G A G C T C	CCATCTTCCG	GAGTTCTGCTT	GGCAAAATATTTTACATCACACCTGGAATCTGCCAAGTCTTCCACTATGAAGGCAATCGTAGAG TGTGCAGGAGGAAAGGTGTATCCAAAGCAGCCATCTTCCGGAAGCTC/GJTGAGGACACAAGCAGA ACTCGGTGGGTAGATGGA
WI-18190b	26	G A ---		---	TGAAAGAAAGTCGACACAGCGGACACT/GA/JTCATAAGTGGAAACAAAGGATGAAGCTAATCATGGAG GCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGATGAGCTGGAGACATTAACTCTGGCGA

WI-18190	62 G A	TGAAAGAGTCGACACAGCGGACACTGTCTAAGTGGAAACAAGGATGAAGCTAATCATGTGA[G/A] GCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGAAATGAGCTGGAGACATTAAATCCTGGCGA
WI-18181	100 A C	AAATATATAC AACACTCCCTT CAGATC	CGTTTACCAT TTGTTAAGCTT TTG	...	GACAGTGAAACACATTGAAACACAAATACAACAAAAACATTAGGAACAAGAAATGTGTAATCCAA TGTTGAAAAATATATACAACACCTCCCTTCAGATC[A/C]CAAAAGCTTAACAAATGGTAAAAACGTA TGTTGTTCTGAAC
WI-18215	78 G A	AGCAGAGTTC CTGCCCTC	CCTCCCTCTCT CCCC	...	ATTATACAAGCATTCTCTGAGTACAACTAGGGGACAGGTATTTACAAAAACAATAGAGCAGA GTTCTGCCCTC[G/A]GTGTGGGGGAGAGAGGGGATTGAGCATTTGGTGGAGTATGTTAATT CCCTCAAGTTAATTCCTTC
WI-18232	60 T A A	TGGTGTGATT GTGATACACTT A A	AAATAAAGGT TTTCAGGGGT C	...	CATTTCCGAAAACTGATAGTTAAAAATATCCCGTCTGGTGTGATTGTGATACACTTAAGT[A/G]AA CCCCTGAAAAACCTTTATTTTGAATTTGAAGTTTGTCTAGAACTGGGACAGAACTTTTCACATTCTG AC
WI-17892	76 T C A C A	GGAAACTTG AGTTTGAGATC A C A	CACAGAAGTG AATAGACTAGT GAGACA	...	TTTAAAAATGCTTAGATTTCCTCAGTATTTATCAATAGTGTGAAGCTGGAAAACTTGAGTTTGAG ATCACAAT[A/C]CTGTCTCACTAGTCTATTCACCTCTGTGGGCATTTGGCAGAAAGTGCC
WI-18242	30 G A A	CCCCAAATGTT AATCGTAACA A A	GCTAACACCTC TACTGTAAACAG CTTTC	...	AATATCCCAAAATGTTAATCGTAACATACT[G/A]GAAAGCTGTACAGTAGAAGTGTAGCAAAAAT TGGATGCCACAACTTATCTACCACTCTTCAAGCAAGTGAAGGTGAGATGTTCTTGCCCTATATC TGCAAAAGATCGAACAAAG
WI-18266c	119 C T	GCATCAGACATCACCACTCCTGAAAAAAACCTTCTACAAGAAATTGAAAAAGTTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAAATGATGCATGAATC[C/T]ACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18266b	124 T C	GCATCAGACATCACCACTCCTGAAAAAAACCTTCTACAAGAAATTGAAAAAGTTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAAATGATGCATGAATCCACAT[C/T]GAGAC CCGCAACTCCGAGGTACCT
WI-18266a	97 C T	AAATAGGAAA TATGGACTATC TTCAAA	TTTCATGCATCA TTTGTCGA	...	GCATCAGACATCACCACTCCTGAAAAAAACCTTCTACAAGAAATTGAAAAAGTTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAA[C/T]TGACAAAATGATGCATGAATCCACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18312	73 A G A A	GCTGTCAGCTA TTGTTATTCA	GGAGAAAAGG GAGCAGAAGA	...	CTGAGCCTCTTGGATATGTGGTTAGTGTCTATCATTAAATTTTGGAAAGCTGTGAGTATTGTTATTC AAAT[A/G]ATCTCTGCTCCCTTTCTCCCTTTTCTGGGATTCTCATTCTGCATGTGTTATA
WI-18330b	66 A G	AAACATCTACAGCTGTCTTAGGCCATCTCTGTAAGAAATCAGGGATAAGAGCTGAGGAACAAGAGGGI A/GTATGTAGGCAGTGTGAGTCAGGACTATGCAAAACCATAAAAATAAGAACATAATTTTGTGAT TCACA

WI-18330a	49 G A A A G A	TCCTGTAAGA AATCAGGGAT	AGTCTGACTC ACTGCCTACA	AAACATCTACAGCTGCTTAGGCCATCCTGTAGAAATCAGGGATAAGA[G/A]CTGAGGAACAAGA GGGATATGTAGGCAGTGAAGTACAGGACTATGCAAAACCATAAAATAAAGAACATAATTTTTTTTGTGAT TCACA
EST37564 5	85 T C A G A	AAATTC AAGC CATCTACAAA	CTATGAGGCC TCAATGAGA	AAATTAGTAGCCATAACAGGCTGGAATTGCTGGTAGAATCTGCATGTTATTTAAGCTAAATTC AAGCCATCTACAAAAGATT[C]CTCATTTGAGGCCATAGGCTGCAACACATCAAAAGGCATTAC TGTACTGGAGAGGACTGAG
WI-18327	104 G A T T	AACAGCTTT CGTTAGGCTAG	CGCATACAATG GCTCAGC	CAAGGGGATTTATTACCTACAACAAGTAAGGAGGAGCAGCTGGGGCAGTTCCCAAGCAGTACCTC CCAAACAATGGTGAAACACAGCTTTCGTTAGGCTAGTT[G/A]GCTGAGCCATTGTATGCGGAGGCAGA GT
EST37624 6b	102 G A ---		---	GTGGCAAGCAGCAGCTAAACACACTCATTTTGCATGAACCTCCAAATACGAACAGTGCACGCTGATGG CCTGCAGTCTCTGCGGTGCTTGGCTCTCTGGACG[G/A]TTCATTCTACATGGCTGCTGCTTTGCGTCC TCTGACCTCCCCATTCC
EST37624 6a	58 C T ---		---	GTGGCAAGCAGCAGCTAAACACACTCATTTTGCATGAACCTCCAAATACGAACAGTGCAC[G/T]GCTGA TGGCCTGCAGTCTCTGCGGTGCTTGGCTCTCTGGACGTTCAATCTACATGGCTGCTGCTTTGCGTCC TCTGACCTCCCCATTCC
WI-18357	89 C G GCATCAA	CCAGCCCTTA GCATCAA	AAGGACTCAA AGACTGAAGAT GA	AATGTTTTAAAAAGTCTACCGTGTGAGGTGGCCATGAAGCCCAAGCCCATGGAGAGACATTTTCAAGA TAATCCAGCCCTTAGCATCAA[C/G]TCATCTTCAGTCTTTGAGTCTTCCAGCCCAAGGTCCAAGCTT GTGGACCAGAGACAAGCC
WI-18012g	117 A G ---		---	TTTTATCTGGTCAGCTCCTTTCTTAATGGCCTGAAGGTCACTCTCTTCAACTTTCCAGACTTGGAAAG ATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCCCTTCGTGA[G/G]GTGTTTCCCTGATACA CGCTGACGTTTCGAGGG
WI-18012f	113 G A ---		---	TTTTATCTGGTCAGCTCCTTTCTTAATGGCCTGAAGGTCACTCTCTTCAACTTTCCAGACTTGGAAAG ATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCCCTTCGTGA[G/G]GTGAAAGTGTTCCTGATACA CGCTGACGTTTCGAGGG
WI-18012e	112 C T CCCTT	GCCACTTTTGC CCCTT	TCAGCGTGTAT CAGGAACA	TTTTATCTGGTCAGCTCCTTTCTTAATGGCCTGAAGGTCACTCTCTTCAACTTTCCAGACTTGGAAAG AGATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCCCTTCGTGAAGTGTTCCTGATACAC GCTGACGTTTCGAGGG
WI-18012b	46 T C ---		---	
EST38390 4	75 A G CTCTGCATTG	GCTAAAGTCAG CTGATTAATAA	ACTTAA	CATATCATAGCCAGATCTACAACCCCAAGAGTAAATCCCATGGTTATGTTACATGGCAAAAAGGACTC TGCATTGT[G/A]TAAAGTTTATTAAATCAGCTGACTTTAGCATTGGGAGATTATCTGGAT

EST38512 7	91 T G	TGACGATGCC AATACTTCG	CAC TGCAC TCT GGGAAGC	TAATAAAAAC TGACCCAA TTTGGTAAACTGTGTCTGGACTGAGAGAAACAATGAAAAATCTGTAAAT ACCTGATGACGATGCCAA TACTTCGTTG/GCTCCAGAGTGCAGTGATAACTGTTATAGCC
EST38519 0	24 C T T	CCTGCACTCC TAAAAGATCT	TCTGTTAGGAC TTGGGGGA	CCTGCACTCC TAAAGATCTTTTTC/TTCCCCCAAGTCTTAACAGAATGGTATATCTCTCTGGAAAA AGATGAACGTCAATCAATGGATTGCTGCTCTCGTTTCAGCTTTGATTTTTTTGTCTTGAGAACCTTG TCCTCCCTGCTGATT
EST38575 1		GAACATCCCA TGTTCTGTTT	AGGGAAGGTA GTATAACACAT	AGTGGTCAATGTAAACTAATGGGGACACCAAGCCTCAGGAAGAACAATCCCATGTTCTGTTTAA T/CJTCTCTTATGTGTATACTACCTTCCCTTCTCTTCTTATACACATAGATTTTCTTAAATTGCAGC CCA
EST38616 9		CCTGCTCGCC CTTC	GAGGAATGGAT GGTGCC	CCATCTAGGCAGGTACCTGAGCTCTGTGCTCCAGAGTGGTGCTCAGCCCGGGGGCCCGGTGG AGTCTCCGCGGGCCCGCCCTGCTCCGCCCTTCTC/G/GGCCACCATCCATTCTCCAGGGG
EST38652 8		TCTGAAC TGGG CATTCAA	TTGCAAAAATG AAAGGAAAA	TATAGTAGGTACTTTCTTGTGCTGCAGCAGGAATTAATCAGTCTGAAC TGGGCAATTCAA/T/CJGCGTG GTATTTTTTCTTTCATTTTGTGCAAGTAAAAAATCAT
EST38654 5		AATGGTCA TTT TAATATATCA	CAGTGATGGTC CTTAATCTTCT	CTCAAGCTGAGAATGGTCA TTTTAATATATCAGTTTTACATA/T/CJAGATAGAAGATTAAGGACCAT CACTGAGGTACATAGCTCAGAGGCAGAGTTAAGATTTGGACCCAGGAGTTGGTTCCAGCATATA
EST38707 9			ATC	GGATCTCACTACCTGGGACAGCTGAGAGGGACATCCACCAAGAACCTACTGATCTGGAGTCCCA CGTTCCOCJAGJAGGCCAGCGGGATGTGTGCCCTCTCTCCCAACTCATCTTTTCAGGAACACGAGG ATTCTGTCTTCTGGAAA
EST38759 2	86 A G	TGCTCCCTGA GGTGATAGG	TCACCATCGTG GACTTAAGG	TGACCTTGATTTCTTCACTAGAGGGGAGAAGAAATCACCTACCTTTTGGATGCTCCCACTCTACTTGT CTCCCTGAGGTGATATGGJAGJCTTAAGTCCACGATGGTGACCTAAACTCAGTTTAAAAATCTTGCC TAGCAGCACC
EST38775 1	40 T A C	AATCAATAGG AGAGGATTGG	GGCTTTGCTCT GAATCAAA	GACTCTCAACCAAGAGAAATCAATAGGAGAGGATTGGCT/AJTTTGAATTCAGAGCAAAAGCCCT CTTACTGAGAGGTGAGCCCCAGCCCCCTCCAAATGCCCTTTTCATGAGTTAGGATCTCCTAAGTGGTAC AAACAACCAACATGGTGG
EST38815 4		TGTTTATGAGA ACCCATTACA	GCTGACTGGCA CATGCTTT	CACCCCATATTTGACCAAGGGATGAAGCCTAGCCATGCTCTTCACTTATGTGTGTTCAATCAACAAG TGTTTATGAGAACCCATTACACA/C/AJAAAGCATGTGCCAGTCAAGCAGATTCTGTAATAA
EST38858 4		CACGAGTAAA AAGAACTCA	GGAGCGAGTCC AAGGAGAA	TCCTTACTGTGCTTACAACCTTCTCCCAAGTTTGGGGTTTCCCATATTGTTATTGTTATTGTTATTA TTCAACACGAGTAAAAGAAACTCATGAC/CJTTCTCTTGGACTCGCTCCTCTCCCAATCTCGAT ACCGACTGCCTGTTG
EST38865 2	72 T C	GCTGTAGAATT TGTTGATGATGC	GGAAGGACGG AGGACACAG	CCTTAATGGATTTTACAGCTCATCTGAGTCTCTGCTGTGTTCTCTGAGGAGCTGTAGAAATTTGTGTCG ATGC/T/CJCTGTGCTCTCTCCCAATGAGCACATATGCAGGGCAGGCAAGAGCATGCTGGA TTTGTCTTAGTTGTTAA

EST38878 9	47 T	AAACATCATT ACTAGCCTAG C ATCCTAA	CCTTCAATAAA TCTCATGTCT CA	CCAAATGAGAACCAAGTAATTAACATCATTACTAGCCTAGATCCTAA[T/C]TGAGGACATGAGATT ATTGAAGGGAAATCCTCAATTAATATGAACATTTCTTGAGAAATGGAAATTTGAAACATTTCCC TTATCAATGTCTACACATCTTTATTTTATTTTATTTTACCTTTCTCAAATATCGGATTGTGC TCATGAGAAATATGGCTGAGGGAGCTGGCAGGCAGTCTCTCA[G/C]GCTCCCTGGATAGCTAAAT TTA
EST38882 6b	113 G	TTATCAATGTCTATCTCACATCTTTATTTATTTAT[T/C]TTGTTTTTCACTTTCTCAAATATCGGATTGT TGCTCATGAGAAATATGGCTGAGGGAGCTGGCAGGCAGTCTTCTCAGGCTCCCTGGATAGCTAAAT TA
EST38882 6a	35 T	TGTCATCTCAC ACATTCTTTAT TTTT	CGATATTTGAG AAAGTGAAAA CAA	GCACATAACTAATTTTCAATTTGCGATTGCACAGCATGGCTAAACG[A/G]TAAAGATGGGAATCAA CAAATACCATTTGAAGATATGGAGCAAGAGAACTCTCACATACCTGCTGGAGGGAATATAAAT AACTGAATGGCAGTGAACACATACACATCAAACTTAGGGAATGTGGTTAGTGTGGTACGTTGAG GGAACTTATAACCTCAC[A/G]CGCTTTTTCACAAAAACACAGACACAGAGATTTCCAACTC CAGCAATGACAGGCTAGGG
EST38909 5	47 A	GCACAGCATG GCTAAACG	GGTATTTGTG ATCCCATCTT T	TAACATTCCCATTTGAATCCCTTGGTGG[G/C]GGGGGGGGTGAGATTGCAGTGTCAAGATAAA TATCACAATATATCAAAAACCTTCAAATTTCTATGCATTCACACACTGACATGAGCCACAAACATT CCTTTCACAGGACTGTAC
EST38911 9	85 A	GTTGAGGGAA ACTTATAACCT CAC	TGTTGTTTTGT GAAACAAGCG	CCTGCTATGATGCCTGGGCAGATCCGGACCTTCGGTGAOC[G/A]CAGGCTCCCTGCCAGGGCTTGG CCCTGACCCGGCTCCCGAGCTCGGCCCTGACTGTGGAGGAGCTGAAATACGCTGACATCCGCAACCT C
EST38955 5	30 G	TGAATCCCTT GGTGG	CACTGCAATCT CAOCCC	CACGTGGCCCTAAGTTCCGGGTCTTCTCAGTCTGGATGGCTGTGTGGAAAAAGCTTGGTGGTAAG GCCTAAGGAATTTGAGGGGCGAGGGGGGATGCCGCCAGCCGAGATGGTCTGTAAAGCCTGTGGGTC AAAGACCTAACTTCTGGA
EST39002 0	42 G	GGACCTTCGG TGACC	CTGGCAGGGAG CCTG	AAAGATAATGTCAACACGCAACATATAGAAACATAAAAGAAAAATAAAGTATCCACCCTAAAT CCCTATTATCCATGATATTTTCA[T/C]JAGCAACTAGTATATATCAATATATTTTTCACAAACCAT TCAGTTACAC
EST39004 8	79 T	GGTGTAAAG CCTAAGGAAT	ATCTCGGCTGG CGC	GGTTGCTTTCATGTAATTTTCTCATTTCTCTATCAGGTTTCTGGTCCCTTTGTCTCAATTTTAAACAT T/CCTTTTATATAGGAATTAGCCCTTAAACTGTGTACATGCTGCCAAAAATTTCTCCCAAGTT
WI-16398	90 T	TCCCTATTATT CCATGATATTT TCA	GAATGGTTGT GAAAAATATA TTGATAT	GCCTTAATGGCTACAGAAGAAGG[C/T]GGTTTTATTTTCTTTTAAACACATCTGGTTCTGGCAGC AAGTATATTATGCATTTAGAGCAATAGGTGCCCTGAA
WI-16403	69 T	CCTTGCTCTC AATTTTAAAC ACT	TAAGGGCTAAT TCCCTATATAA AAAG	
WI-16406	24 C	GCITTAATGGC TACAGAAAGA AGG	CCAGAACCAG ATGTGTTTAA AA	

EST39236 0b	57 C G	TCATCTGAGA ATAAACTTCCT GTCT	CATTATAGGTA CTGAGTCATAC ATTAAACA	TCCTTTTATTCATGATTGTTTCATCTGAGAAATAAACTTCCTGCTAAATTTCCAA[C/G]ACTATGTT TAATGTGACTCAGTACCTATAATGAGACTGGAAATATATTACCTGGCAAATGAATGAGGTGCTCTC TTT
EST39294 4	63 G T	CCTGAAACAG GGATGOC	GCACAATTAA ACATAGTACCG AGAA	CAACAGACCTTGGTTTGGCTCACCTGGTGACAGGAGACTCTACCTGAACAGGGATGCC[G/T] TTCTCGGTACTATGTTTAAATTTGCTGAGCCAGCAACCTCGAGTTACCGGCCCTTTACCCACAGCC AGCTGCTGTGCTGCAAT
EST39366 2	72 T C		...	AGAAACATTTCTGCTGATCAGAGGAAGATGTATGTAGAAATCAGAAATCTGACTGAATTCCTAAA ATCTATT[C/J]ACACTGAGAGGAAATGGAAAGAAATGTTTGATAAAGCTTTTCCCTGACTCTCA GAGGGGTTTCAGA
EST39371 9	86 A G	CATTGGATTA GGTGAGG	TGATTTGAGAC ATTTCACATTT TT	AAAAAGCTGTAGCTGGCAAGTCAAAGTTTATTTATGTGTAAATCCCAGTTGAGCATTTTTCAT TTGGATTAGCGTGAGAGG[A/G]AAAAATGTGAATGTCTCAAATCAATGCTTCTTCTAAAGATTA GACATTGCCCAACCTGC
WI-17177	23 A G		...	ACAAGTGACATATCCAAACCAAC[C/G]TCCATCCCCACCTGTGCCCTATTCTTCCCTGTGTTCTTT AGAGCCTTTTCAGCTATTTCTGTGAAGCAAACTGCACGAAGGCTCCCCGTACTCCTCCCTGGAA G
EST39428 8	31 C T	GCCTCCCA ATTGATT	GGTCCCTTATG AAGCCACC	AGTTCTCTGGTTGCTCCCCACAATTTTGATT[C/T]GGTGGCTTCATAAGGGACCCAGGATTCTGCATT TTCTGGGTGGGCTAGGTAATCTGTGCTCTTTGGTCCACAGAGCACAAATTAAGAAGATCAGGTCT GGCTGTTC
EST39430 2	45 A C	GGCAGAGGAA TAACTGATGT	CAGGGGTGGG GTAATG	AATTTAGCAGAAACAATGAAGTTGGCAGAGGAATAAAGTATGTT[C/A/C]CAATACCCCGACCCCTGA CCAGTACCTTTCCCTCAGGCCAGGCTCCGGTGAGGATGTCCTGGG
EST39446 7b	117 C T	CTACTGACAT AGGACTTCA GAGTAA	TCCTGGAAAC TGACATAAAC	AAAGCCCTGTAACTGAAGCTAGACAACGTCAACTTTGGAAAGAAATAACAGGAACCTATTATAT ACGTAATCAGTTTTCATACCTGCCTACTGACATAGGACTTCAGAGTAATA[C/T]GGTTTATGTCAGT TTTCCAGGATTGTTCTCCC
EST39465 2	80 A G	AATGCAGGAG GGTGC	CAATCTGGGC CCTCT	ATGGTGTCAATTAGAGGGCCACAGGGGATGGGGAGTAAATAAATAACATAACGAACCTGAACAGAAA TGCAGGAGGGTGG[C/A/G]AGAGGGCCGAGATTGGGTGTTTCAGGGCAGAGAGGTGGAAGACCAG
EST39501 0	81 A G	AAAGATTCT GTAGACATCT AACATTAG	CACCTGCAATT CTGAAGGCT	TGCTTACAACCCATAACCATAGGCCATGTGTTCAGACATTTCTGACCAAGCCTAAAGATTCTGTAG ACATCTAACATTAG[A/G]TAGCCTTCAGAAATGCAAGTGCAAGTTCAAGTCAAAACCAATTC
WI-18387b	84 A C		...	CACAAATGGGACTGCTGAAGAGTGGACAGTTGGACCTTACTTTGGTGACCCCATACATTTGTGGTCA CATGCTTTAGCCATAC[A/C]CATGGTAACATTGACTATGGAGCTTTGTGAAAGTGAATGTGCGGATG GCTATGTAGACATAAAGA

WI-18387a	EST406019	57 A G	CCTTACTTTGG TGACCCCAT GCGTGAACCT GAAACAC	GCTAAAGCATG TGACCACAAA TTCTTGGAGA AAGCGTC	CACAAAAATGGGACTGCTGAAGAGTGGACAGTTGGACCTTACTTTGGTGAACCCATAC/GJTTTGIGTGCACATGCTTTAGCCATACACATGGTAACATTGACTATGGAGCTTTGTGAAAGTGTAAATGTGCCGATGCTATGTAGACATAAAGA
EST41935		32 A G	AGTGATTCAC ATCTTCAGGAT AGGT	GCACACCCCTC ACACTGTTA	TCCATTCACTGTATCACATCTTCAGGATAGGT/GJATAACAGTGTGAAGGTGTGCTCATTTTTCTTCAGCTGTAGAGGAGTCTCCCGAGAGTAGCAGTTGTGA
EST43091		28 C T	CACTCTGGCT TTAATTTTGA CA	AAAACTGAATT GTTAAACATG CTAC	ATGTCAATCTGGCTTTATTTTGGACA/CJTGTAGCATGTTTTAACAAATCAGTTTTTTCATAGGCAAACCTTTTGAACATCAAAAGAAATACAATATATTTTCACAAATTTCTCATCAGTGTAAATTCAC
WI-18420c		108 T C	TTCCATTAAAC AGGAAGTTTC C	AAATTCACG ATTGCTATAAG C	AGAGAGACAAACAAGAAGAAATAGGGAATAATGGGAAGAACAGAGTGAATTAAGCAAAATCTTGGATTCAGATTCCATTAAACAGGAAGTTTCCCTCAAAAAAAAAATCAAA[C]/GCTTATAGCAATGCTGAGAAATTCATAGGTACTTCATGGGA
WI-18420a		38 C T	GAATAAGGGA AAATGGGAAG AA	CCAAGATTTC TTTAATTTCAC TC	AGAGAGACAAACAAGAAATAGGGAATAATGGGAAGAA[C]/TJAGAGTGAATTAAGCAAAATCTTGGATTTCAGATTCCATTAAACAGGAAGTTTCCCTCAAAAAAAAAATCAAAATGCTTATAGCAATGCTGAGAAATTCATAGGTACTTCATGGGA
WI-18425b		101 T C	--- CACCTGTCT AGACAGATT	--- CCTCTGTGT TGTGTGA	AGCTGATCAGCTGTCTGTACTGTGTTTTATGTGTGGCCCCAGGGAAGCCAAAAGATCAGACACCTGTCTAGACAGATTCA/CJTGACACAAACAAGGAGTGGGGTTCACACGGCGGAGAGCCAAAGAC TAGGGC
WI-18425		81 A C	A CCTTTGGCTCT AAGTGGGACT	GTATCCAGA	AGCTGATCAGCTGTCTGTACTGTGTTTTATGTGTGGCCCCAGGGAAGCCAAAAGATCAGACACCTGTCTAGACAGATTCA/CJTGACACAAACAAGGAGTGGGGTTCACACGGCGGAGAGCCAAAGAC TAGGGC
WI-18449		129 C T	---	---	AAATTTAGGTCGGGTGGAACTATAAAAAGGAAGAAAGAGAAGTAATCAAGGGAGGCCAAAGTGGAAGCTGTATTGCTGATCTAAACGTGCTGTTCAGTTCTCTTTTGGCTCTAAGTGGGACTA/CJTTC TGGATACAGTCAGGGGAG
WI-18457		120 T C	---	---	ATCGCTTCATTGAAGCCCTGCTTAATTTCTCTCAGTCAACTGGTGCCCCCAAGACATATTTTATTTCTTAAATGTCCAATACTCGCCCTGATGTCTGTGTTGTGCACATTTGGGGCCACAG[C]/JAAATAGGCTAAA AGGCAGTCCCACCTGCT
WI-18462		39 A G	CCAATGGC AGAGGTGA	TTTAGGCTTTG AGATGTTTCT	GGTGCTATAGCTGCTGTACACCACAATGGCAGAGGTGA/JGTAGAAACCATCTCAAAGCCTAAAAATTTACCATACATCCCTCAGCAAGAAAGTTTGTAACTCGGGTTTAGGACTCCATTGAG
WI-18476		60 C T	GAGG GGTGGGGTGC	GCACGATGGGA GTGAOC	TGAGGACGTGTGACAAGCTCAGCAGGGGTGGGGCGCGGCTGAGGGTGGGGTGGCGAGG[C]/TGGTCACTCCCATCTGGCCGTCCTCCACTACCCACACCTGGCCAGTCCACGTTGAGGT

WI-18491	109	GA	AACAAATGGT AGGTGGTATT	OGTGTGCATTT TCTTGTAAATCC	CTAATGAGATGAATACATGGAAGGCGTTTAGCACAGTGCCTAAACACACAGTAAGTAACCAACAAT GGTAGGTGGTATTAACTATTATTAAATCCAGAATGAC[G/A]GGATTACAAGAAAAATGCACA CGT
EST50757 b	79	CT	GAGCTGAGG CTGCTTCT	ACCTTCACCC GCCC	AGCCCCCTCACCTCCACTCTGCTTCCACAAAGTCGGCTCCGAGAGCTCGAGGCTGCTCTTTTATAT GTGCAGGGCC[CT]GGGCGGGTGAAGGGTCAGAGA
WI-17675	103	TC	GGACATTTGG ATGGTGACTT	GGGGAACCAAC CAGG	GATCTTGGAAAGCACTAGAACTAACAATCTTACCAGGTGCTGAAGAAAAAGTGTCTCGTTTAAAT TGCCAAGCAGGGATGTGGACATTTGGATGGTACTT[C/C]CCTGGTGGTCCCATAGATTACCAT TGCTCTAATGGTGCTA
WI-16543	67	GT	AGATAAACTA CATTTGGGTT	GATTCATCAT ACAGGGGACTT	GATCCATTACCTAGGGTAAATTTCTCTGAATGTCAAAACAAAGAGATAAACTACATTTGGGTTTGG G/TAAGTCCCTGTATGATGAATCAAGATCCTCAAGTCTGTCTTGCCACCCATTAAATACGTATT TTTGTAAAGGCTGAAGTT
WI-17687	107	CG	GCCAAAAAGG TTGGGAA	TTACTTTTGT CCGACCAAGCA	ATCTGAGATGGAAGAGTTTCATCCCAAAACCATCTCCCCCTGACCCAGTCCATGGAATAATGTC TTCCACAAAACCGGTCCTGGTGCCAAAAGGTTGGGAA[C/G]TGCTGGTGGTACAAAAAGTAATT G
WI-17690b	79	AG	ACAACATGTGAAAGAAGATATGTTGCTTTACTCACAGTGGAGGCATTTTCTAGCTGTGTTGATTT GGCTTCCCTAT[AG]GATTCAGGACCCATAACTCTTGTCTCACTCATCTGCTATGCTGCTG
WI-17690a	63	GA	AGGCATTTTC TAGCTGTGTT	CAAGAGTTATG GGTCTGAATC	ACAACATGTGAAAGAAGATATGTTGCTTTACTCACAGTGGAGGCATTTTCTAGCTGTGTT[G/A]A TTTGGCTTCCCTATAGATTACAGACCCATAACTCTTGTCTCACATCTGCTATGCTGCTG
EST51717 b	128	CT	GCGGAAGACA GTGAGCTGTT	TTGAGGCAATA ATCCAGCTC	GATCCAATCTCAGTGTCTAACTCATCCAGATTATTC/TTGAAGTGGAAACCCACCTCCGACCC CAATGGCAACATCACCCACTACCTGTTTCTGGAGAGGCGGGAAGACAGTGTGAGCTGTTTCGAG CTGGATTATTGCCTCAAA
EST51717 a	39	CT	GATCCAATCTCAGTGTCTAACTCATCCAGATTATTC/TTGAAGTGGAAACCCACCTCCGACCCAA TGGCAACATCACCCACTACCTGTTTCTGGAGAGGCGGGAAGACAGTGTGAGCTGTT[C/TT]GAG CTGGATTATTGCCTCAAA
EST53012	97	CT	TGGTCACTTTG GGGOC	GGCTCTGCOCA GGC	TTTCCAGGTTGACAGGTTTATCCACCCCTTCCATCCCATGGCCACCCAGGAGGAGGAGACAG GTGTGCTGGAGTCTGGTCACTTTGGGGCC[C/TT]GGCGTGGGAGAGGCCACTGGGTTTACATTCTCTGT GGGAGGTTGTGGACAC
EST53349	96	AG	TGTTGAAAGC AGTCACAATG GTAC	CATCTGGATAT CTTGTACATT TT	AAACTGCAAAATAACAAAAACAAAGAGTCCAAAGGCTAAAGTCTAAGCTATAATTACACATG AAGTATATGTTGAAAGCAGTCAATGTAC[AG]AAAAATGTACAAGATATCCAGATGTTTAA
EST53389	74	AG	GGAGACCTGC AGAACTTAAA CA	GCCCTTCTAA CAATAAATGCT C	TTTCCAAATGTCTCCTGACTTGACAGACTGAGAGCCAGCCAGCCAGGAGACCTGCAGAACT TAAACAC[AG]GAGCATTTATGTTAGAAAGGCAAGTCTTACACTCAAAATAGGTTTAAACATGAAC ACATTAAGGGAGATGGCC

[illegible]

[illegible]

TIGR- A003P30	117 C G	ACAAGTTCAAAGGAGAACTTCCTTTTGTTTAAATGCAGCTGTGCTCAGAAAGCCTGTGATTTCTCTAGGA AACCATCTGGGTTTAGCCCATTAGAAAAATGCAGTTTAAAGCAGTGTCAC/G/ACTGGCTGCCTGAA GGTACCTTGGAGATACT
TIGR- A004S34	156 C T A	CCAAACCTCCT CATTCTATAA	TGTAACAGCT AACTGTTTTTG TTAAA	GCTTGCTTTTATGTTTAGTTCGGGGGAAGGAGGGCTGACACCCGACACATCTGGACACCAGC AAGGTCACAGGGAGGTTTGCAAACTTCTTTGCTTGGCTAACAGTGTGTCATGTGACATAGCCA AACCTCCTCATTCCTATAAA/C/TCTTAAACAAAACAGTTAGCTGTTTACAAAACAGTTAGCTGTT TACATG
TIGR- A004T44b	97 A C	AACAACAGTGTAACTTTAACAGGGGATGTTAAAGGTAAAGTCAGGAAGATAAACCAAAATGAT TGAGTATGATAAAGAAATTTGCATGGCGATT/C/JAAATAGAAAACCTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAGAAACAATATGACTTAGCAAGAAACAATATAG
TIGR- A004T44a	69 G A TGA	GGAGATAAA CCAAATGAT	GCCATGCAAAA TTCITTATCA	AACAACAGTGTAACTTTAACAGGGGATGTTAAAGGTAAAGTCAGGAAGATAAACCAAAATGAT TGA/G/ATATGATAAAGAAATTTGCATGGCGATTAAATAGAAAACCTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAGAAACAATATGACTTAGCAAGAAACAATATAG
TIGR- A004V08	60 T C	CAGGAAACA GGCATTCTCT	TCCTCCACA AAAGGC	CCTACAATCCTATAATATTCAAGGGTGGGAGGATGCAGGAAACAGGCATTCTCTTAT/C/JGCC TTTGTGGGAGGATCAATTTGGTGCATGCACTTTAGGGGACAATTTGGGAGTAGCTGTCAAAATTC AGTAGCTCAAAATTTCAA
TIGR- A004V26	125 A G	TCTAGCTATAAGACCAGATTTTAAATATTCTAGATATAGAATTATCCAGAATAATCTATTGAATTGA CTGATTACAAAATGTTAACAGCTGGATAAACGGTAAATATGCATTATCTTCACATGA/G/JAAGGT TTCAGTTTATAAATGCTTAAATAGTATCTATTGCTTAAATACTGTATCTATTGG
TIGR- A004V28 a	29 A G	TGTTGGGGTG CGATCTC	CGGAGGTTGCA GTGAGC	CCAGGCTAATGTTGTGGTGGGATCTC/J/GGCTCACTGCAACCTCCGCTCCAGGTTCAAGCAA TTCCTCGCTCAGCCTCTTGAGTAGCCGGGACTACAGGCACCCGCCACCTAACTAATTTTG TATTTTGTAGTAGACATTGTATTTTGTAGTAGACAGG
TIGR- A004X20	25 T C GA	AAGTTTTCCTT CTCTCTGTAG	TTTTATAGTTG ACTGTAACATG GAGAC	TAAGTTTCTCTCTCTGTAGGA/T/C/JGCTCCATGTTACAGTCAACTATAAACATGGCTCATGT TCACTCTGGGCTCGCTTCAGAGGAGTTTGATATTTGGAAAGTGGTACCTTTGTTCTGTGCTTTTCA GACCAACCGCTTCTTTCATTCTTCAAGGCTTCTTCCAAAGGAGTTAAATCATCATGTGTCCAATC ATCATCATGTCTCT
TIGR- A004X30	26 T C	TTTGAATCTT AGAGTAGAAC CCAC	TTCTTTATGGA AGTGTTTAAAA CTATTTT	TTTTGAATCTTAGAGTAGAACCCAC/T/C/ACTCTAGTAATACTTGTAAATAAAATAGTTTT AAACACTTCCATAAAGAAATTAGGGTGCCAGCTCTTGAATTTCCCTTAGGGATAAAGATATCCAT GTTAGGGATAAAGATATCCATGTAC
TIGR- A004Z04	102 T G ATGCAAAACT	TTTCAATTTGGGT TTCATTTCATGA	CTTATAATTAG AAATTTTCATGA AAGCAA	CACGGTATATGCCCTTATATAGGTATATATACAGATCGTACACATATATTTAACAGTTTGACATG GGGTCCACAGTACCTTCAATTTGGGTATGCAAAACTT/G/JTTGCTTTCATGAAATTTCTAATTAAAGG ACTGTTGCTTCTTTCATATTCAATGGACATTATACAAAATACAGTCTCTTTAGTGATTTAAGACGTC TCTTTAGTGATTTAAGACTG

TIGR- A004Z19	85 C T	GAGAACAAC T GCAGCATTTT	AAGATGGTCAT CGGGAAGA	TAAGTGGAGACAAGTTTATTGGAGGAGCTTGACACCCCTCTTCTGCCCTAGCTTGAGAGAACAACTGC AGCATTTTTTCTTTTTC/TCTTCCCGATGACCATCTTTTGGGCTGGCGGCCAGGCCCTGGGTGTC TCCCATATCGCTGCTCTTATGTAGAGACTGAGGATCTGGTATAGGAACAGATC
TIGR- A004Z42c	89 C T	TTGGGGGAGGT AGGAGACT	CAGGGCTGCGG GTCC	GTCTTAGCAGAGGAGATAACTTTGAGGGACAGCCCCCAAGGGCCAGGTAGCCTTCAGGGGCGGGCA GGGTTGGGGAGGTAGGAGACTCTGGACCCGCGAGCCCTGGCTCCAGCTTCATCATCTGTGTCTCTT CATCATCTGTGCTTC
TIGR- A005D17 c	81 T C	---	---	TATGGACTGTGTAGAAATATGATTTGGACAAGAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGCAAGGC/TCTGTAGATCTCTTGGCCTCTCTGTGAGGATCTCTCTCTCTGGGCAC GGGTGGGACCCCTCTCTGGAATGGGTATCTTACGACAGTCAAACTCTTACGACAGTCAAAAC
TIGR- A005D17 b	79 G C	GGGAAACCC AGCAAG	GAGAGGCCAA GAAGAACTAG AC	TATGGACTGTGTAGAAATATGATTTGGACAAGAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGCAAGGC/TCTGTAGATCTCTTGGCCTCTCTGTGAGGATCTCTCTCTCTGGGCAC GGGTGGGACCCCTCTCTGGAATGGGTATCTTACGACAGTCAAACTCTTACGACAGTCAAAAC
TIGR- A005D44	97 G T	TTAACATTATT GAACCTTAAA CTGTTACAC	TTGCTATTAT TTAAGGCCAAC AAAA	CATCAGTAACATATACACAATTGGTCATCAACTGAACCTTGCCTCCAATATATTTCTATACAATACTT AACATTATTGAACCTTAAACTGTACACTG/TJTTTTTGGCTTTAAATAATAGACAATGATTTTTG TCTATTACTTAGTGATAGACAAGAGTACTTTGTTAGACAAGTGAATCTTTGTTAC
TIGR- A005E31b	27 G A	---	---	GGAGTTCAAATTTATAACCCAGGCCTCTG/AJCTCAGAGCTGACTGGCTAGGCAAAGCTTTCCAGAC ACAAAGCCACCTGCCTGCCATGTGGATAGTACTCTTTGCCCTGCTTGCCCTACAAAGCCACCTCTAT TTCATACCAATACCTTCTATTTCATACCAATAAG
TIGR- A005E39	182 G C	---	---	CTCAGTGTAAAAACTTTGTAGGGAAAAAATAAATCCAATGGATATATGGGAAGAGAAGTG CCAGGCTGGATGGTGTGAGACAGAAATGACCCCTTGGGCTCTCTTTATTTTGTCTTTTCAACAGGACC CCACAGATATTTGCGGTATGTCATGAGGACTGGGGATGCTCTTATG/CJGGATGCTCTCTATTT
TIGR- A005E42a	42 A G	AGTAAGGTTA CTGCACCTTAC AGAG	CCTAAATCAGG GGAAATTGAG	GCTGAGTTTTGTATCTTAGTAAGGTACTGCACCTTACAGAG/GJCTCAATTTCCCTGATTTAGGA AGCGGATGCTAATGGGTATTGCATAGGTGAAGTATAAAATGTTGTATTTAAGAGAATCCCACAAG CTTGGTATAAGGCAGAAAATAAATGGTATAAGGCAGAAAATAAATAG
TIGR- A005E46	76 A G	CACCTGACTCG GTGCTTTAC	CCCTGGCTGTG AGGTAATGT	ATGACAATGATGATAGTATTAGCCCTACCGTTTGTCTAAGCACTACTGCTGATCAGGCACCTGACTCGG TGCTTTAC/GJACATTTACCTCAGCCAGGGTTGGCAATGGTCAATTTTGACAAATGGTCAATTTTG ACAC
U20979	24 C T A	GCAGGGGTGA CGTATGTAGA	GGGAGGAGAC CCTAAGC	AGAGCAGGGGTGACGTATGTAGAA/CJTGCTTAGGGTGTCTCCCCACAGAGAGATACTTGAACCG ACTCAATCTCTGTGTAAAGAGCACTTTGTCTGCTTACAGGACCTCCCCAAAGTGTGAGAGTTCTAT ATAGGATGCTGGATTAGTTCTCTTGATATTGTAAAAATCCCCCAAGAGCCGCATATGAAATCTGCCC

X57830	106	G C	CT	AGTGAACCA ACGATCATAT	CATTGACAGAA TAAATGAGGC A	GTGGCAACTGTGGAAGGCACACTGAGCAAGTTTTCACCTATCTGGAAAAAATAATGAGATTGGA AAAAATTAGACAAGCTAGTGGAAACCAACGATCATATCTG/CJATGCCATATTTATCTGTCAAT GAAAGCGGGTTCAATGCTACAAAATGTGCTTGGAAAATGTTCTGACAGCATTTTCAGCTGTGAG CTTTC
X74070b	72	T G	TGGATC	CTTTTAAAGAA ATTTTGTGTTA	GGGCTTAAAAA TATTAGAGATC TAGATTT	AACCTGAAGAAGTTACTGGGAGCTGCTATTTATATTATGACTGCTTTTAAAGAAATTTTGTATTATG GATC/TGJGATAAAAATCTAGATCTCTAATATTTTAAAGCCCAAGCCCCCTTGGACACTGCAGCTCTTT CAGTTTGTCTTATACACAATTCATTTTGCAGCTAATTAAGCCGAAGAGCCCTGGGAATCAAGTTT GAA
Z48804	44	C T	---	---	---	ACTGCCGAAGTGTAGCGGCCCCCAACCCTTCTCTCATCACCAAG/C/TJTAGAGCTTCTTCCCGAAGGG CCTTTAGGATAGGAGAAAGGTTTCATGCACACACGTTGTGAGAAATGGAAGAGCCCCCTCCAGACCACT CTACAGCTGCTCTAGCCTTAGTTGCCACTAGGAAGTTTCTGAGGCTGGCTGTAAAGTAAGTGAAGG TCCA
D28513b	133	A G	---	---	---	ATGACCAAGCCACCACATTTAGAACCTTTGGCTGCCCTTTGGAAAGTCCAGAGCTGGATCTCTCAGCTCC CGCCCCAGAGGGTCAAGCACCTTTGGACATGGCTCACAAGCAGTTTTTATTGACTGCATGAATGCJAV GJTGCGTGAAGCATGAACCTTGTTTAAATCAAGAGGCTTACATAATTTTAAACAGTTCTGTCTTC AGCTGTACATA
D29833b	85	A G	---	---	---	CCACTCCATCCTGATGCCCAAGTTATCCACAGCCTCCTTCCCGACCAAGACCCCTATCCACCTGGACC TCCATTTTCCCTGTAAJAGJTTCTCCAAGTATCCTACCTCCCTACTCCTGACACCCCAAAATATGAA CAACTGCAGCAGGTGCCACCACCACCAACCAAAAAGACACCCTACCTTGTAACTACTGCTTCTGCTAC
D29833a	21	A G	---	---	---	CCACTCCATCCTGATGCCCAJAGJTTATCCACAGCCTCCTTCCCGACCAAGACCCCTATCCACCTGG ACCTCCATTTTCCCTGTAAATCTCCAAGTATCCTACCTCCCTACTCCTGACCCCAAAATATGAA CAACTGCAGCAGGTGCCACCACCACCAACCAAAAAGACACCCTACCTTGTAACTACTGCTTCTGCTAC
D31762	82	G A	---	---	---	CTCCCTGCCCTCCTCCTCCTGCCCTGTGATGCTCCGCTCAAAACAGCCGAACCTGTCTTGCAATGGGGG GAGGGGGGTTTCTG/CJCTTCTCCTTCTTGGCTTCTCTTATTCTCCACAAACCAATTCCTCAATAAA GCCAAAATCTTTCTCTTCTCCCTCAGGCCACCTCCTGCTCCTCACTGCTGCTGCTGCTGCTGCTTTT CTGGA
D37931	64	T C	---	---	---	ATTATCGCAGTGTGACCTTACACTTACTCCTTAAATAGCAGTGAGTAATGCATTTGAGCTG/T/CJ CCCAGGCTCTGCTCCTCAGCTCATTTCTACTCTTTTCTCTATAAAGTCACTTCTTAAATACAT GCACCAAGAGATATGGAGACATAAACCTGTAAATGAATGAGGCTGGGCTTTTCTGTAAATAGCTTCC TTT

D63807	101 C T	---			CAGCAGGAC TTCAGTGCAGTATCCCTGCCTCAGTCTCTTTAGAAATCACATCTGTGTTCAATCC ATTGTTTAGAGGGAGTGATTTTCCCTGTTCCAC/C/JGAGAGGAGACTTTTGTTCACAAATGGATCAC AATGCAGAGGAGTCTGTTCTCTCCCGCTCGCTCTCGGTGCTGGAGGGTGACCTGTCCAGATGAC
D90145	21 T C	---			TGGGAACATGCGTGTGACCTC/JCJACAGCTACCTCTCTATGAGACTGGTTATTGCCAAACAGCCACA CTGTGGGACTCTCTTAACCTAAATTTAAATTTATATACATACTATTAGTTTTTATAATTTATTTTGAT TTACAGAGTGTTGTGATGTTTGTCTGAGAGTTCCCTGTCCCTCCACCTTCCCTCACAGTGTG TCTGGTG
EST14035	59 T C	---			ATTATCACTCTCAAAAATTTGGTGTGTGTGTTAAGTACTTCTTATTTATGAGCCCC/C/JGAGGA CCAGACATGTTATTATCAAGCCCCCTTATATACCATCTAAT
EST16668	71 C T	---			GCATTTTAAAAATTCACATTGAATCATTATTACTATTATGATGTTTACATAACAATTCAGTATCAT ATG/C/JTGTAGATTTCAGATGTAGGTGCTCAATACTGAGCAGCTTATCT
EST16904	57 C T	---			ACAGACTATCGCCAACCTTATAATGCTTAACTTTATGATCAATAGTAATAAATTACA/C/JGAGATA TTCACACTTTATTATAAATAGGGTTTGTGTAAGATGATTTTCCCAACTGTAGGTTAACAT
EST21863	49 A G	---			TTTTAAGTACCAGAGGCACTGCTGGAACAGGATGAAACTGATACACC/JG/JGTTACTACTTACTC TTCACCTCTCAACCTGATTCCTCTAAAGACTTCTACTTAGCAA
EST21885	80 G A	---			GGCTGTAAGTAGAATCAAGTTAAGAACATTTTATGCCTTATTCACAAACATTTACTGAGCATA CTAGGTGCTGGG/C/JTGTGACAGTGAGCAAAAACACAA
EST22623	26 A G	---			ATTTTAGTGAATGACAAAGCCCCAA/JGJAGAACAGAGGATCAATAAGATTGAAATGTATTACC TTCTCATAGTATACGAAGTTTAAACACAAGTATGGGAGT
EST22644	98 A G	---			AAAATGATTGAATTCAGCAAGTACATTTATGATCTATCTACATTTGTTAAACAGCACTAAAAATAA AAATTTTAAATGATTATCCATTATTACAG/JG/JAAATGTGGAAGATGGCTTTTAAACCC
EST23587	31 T A	---			CCTCATTTATTTAAAAAGACGGACATAAAAA/T/AJATACAAACAAAAAACCCCAAGTCACATTTTCAG GAGTAAAAACTAAAAAGTCTGATATGAAAAATATGGTGG
EST24246	106 T C	---			AAAGATCTGGCATTATTCACATCATCTAAATATTTTGTAAATACITTTTCCATGAGTATTTTTTCA TGTCGAAGCATTTTAACTATCATTTAGCGTAAATACC/C/JGAATAACCCATAGTTACAGAATTGG GTCTGTGAACCTCAAT
EST24308	45 A G	---			TAGTTTAAATTTCTGAACCTTTGGCTTATAAAATTTTCTCAACTT/JG/JCATTTAAAAATGTATCAAT GCACCTTCTTCAGTAGTACCACATGAAATATATAACCTCGTTC
EST24435	73 G A	---			CTTGAACCTTCTGGTCTCAAGTGGTACGTCGCTCAACCTCCCAAAATGATGCGATTACAGGCATAAG CAGCC/G/JTGGCTGACCCACATTTCTTTATCCGATCTGTGATGGACATTCAGGTGTTTC
EST25089	25 T C	---			TATTGTTGCATTATCAAAATGGTTA/C/JAGTTTTCAATTAACACTGTAATTGATTCTATGTATAAA ACAGCTTGAAGTTGTAATGTAGTTTCCAAATCGTTAGTTAATGCTACAT

EST25476 9	33 GA ---				AATGATCTTTATTTTCAGACCTGCTCCTAAA[G/A]CTTTCTCCTCCTCTAAACAAACACA AGAGGTCCTCTTGCTGCCCTTCCATGGACTGGCGGCTGTGGACTTGGACCGTCTGCTGA
EST26183 2	70 T A ---				AGATAATGCATTAGAGCCTGCCCTCATTGTATCTTGATTAACCTTTGTAAAGATTGATCTCTAAATAAG ATT[A]ACATTTCTGGGTACTGGGAGTTAGAACAAC
EST27231 1a	28 T C ---				AGAAAATAAGGTGCTACAGAACTCATGT[C]GATAGCGCTTTCTTTAGGCACATATTATAGCATT CAGATGAAAGTTCTGTAATCACACACACACTGTGCCCTAACACAAACACGGTGACTCTGA
EST27816 5a	26 T C ---				CAACTCAAGGTACAAGACAATTGCATT[C]TAACATTGTTATAATAAAGGAACATCAGATCAAT CATTAAGGGCTCCAGAGTGAACAGCATCTTCATAACTTCCATGTT
EST28588 0	78 A T ---				GTTTAATTGGCGTATGGTTCCACAGGCTGTACAGAAAGCATGATGGCTTCTGGGAGGTCTCAGGAA ACTTACAATCA[A/T]GGTAGAAGGCAAAAGAGAGCAGGCATCTCTCCATGACCACAGCAGGAGG AACAGACAGAGGAGGGGAT
EST30226 5	25 A C ---				TACTCACCCGACATACATATCTCA[A/C]GTAGAATTAGCTATAGCTACTGACATACTTCTATTGTAGT AGGGAATATAAACTACTGAACAAGACAGACTTGTCTAACTTAAACAAGACAGACTCATTTCCCTTTGA G
EST30935 9a	59 C G ---				AGCTATGGTAGAGCAAAATCCAGTGGTGGTAAATCAAGAACTCTAAAGTTTCAGTAGAGA[C/G]AGGT GTTTGAATGTCAAGGAAATCACTGAGGTAGATTGGGATTACAATAAGACAGCTGCCCTGTGAGGT CATAAGAGCTTTGTGAGG
EST32515 7	25 GA ---				CCGAATATAAGGAAAAAATGGTGG[C/G]ATGGCTCTAAACCTGTTGAATAGATAATATGGCCAAAT ATTACAGTTTCTCACCTTCTCTATGAATACTGGCAGCTGTTATTTTCATGTTATGTGAGTTTCTATGC ATAAAAATCCCAGTAAGA
EST33274 4	27 T C ---				TGCTTTGTTTCCCTCCAAATCCTAAAAT[C]GTGTGTCTTCAAAGAAATTCGTGGAAAGGACTTTGAA TACGAGTTTGTAACCATATTCAAGTATTCTTGAATACAGGTTTCAGATAACTATGGAGATGATACCATT GGACTAGGTA
EST33352 7b	75 C G ---				TACACATTATTCAAGAGACCACCTGACATGCATCTCCTCCGCAAGATACATTCCGTCCTCTCTTAGAGA AGTTTAA[C/G]GACACATAGTATTATTTTACTAAGAGAATACTCTTGGTGCATATCTAGGGG
EST33424 1	126 A C ---				ATTTTCCACAGCAGAAGTATATTATTGTGCTGAAATCAGGTAGCAGGGAATGAATAGCTCTTGG GAACCAGTACAGAATGTTTCAAAAAGATTACAAATCTCAGTCATTACACACTGAGCAAC[A/C]AAA CAAAGGTGTGAATCCCTCT
EST33488 7	90 A G ---				CCTTGGGGGAGTTTAAAGCCAGAATGTGACAAAGTCACCTTACAGGAAGACTGGAATGTAGCCATAG TTGAACTCTAACATCGTCTATAG[A/G]JACCATTTCCCGTCTCCAGTTAGGTTCTAGGCATACCTAAGCT GCTC
EST33508 1b	45 C T ---				AAAAACATGCTATTGAAACAACTTTTATAAAGAATAAGTTGA[C/T]TGAAAAGCAGTTTAAAT AACATCAACTCACAATGACTTTTAGAAGCCAAATAA

EST33508 1a	36 A G ---			AAAACATGCTATTTGAACAAACCTTTTTTATAAAGA[A/G]TAAGTTGACTGAAAAAGCAGTTTTAAAT AACATCAACTCACAATGACTTTTAGAAGCCAAATAA
EST33863 4	77 C T ---			ACAACATAGGACTGGTATCTTGTTTTGAAAAATATGTTGCCACTTCCTATTGTTTTAAAAATGA TCATTTAAC[C/T]CTTTGAACACTACAGCCTGAATCCCC
EST34739 3	97 T A ---			GAAGTATCCTCCAGTGGCAGGAACCTGAAGACTCCAGATCAACCAGGTGGACCTTTTCGTTGATGA GCTGATAGCTTCTAGGCTGTGGGAACCTC[T/A]GGTGCCTTACAACCTCCAACACTGCAGAAATTTCT TGTTGTGCCTCATAAACA
EST34792 6b	104 A G ---			ACCTGACTGCTTTAAAGCTCTTTGTAAGCTGACCGTAGCAGACAGATCACGTGGCATCCACTATCAATA CTCATAAGTCTAATTTATCCTCAGGATGTTCCCTGA[A/G]GATTCAGGAATTCCTAGTCCTATTACA AAGATTTGTGCTGTG
EST34835 9b	93 T G ---			GGAAATGTTCCCTTTGCAACAAGGTACGTTTATCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGAGTCTATGTTGTGCTTCTGGT[G/G]GGCCTTAAAGAACAACAGACAAATTTGTGCTAAAGAT
EST34835 9a	82 G A ---			GGAAATGTTCCCTTTGCAACAAGGTACGTTTATCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGAGTCTATGTT[G/A]TGTCTTCTGGTGGCCTTAAAGAACAACAGACAAATTTGTGCTAAAGAT
EST35230 0	93 G T ---			CACAAAGGTCCACTTTACTTACATGAAGGAACATAAAGGCATGAGAAACAGTCATCAATAAATG CAAGACATGAGCATAAAGAGGTTCTC[G/J]GCCCTTCCAGCGTTGTTATTACAGAGAGAAACCT
EST35337 9	33 C T ---			TCTTTTCAAAATTTTGTATGATGAGGCATTTAATG[C/T]TATAAATTTCCCTGCTTAGGAATGTATCTGCT ATATCTCAGAAAGTTGGGCATGTTGTTTCCATTTTAC[TAG]TCAGAACTTTTTCATTTTCATCT
EST35708 9	32 C T ---			CTGCCCCAAATTAACITTTAGGCAATGGAA[C/T]AGACTTACTGTATGGGACATTTTTTAAAAAG ACAGCTTAGTAATATGTTTCATATGCAGCGTGTGCTCCCTCTCTGAGGTGGCACCTTCCCTGTTGTG ATGTGCAAGTGTGGCT
EST35747 9	51 C G ---			ATCCAGTGCAGAGTTGTAGCTGGAGACATATTTCAACCCACAAAGGCTCCA[C/G]ATGTTAAAAAGT TTCCCAACATCAACCTAATACAGTGACAGCAACACCTCCCTCCTGCCCCCTTCCAGTAGGGTTGAGATT G
EST35751 9	89 C A ---			TGGTCCATTATATAAACTGAGGGAAACAACGGTGTGACATGGCAGACATTTATTTCAATGGAGA AGTTCTCTCCCATGAACCAAGA[C/A]CTTGCTCATGATAAAGTGGAGACAATAAGAAAGCCAGGT ATATAATTAAGGCTGTGA
EST36301 4	93 C T ---			CACCTGTTTCATTTGTTCACTGGGCTGCTATCTGTGGGCTGATGCTCTACCAAGTGTACGCTACAGC AGTCAGGAGGAGCCCATGGCCCTG[C/T]GCTGATGGAGCTTGTAATTTAGCCCCAAACTGATCTTCA GAAAGAGGTACAACAAA
EST36519 0a	33 G T ---			GCCATCAGCCCCACAAGACATGACTACCAACG[G/T]GGCCCCCTGCACCCCATACTGGCCTCAGCAC CTAAGACTGGACAACCTTTGTACCTAATGACCGCCCCACCTGGCAATACTGGCTGGCCTCTTCTCTGT CACAGGGTCTTAGTCTG

EST36620 6	50 G A ---	---	---	GAC TTATTAGATAAGGGTTTCGGCTACOCCTCAAAGCTCTCAGGACTGG[G/A]GCTAGGGTTTAAGG AAGGCTTATTTAAATATGGAAATAAAATACAAAAGGGCCACACCCGATGCAAAAGACTTT
EST36690 0a	89 C G ---	---	---	CCTGTGATGTGCATGGTGCCTGAGCAGTCGTACTTACTATCGTCAGACAGCTCACGTATGTCAGGA AAGGAAGTCTGGGATTCTTAC[C/G]AGGGGACATATCACACATATTCTAAGTCACTGTGTGACTCGG CTTGAGCAAGTCATTCA
EST36729 9	62 C T ---	---	---	GAGACAGAAGCCATCAGTTAAATGAGGTAGGCCTCTCCTCCTAATATACTGATTGACAATG[C/T]A TATTAGCCAGTAATGCACITTAGCTACCTGGACAATGCTATCAAGTGTCTGGGAAGGGAG
EST36823 6	103 A T ---	---	---	ACTGTCTGGCCGATGATTGGAGCTTGAAAAAACTACCATGCCAGATCTCCACCCAGACCAATTAG GTCAGTATCTCTGGGGTGCTATTCAAGCAACAATT[A/T]TCTTTTATGTTCTTAAGCTCATCATGAG TTAA
EST36987 4	126 C G ---	---	---	ATGATCGCTTATGTAATTTGAGGGCGACATGGGTAATGGGAGATACCCACAGGACCTGTAAATATT TAAATAATATTAAACAGCTGATCAGAGGCTAAATTACAACCTGACATTTTGTATGCAGTTT[C/G]TTA GGGAATTAAGACAATGCAG
EST37054 3	88 T C ---	---	---	GGTCTACTCTCTTGCCAGGAGCGTTTGAACTCCTGAGCTCAAGTGACCCCTCCACCTTGGCTTCC GAAAGTGCTAGGATTACAGG[T/C]GTGAGCCACCACACCTGGTCTTAAAGTAACCACTGAA C
EST37269 3b	105 T G ---	---	---	AATAGTCTATGGCTACGGGCCGTGGGATGTTAAAAATGGGATTTTAAATTAGATTGTGAACATG CAACCCAGCAAAATTTCTCAGCTTATATTTGAAAGT[C/T]GICAGGAGAAAAATGGGGTCC
EST37284 2	93 G T ---	---	---	AAAAGACCTTTCTCAAGCAGTAACCTTTGAGCAGAGACTCAGATGAAGTAAGGATGAACCCAGGAA GCTCTCTGGATAATGTCACTCTAGGAA[G/T]AGTAAACAGGTGTTAAACCCCTGAGATAGCAACCT CTTGGCTTGCTTGAGGAATA
EST37315 2a	90 A G ---	---	---	AGATGGGGCTTGCTAGCTTGCTCGGGCTGAACATAAGATATCCTCCTGCCTCAGCCTCCCAGGTAGT TGGAACTATAGTAGGAGTATCT[A/G]CCCTGCCCTGCTAGAACTTCAAGTTTGTATGGGCAAAATCCA CCCCAGAGGACAGGACAA
EST37374 1	45 C T ---	---	---	CCTGCCATGATAATGTTAAACATATCAAGATCCTCCTCAAACTT[C/T]AAGGGTGAAAAGCATACC ATTCCATTTTAGTTGAAATATTCCTTCACATAGCCCAACACATTTTTC AAGGCACTCTAGCTACTACA GGA
EST37376 8b	101 G C ---	---	---	GTGACATCATGTCTCTCAATGCCCTTCAATTAAATAGTAGTTGAGCGCTGGGGGCTGAAGTCAGACT CTCTGGGTTCAATCACAGTGTGTGCTGCA[G/C]GCTGTCTCCTCAGGCAAGTTGCTGACTTCTCTG TGTCAGG
EST37376 8a	41 T C ---	---	---	GTGACATCATGTCTCTCAATGCCCTTCAATTAAATAGTAGT[T/C]TGAAGCGCTGGGGGCTGAAGTCAG ACTCTCTGGGTTCAATCACAGTGTGTGCTGAGGCTGTCTCAGGCAAGTTGCTGACTTCTCTGT GTCCAGG

EST37378 9	63 T G ---	---	ACACACAAAAAATGTTGGCAGAAAAATCTGGAAGATTCTAATAACCTCAATTCTGTGAAAAACIT/G JAACATGCCTCAAAAAAGAGGGGAAAAAACITTAACAGAAACACTGTGCTGACATGATTAGCTT
EST37452 4	46 G A ---	---	AAGACATAAATCTGCAATGAATCAGTTATGAATAATTAAACCTCT/GA/JCTTCTCAGGAGTGACAC TAATCATGGTCTGGAAGCTAGCCTATCGCATTTTAAACACCCCTTAATCAATGACGTAGAA
EST37613 6	34 A G ---	---	CTAGGCATGGGGCTTTTACAGTCATTTATTTACC/A/GJGTCATGAATTCATTAAAAACCCACAGCGAT ATAGCAATGAGCAAAACAGACCCCTCCCCAAATACCCCTGCGTTTCATGGATCTTCCATTCTAA
EST38025 4	56 T G ---	---	TTATTGAGTAGCTACACTGTGGCCAGAACTAAGCTTTATACATGTTTTATACACTAT/GJTTATCTCA ACAATCTTGAAGGGTGGTATTATTTCCCGICTTATAGGIGAAGACICTGAGGTTTCAGAA
EST38068 6	57 C T ---	---	TCTACAGGTCACCAAGTATCTGTATATGCTTTAAGTGGCATTTTCATGTCACTT/CJTCGCATGG AAGAACGCTCTCCTTTTAAATCCCTAACCTCTCTCTCTCTGGGAAGACAGAACGTCACAA
EST38420 6a	100 T C ---	---	TAAATCAAGGCCTCTTTTCATTACCAAAACAAACAAAAAGGGAACAAAAATACGATGGGAGAGG GAAGAGATGATGCCGAAGTGTATCCTCGACTGACIT/GJGTCCTGACGTGCCATGGTCCCGTGCCT TATTCATTCTCCTCTCTCA
EST38950 5	25 T C ---	---	TTATTGCAAAAGTAAGCAGCCGGT/CJTGCTCCCTGGATTGAGGCTGAGGAAGACATTACTTCCTG CTGGAATACTTTGGGACTTACATTTGACACAGGCTAAAGTATGGGATGAGAGAGGAACAAAAAGCTT ACAAACAAAGAGCAGCCA
EST39053 6	90 T C ---	---	TTTTTTGTTACTCTGTAGCCAGTCATTAATCTGAAGTTTAAATATATCATATTTATTGGGATGAGATCA TAGCTTTTACACAAATGCTATG/T/CJAAACAAAGTTACTGAATATTTTACCTCTCGTGGAGTTG
EST39331 1	70 G C ---	---	TCCTCTTGTCTCTAGCACTCAGACCACCAAGAAAGCCCTGGAAAGACCAGCCATGGAAGGAAAGTA TGQ/GJGTGTTTTAGGGAGAGCTGGCACCTGGCCTCTAATCTTCCCTCTGCCATTGAACAGATGGGT GCCTTTGGATACATCACT
EST40544 7	31 C A ---	---	GTCACCATGACCTTACATAGTGCCTCTAGT/CJACCTATGAGGCACCTAGAACTCTATTGTACTTCT CACTTTATCACATTAGCTATCGAAGTTTGAAATTT
EST40548 4	37 T C ---	---	TTCTAATAGCATGCCCTGTGACAGGGGAAACTAAGCTC/T/CJTCAAAATAACTGAAACTAAATCTGTA AGATAAAATGCTGGAATTTGAGAAGGCACATGCGCTTTGTAGTTTTCTCCAGAAGGCTCAAGGTGTC AATAATCTGTGGGACTCA
EST40549 1	42 A G ---	---	TGTTTCTCTAGAGAACCCCTGTGTGTATACACTACGTCACAC/A/GJATAAAGTCACATCAAGACTAA TAATCTAAATGTTAGTTTGTGTACCACCATTTCTCACTTTGAACCTAGCTCCCTGCAAAAGCACCTTCTA CCCTGCACITTTGGGGAG
EST40579 1	81 A C ---	---	TGTGAATTACACATCAGTAAGGCAGTTTACAGAATTTTTCATCTCTTACCTAAAGTCTGTGCTATCTG AGCTGGTGGAAA/A/CJGGACTTGGAGACAGCGATTAAATACGGAACAAGGTTCTCCAGGAAG
EST40584 3	68 A G ---	---	TTGTATGGTTGTAGGAATTTGGGAAGAAATTATCTGTGAAGGAAATTTGCCACTGTAAATGCACACCC A/A/GJCTGTACTCCCAATATCCTATGTTTTAAGCT

-228-

EST51340	51 G A ---				GATCAAACTGTATTGCCAGGCCAGCTCCTGAAGAACTGTGAACATATGAAC[G/A]TCTCAGCCTAGA AGGATAATGTGACCTTCAATTTGCACACCATCCATTGCTCTTTCAAACCTAAGAGCCTCTCTAAGCTA GATAGGCCAAGGATTATT
J04162	134 T C ---				CATGGGAGTATAAGAGCAGTGGCAGCAGCATCTCTGAACATTTCTCTGGATTTGCAACCCCATCAT CCTCAGGCCTCTCTACAAAGCAGCAGGAAACATAGAACTCAGAGCCAGATCCCTTTATCCAACCTCTGGA T/CJTTCCTTGGTCTCCAGTGGAAAGGAAAAGCCCATGATCTTCAAGCAGGGAAGCCCAAGTGAGT AGCTG
K01506	63 T C ---				CTGAACTCCAGCTGCCCTACAAACTCCATCTCAGCTTTCTCTCACTTCATGTGAAACTAC[T/C]C CAGTGGCTGACTGAATTGCTGACCCCTTCAAGCTCTGTCTTATCCATTACCTCAAAGCAGTCAATCCT TAGTAAAGTTTCCAACAATAAGAAATTAATGACACTTTGGTAGCACTAATATGGAGATTATCCTTTC ATTGAGCCCTTTATCCT
L18877	69 T C ---				TGAGCTGAGCAGAGTTGCAGCCAGGGCCAGTGGGAGGGAGTCTGGCCAGTGCACCTTCCAAGGCC C[T/C]ATCCATTAGTTCCACTGCTCGTGACATGAGGCCCATTTCTCACTCTTTGAAGAGAGCAG TCAGTATTGTAGTAGTGGTTCGTCTATTGGATGACTTTGAGATTATCTTTGTTCCCTGTTGGA ATTGTTCAAATGTT
L31848	36 T C ---				GCTATTTTACATATCCAAAGCCCTTTAGGGTACAGT[C/T]CTCTTGCTGACCCCTGTAGGGTGCCA TTTGGAGTTACAGCCTAGAAAGAAAGGCTTTGGGCTGGTGGTGGCATAGGCTGTAAATCGT AGCGCTTTGAGAGGCTGAGGCGAGGAAGATAGCTTGAGCTCAGGAAGTTTCGAGACAAACCTGGGCAAT GT
L38517	137 G C ---				GGGTCCAGAAAGCCTCTCAGCCAGGAGGGAGCTGGCCCTGGAAGGGACCTGAGCTGGGGGACACTGGC TCCTGCCATCTCTCTGCCATGAAGATACACCATTGAGACTTGAGCTGGGCAACACCCAGCGTCCCGAC CC[G/C]CGTGGTGTAGTATAGAGCTGCAAGCTGAGCTGGCGAGGGGATGGTTGTTGACCCCTCT CTCCTAGAGACCTTGAG
L39059	123 T G ---				ACTTGAGAAAGCAGAGCTGCCACCTTCTGGAGGCCACTGTGATGATGAGCCAAGCAATTTGGAGCCA AGTTGAAGGGACAGGGCAACAAAATACAGTAGTATTTCTTTGTATTTTGTATAT[T/G]CGCCTGA AGATCATCCCGCAAGCAGGCTGGAGGTGCCGGTGGGCTGTGTTGCTGGGATTTTAGTCTGTGCTGG GAG
L41268d	173 G A ---				CAAAGTTGTCTCTCTGCCCATGAGCACCACAGTCAGGCCCTTGAAGGGATCTTCTAGGGAGACAACAGC CCTGTCTCAAAACTGGTGGTCCAGCTCCAATGTACCAGCAGCTGGAATCTGAAGGCGTGAGTCTGCAT CTTAGGGCATCGCTCTTCTCACCACCAAAATCTGAAC[G/A]JGCCTCTCCCTTGCCTTACAAATGTCT AAGGT

L48728b	111 T C ---	---	---	AAGTGAACAGAGAAAGATGGATTGTTCCCTATAAAGCACATAGTATGTTTACTGGTATCGT AAGAAGCTGGAAGAGAGCTCAAGTTTTGGTTTACITTCAGAAAT/CJGAAGAACCTTATTCAGAAAG CAGAAATAATCAATGAGCGATTTTAGCCCAATGCTCCAAAAACTCATCCTGTACCTTGGAGATCCA GTC
M18079	52 G A ---	---	---	GCGCACAGTCCAAAAATACAAATTGGACAGAAGATCTATATTGTACCAGAACTG/AJTTTATTTACCC CCATCAAGTATAAGGTTACTGATTGATTGGTCCCTTTTATAAACATTGGTATATTCCATTCATGCCAA AGCAAAAGAAGTAAAGCTAA
M19169	113 T C ---	---	---	TAGGATCTGTGCCAGGCCATTGCGACCCAGCCACCCACTCCACCCCTGTAGTGTCCACCC TGGACTGGTGGCCCCACCCCTGGGGAGGCCCTCCCATGTGCTGT/CJGCCAAGAGACAGACAGAG AAGCTGCAGGAGTCCCTTTGTTGCTCAGCAGGGGGCTCGGCCCTCCCTCTCTCTCTCTCTAATA GC
M21539	114 T G ---	---	---	TCACCTCGTTCCACAGCTCCACCTGCATCTTCTCATCAAGCCATCCAGGGATACACAGGGAGCTTCT TTCCCCCTTAGCCCTGTGATCTGCCCATGATGATCCCGACAGCAAAAT/GJTTTCTCTTCTGAGGCTG CCATGCTGCCACTGTCCAGGTGGAGACTGAGCAAGGAAGTCTCAGCTGTACCGGCCCTTTCAGAGCT TCTCTTTGGGTGC
M26041c	173 A G ---	---	---	CCTAGCATTTATTTCTGGCCCATTTATCATATCCCTTTTCTCCTCCAAATGTTTCTCCTCCTCCTCT TCTGTGGGACTTAAATGCTATATCTGCTCAGAGCTCAAAATGCCCTTTGAATTTTCCCTGACTTC CTGATTTTTTCTTCTCAAGTGTACCTACTAAAGJGATGCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041b	157 A G ---	---	---	CCTAGCATTTATTTCTGGCCCATTTATCATATCCCTTTTCTCCTCCAAATGTTTCTCCTCCTCCTCT TCTGTGGGACTTAAATGCTATATCTGCTCAGAGCTCAAAATGCCCTTTGAATTTTCCCTGACTTC CTGATTTTCTTCTTCTCAJGJGTTTACCTACTAAGAGATGCCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041a	45 C G ---	---	---	CCTAGCATTTATTTCTGGCCCATTTATCATATCCCTTTTCTCCTCCAAATGTTTCTCCTCCTCACC TCTCTGTGGGACTTAAATGCTATATCTGCTCAGAGCTCAAAATGCCCTTTGAATTTTCCCTGAC TTCCGATTTTCTTCTTCTCAAGTGTACCTACTAAGAGATGCCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M63967	57 G C ---	---	---	TAAGGCAGCTGTACGGAGGCCAGTCCAGTCCAGCAATTCACAAACCCTTGACJGJJAATGCT TGCCAAAGCTGTTTAAAGCCAAAGAACACCCCTTCTTTGTTCCAAATTAACCTCTTAGAAGAAACCCCA CAATAAAGCAATTCATC
M81695	34 G A ---	---	---	ACTTACTTACCTCACCTGTACGGGTGACGGGGAJGJGAACCACTGCACCACCGAGAGAGGCTGGG ATGGCCTGCTTCTGCTTTGGGAGAAACGCTTGTCTGGGAGGGGCCCTTGTCTGTCAAGGTTG CAACTGGAAACCCCTTAGGACAGGGTCCCTGCTGTGTTCCTCCCAAAAGGACTTGACTTGCAATTTCTACC T

U06641d	166	CT	---			CTCCTCCTTTATTTCAGCATGGAGGGTTAAATGGAGGATCTCCTTTCTGTGACAAACATCTTTC ACAACTTACCTTGTTAAGACAATTTAAAAAGATCTTTTACAACTTACCTTGTTAAGACAAAAT TATTTCCAGGCTATTTAATACGTACTTTAG[C/T]TGGAATTATTCTATGTCAATGATTTTAAAGCTA TGAATAACAATGGGGGA
U09607	39	TC	---			GAGGCCTTATGAGGGTCTCTACTTCAGGAACACCCCCA[T/C]GACATTGCATTTGGGGGGCTCCCG TGCCCTGTAGAAATAGCCTGTGGCCTTTGCAATTTGTTAAGGTTCAAGACAGATGGGCATATGTGTGAG TGGGGCTCTCTGAGTCTGGCCCAAGAAAGCAAGGAACCAAAATTTAAGACTCTCGCATCTTCCCAAC CCCTTA
U09608	82	TC	---			GAGCAGAAGGCAAGAGCGGCAAGATGAGTTTGAGCGTTGTATCCAAAGGCTCATCTGGAGCCTC GGGAAGTCTGGTCQ[T/C]ACATCTGCCGCCCTTCCAGCCCTTCCCGAGCCCTCCTCTTGTCTTC ATTCATTCAACAAAATTTGGC
U10694	20	CG	---			GTGACATGAGGCCCATCTT[C/G]GCTCTGTGTTTGAAGAGAGCAATCAGTGTCTCAGTGGCAGTGG GTGGAAGTGAGCACACTGTATGTCATCTCTGGGTTCCCTGTCTATTTGGGTGATTTGGAGATTTATCCTT GCTCCCTTTTGGAAATTTGTTCAAAATGTTCTTTTAAATGGTCAGTTTAAATGAACCTTCCACATCGAAGTTAA TGAATGACAGTA
U13877b	162	TC	---			AAAAGGACTCTGGTTCAATCCAGGTTCCATTTGCTATCTTTGTGACCTTGCACAAGTTGTTTAAAC CTCTTTGTTCCAGAAATTTCTCCATGGAGTAACAATATCTAGGTGGGAGGATTAGTGAAGTTACATGT AAAGCACAGAGGAAACAGCCAAAGAGAT[T/C]TTACCGTGGTCTTACTAAAGTACATATCCTAACTTGG GGTTACCTTCAGCA
U15555	187	TC	---			TTTCTGTCCACTTTCACCTGGTTTTAATAGCCAGCCAGTCATATAATAGTAGGGAATCAGTCAAGCAA AAATGCTTTGGAAGAAATTAATAAGCAATGCTGAACATCAGGAATTTAGATATCCGTACAGAGAGT TCCAGTAAATTTTATGAGTCCACGACCCCTTTTCTAAGCAGTCTGGTCCATG[T/C]TGGTCTCATAC CTCATATGCAGGATTCATTCA
U17077	122	TC	---			TCCAATTATTGGTCCCCAAAGCAGCTTCCAACGTTTGCCATCTGGATGACAAACGGAAGATCCACT AAAAAGTCCACGGGATTACAGAAACGTCCTTGACAGCTGAGCGATGACACACACAT[C/T]TGTGTTGG ACATTTAAATTCACCTCTGCTGAATAGGAGGAAGCTTTCTTTTCCCTGGGAAAACAACACTGTCTCTTGG AATTA
U18543	58	TC	---			GCACATGCAGAAATAGACTCAGCCTATGTCTCTGATTCCAGCTGGGTAGTCTAGAATTT[C/J]AGAAG CTCCATCTTTTAAATGTTTTTATTGTTATGTCCCTCCCGCTCCACCTAAATTTAGAGCTTTAAA AGATGCACTGCCCAATAGGACACACGATGGTGTAGCTGAAGTTTGATTAGCAATTAGGCACCTTCC AAGGCTTTAGTAGAGAGGCC

U25975b	164	C A ---	---	TCAC TGTGTGGCCTCATACTCTTTTCCATTTTCTACAAGAAGCCTTTGTATATGAAAAATTATT ACTCTTTTGGGTTTAAAGAAATGGTCTGCATAACCTGAATGAAAGCAATGACTATTCTCTG AAGACAACCAAGAGAAAATTGCAAAAAGAG[C/A]AAGTATGACTTTTATATGAACCCCTTCTTTAGG GTCCAGAAGGAATTGTGGACTGA
U25975a	143	C G ---	---	TCAC TGTGTGGCCTCATACTCTTTTCCATTTTCTACAAGAAGCCTTTGTATATGAAAAATTATT ACTCTTTTGGGTTTAAAGAAATGGTCTGCATAACCTGAATGAAAGCAATGACTATTCTCTG AAGACAAC[C/G]AAGAGAAAATTGCAAAAAGACAAGTATGACTTTTATATGAACCCCTTCTTTAGG GTCCAGAAGGAATTGTGGACTGA
U25997	61	A G ---	---	CAGGAGAGGTTATTCAACACCTCACCAACTAGTATCATTTTAGGGGTGTGACACACCA[A/G]TT TTGAGTGTACTGTGCCTGGTTGATTTTAAAGTAGTTCCTATTTCTATCGCCCTTAAAGAAAATT GCATGAACTAGGCTTCTGTATCAATATCCCAACATCTGCAATGGCAGCATTCGCCACCAACAAAA TCC
U28413	29	C T ---	---	ATTCTGACAGCTAAATTAGCCCTAAATG[C/T]GGGTAATATTTTCTCATGTTTAAATGAGGTT AATATTGTCATAAAATCCTAAACAGACTTCTGTATAGTTTATTTAGTCAAAATGTGTTCTTGATCC CAGATGTTGTGGCCTGGGAAGCCCTCATTGCTACAGTACAAGTAACACAAAGTCGTTGTACCTCAGTT G
U30884c	89	A G ---	---	TAGGGGTAGCATTAAAGATTCAGGAGTCATTAGCAGTGATGATTTTGGGACCTGCCGTATAATCTGT CTTCTATTTCCACGTTAGCCA[A/G]TTGTTCTTGATGAATCTATATAGTCAATAGACACAAATCTAT TGACGGAAGTCATTAGAATGGCTTGTGATACTGATGGCTTGAACCTGCCCCACAGTTGAACACAAGT GCTGTCA
U30884a	34	A G ---	---	TAGGGGTAGCATTAAAGATTCAGGAGTCATTAGC[A/G]GTGATGATTTTGGGACCTGCCGTATAATCT GTTCTTCTATTTCCACGTTAGCCAATTGTTCTTGATGAATCTATATAGTCAATAGACACAAATCTAT TGACGGAAGTCATTAGAATGGCTTGTGATACTGATGGCTTGAACCTGCCCCACAGTTGAACACAAGT GCTGTCA
U31216b	78	A G ---	---	GGGACAGCATATGTGGCACCGCCTCTCTGTGCACGTGAAGACCAATGAGACGGCCTGCAACCAACA GCCGTCA[CA/A/G]CCCCCTCACTAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA CCAGCACCAAGACCCCTTACACGTAGAGGAGGAGGATGCCACGCCGATTCCGCTTAGCCCGCC TGGTAGCCCTTCCAT
U31216a	70	G A ---	---	GGGACAGCATATGTGGCACCGCCTCTCTGTGCACGTGAAGACCAATGAGACGGCCTGCAACCAACA GCC[G/A]TCATCAAAACCCCTCACTAAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA CCAGCACCAAGACCCCTTACACGTAGAGGAGGAGGATGCCACGCCGATTCCGCTTAGCCCGCC TGGTAGCCCTTCCAT

U31416c	76 G A ...				AGTTGCCAGCTCCCATGTACACAGCAGCTGGAATCTGAAGCGTGAGTCTTCATCTTAGGGCATCGCTC CTCCTCAC[G/A]CCACAAATCTGGTGCCTCTCTTGTCTTACAAATGCTAGGTCCCACTGCCTGCT GGAAGAAACACACACTCCCTTTGCTTAGCCCCACAGTTCTCCATTTCACTTGACCCCTGCCACCTCTCC AACCTAACTGGCTTACTTCCT
U31416b	68 C T ...				AGTTGCCAGCTCCCATGTACACAGCAGCTGGAATCTGAAGCGTGAGTCTTCATCTTAGGGCATCGCTC [C/T]TCTCACGCCACAAATCTGGTGCCTCTCTTGTCTTACAAATGCTAGGTCCCACTGCCTGCTG GAAAGAAACACACACTCCCTTTGCTTAGCCCCACAGTTCTCCATTTCACTTGACCCCTGCCACCTCTCCA ACCTAACTGGCTTACTTCCT
U37519a	78 C T ...				ACGGGTCACACAGAGAAACCTGAGTCTAGCCATGAGGGCTTATGCTCCCACTCACATTGTTCTCC AGACCGCAGG[C/T]TCCCCCAGCCTCAGGTTGCTGGAGCTGTACATGACTGCATCCTGCCTGCCAGG GCTGCAAGCAAGGCTTGTCTTCTATCTGCGGACGCTGCTCGAGAGAGGCCGAGAGGCCGAGAAC ATGCCAGGTGTCC
U37690	54 A G ...				GACCACGCTGAACCCACCCACCCGCTGTGCTGACCATGGGCCCTGAGCGTCTT[G/C]CCCCGAATTC ACGAGGCTGAGGCATCCGGGAGCTGGCGTAATGCCCTGGCCGAGTGTGTATCCCATACCCCACT CTGGAAGGAACCATCCAGTAAAGGCTTT
V00540	39 T C ...				TGAACCGTTTCAACATGGAATGATCTGTATTGACTAA[T/C]ACACCAGTCCACACTCTATGACT TCTGCCATTTCAAAGACTCATTTCTCTCTATACCCACCGATGAGTTGAATCAAAATTTTCAGATCTTT TCAGGAGTGTAAAGGAACATCATGTTTACCTGTGCAGGCACTAGTCTTTACAGATGACCATGCTGAT A
X15943	106 A T ...				TCAAGAAGGTGACTGCCCTTGTATGATGGATGGGAAGATGAATGACTGGTTTTACTGGGGTGTA AACCACTCTGAGCCTCTCTGAGACCCTGTTGTTTAAA[A/T]ATCCATAAGGGAAGGTACCCACAC CAGTATCTGAGTCCAGTAGCTAAGACCCCTAGAATTTGGATTCTCTGTTTTTTCATGCTCTCCTT GTAACCCCTGAGATCATCAG
X52011b	148 C T ...				AGGAAGATCCACCGACCCCTCTGGCCTAATCCTTTAGATTAGGTCACATTACATTAACTTAGGA ACCCAGACCCGAAAAGTTGCTGAAGGGAAGGAGACACATTACAAAGAAAGTTGGGAAAATTGCG AAATCTGTTGTGCA[C/T]GCTCAAATGAAACGCCCTTCGGCTTTATTTTTTTTGGAACTG CGAGTGGCTTAGGCTAGCCT
X52011a	118 A/C ...				AGGAAGATCCACCGACCCCTCTGGCCTAATCCTTTAGATTAGGTCACATTACATTAACTTAGGA ACCCAGACCCGAAAAGTTGCTGAAGGGAAGGAGACACATTACAAAGAA[A/C]GTTGCGAAAATT GCGAAATCTGTTGTGCACGCTCAAATGAAACGCCCTTCGGCTTTATTTTTTTTGGAACTG CGAGTGGCTTAGGCTAGCCT

X54741	24 A G ---	---	CAGGCCACCTGCTTCTCTCCAC/GJTGACAGCTTCTGAGTACCCCTCTGTCCAGCCAGCTCCT GCACAAATGGAACTCCCCAGGGCTCCAGGACTGGGGCTTGCCAGGCTTGTCAAATAGCAAGGCCAG GGCACAGCTGGAGACGATCTTGTGGCAGGGCTGGCCCTGTGCCAGCCACCTGGCCCTTCTCC
X54869	99 A G ---	---	AGCAAGCAGTGC AAGCATTTGCGTTTACAGTGCATCAGATACATTTATATTTCTTAAATAGAAATATTATGATGCAT AAATCTGAAATGAATATGTTATTTGCTCT/GJATACAAAAATTCATAATCAATATTGAAATAG GATGCACACAATTACTAAGTACAGACATCTAGCAATTTGTGCGGCTCATTTTGTCAACATGGTA
X66924	147 G A ---	---	GCCGTGCTGACACCTCCAGAACGAGTGTGGGCGGCTTCTGGTGGGACCCGGGAACCTCTC CTGCCGGAAGCCGAGCGGAGTGGGCCCCAACTTGGCCCTGCCACTTGACTTCAGCAATCCCT TCCTGGAGACT/GJAACTTGGTCTCAGGAGCGAAGGACTGTGAACCTTGTGGCTGAAGAGCCAGA
X78932	62 T G ---	---	GAAATGTGAAGAAATGTGACAAAGCCTTTAAAGCGTTGTACACATTGATTGTATATAAGATAAT/GJT CATACTGGAGAAAACTCCAGAAAGTGTGACAAATGTGACAAAAACATTTAATTAATTCATACCTTA TTGCACAGGAAAGCATTTATATCTGAGAAAAATTTGTATAAGAAATGGAAGTGCATTAAATATCTGCT CATATCTTAACATCAGCGAGTT
X80026	25 T C ---	---	CTAACCCATAACTCAACACATCT/GJATCTCCACCCACATCCACACACATCCACCTCCATCC CCAACCCATCTCATCCCCAACTAGAGCCCCAAACCCAGCCCCAGACTAATCCACAGCCATCCCCAA CTCATCTCATCCCCAACTGCAGCCCCAAACCCAGCCAGGGCCATCCCCAAACCCATCCCCAAGCC AACTCAACACCATCC
X80197b	99 G C ---	---	ACCCAACTCAAGTCCAGGCCCCAGGCATCTTCTGCCCTGCCCTTGTGGCCCATCCAGTCCAGG CGCCTGGAGCAAGTGCTCAGCTACTTCTCTCTG/CJACATTTGAAAGACCCCTCCACTCTGGCCTCA CATTTCTGTGTGATCCCCCACTTCTGGGCTCTGCCACCCACAGTGGGAAAGGCCACCTAGAAAG
X80197a	28 A G ---	---	ACCCAACTCAAGTCCAGGCCCCAGGC/GJCTTCTCTGCCCTGCCCTTGTGGCCCATCCAGTCC AGGCGCTGGAGCAAGTGCTCAGCTACTTCTCTGCACTTTGAAAGACCCCTCCACTCTGGCCTCA CATTTCTGTGTGATCCCCCACTTCTGGGCTCTGCCACCCACAGTGGGAAAGGCCACCTAGAAAG
X85106	150 G A ---	---	GGCACCCAGAGTGACCAAGTCCAGAGGGAGCGCGCCGCTCGCCGTGTCCGTGTTTTCTTTTT CAGCCCGGAGAGTGCTGACCTGGGGCTTCTCCAGGCTCACTGGCCACGCTCCCGCCGCTCT CTTTTCTCCCAAGC/GJAAACCAATGCGCCCTTCACTCGCTGCCGTGCCGAGGCGGGGGCTT CTTTCAGAGC
X87160	128 T G ---	---	ACCACCCAGCATGGTCTAAGGACATGGATCGGGTGGCCCGACAGCGTGTGCACAGGGGACCTCTGCCC CACTCTGGGCTTTTCAGATACTCTGACCAAAAAGCCTGCTTTAAACCCGCAAGATGGGGCT/GJGGG ATGCGCAGGAGGAGCCATCGGGTACTACGCAGCAACACTCACAACCTGTCCAGGCTGAGATAAATCCC GGGA

[illegible]

1282	130	C T ---	---	---	GTGCGATCACCACACAGTCTAAATTCAGATGTTTTCATACCCCTAAAAGAAATCTTGTACCCATTAGCAATTTCTCTCATTCCCTCAGCCACCCAGGCCCTACTCTTTATCGCTATAGATTTGCCIC/TJACTTGACATATACATACACATGGAGCCATACATATGTGTGCCCTTCATGATTGGCTTCTTTCACACTGAGAATAATGTTTTCAAGGT
6810	68	C T ---	---	---	AGTATCACACATCTTAATATATTAGATATACACAATAATAAATCACTCCCTACCTTGAACACCTTTA/C/TJAGAAGCATTTTTTAATTTACAACACAAGCTCAACGAACCTACAATAAGTCTAGTAGTCTGTTTACGTGCCAAGGGATAAGGCTGAACAATAAATTAAACCTTTAAACCTATGCTATGAACAAGTACAAATTTCTTTTTGAGTTCTGCAGAGCAATGACCACIAAGAAATATTTTTAAAGGC
6817	118	A C ---	---	---	CCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTATTTTGTATTCAGTTAAGACCACTCAGCATATACAACATCATCACTAACTCAACAATGATAGCTGAGGGTAAC/C/TJGTGGATACCCCTGTGTCTCTACTGGCCTCCAAAGGCATTGAGGGGATCATCAAGATGTTGGACACCTTGTGTCAAATCTTGGTTCAGGTGCGGCCCTGTGCAGATCGGCTTTTGGTTGGTCTTAG
6819b	212	C ---	---	---	CCATTTTATTTTCTCTAAATTTAAATAGAAAGACTTTAATGGAAAACATTTAGTACCATCATGTCAACCTGAATGCCAGCAATACCTCGACTTTTACACACGAGGAGCCTAGTAAAGCCCGTCAGTAGTACACATTTCTCTATGGTCTTCAACAGTTTTGCATATACAAAATTTTCTGCTATTTTGTCTTAGCAAAAGCAATAACTTTTGTCTTCTATATGACACCTAATATCCA
6819a	166	G T ---	---	---	CCATTTTATTTTCTCTAAATTTAAATAGAAAGACTTTAATGGAAAACATTTAGTACCATCATGTCAACCTGAATGCCAGCAATACCTCGACTTTTACACACGAGGAGCCTAGTAAAGCCCGTCAGTAGTACACATTTCTCTATGGTCTTCAACAGTTTTTGTGCATATACAAAATTTTCTGCTATTTTGTCTTAGCAACAGCAATAACTTTTGTCTTCTATATGACACCTAATATCCA
681xx	39	A G ---	---	---	CTGGTATGTCATAAGCAATCCATAATTGTTATAGCTATTIAGTATACTATGGCACCATTTGGGACACAGATTATATGTCAGACACCCAGCAATGTCTTAAAGATATGCAGCAAGCACAAATCTGTCATGGTTAACAAAAGAAATGAACGTCTAGG
6972b	149	G T ---	---	---	AGGATCCCTCTTTTCTATTGATTGGAATAGTTTCAGAAAGGAATGGTACCAGTTCCCTCTGTACCTCTGGTAGAATTCGGCTGTGAATCCATCTGGCTGGACTCTTTTGGTTGGTAACTATTGATTATTGCCACAAATTCAGAGCCTGTTATTGGTCTATTACAGAGATTCAACTTCTCCCTGGTTTAGTCTTGGGAAGTGTATGTCGAGGAAT
6972a	122	A G ---	---	---	AGGATCCCTCTTTTCTATTGATTGGAATAGTTTCAGAAAGGAATGGTACCAGTTCCCTCTGTACCTCTGGTAGAATTCGGCTGTGAATCCATCTGGCTGGACTCTTTTGGTTGGTAAAGTAA/GTCTATTGATTATTGCCACAAATTCAGAGCCTGTTATTGGTCTATTACAGAGATTCAACTTCTCCCTGGTTTAGTCTTGGGAAGTGTATGTCGAGGAAT

7598k	210 A C ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCCAGATTTACCTTGAGAAATGAAAATTATTTCTTGAGGATGCCTTTTA ATATTTGATCCCAATTATGTGAGAGATTTCCCTGATATGTTATCTTATTATATTTTCCCGTATTTTCCCT CAATGCAG[A/C]
7598j	208 A T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCCAGATTTACCTTGAGAAATGAAAATTATTTCTTGAGGATGCCTTTTA ATATTTGATCCCAATTATGTGAGAGATTTCCCTGATATGTTATCTTATTATATTTTCCCGTATTTTCCCT CAATGC[A/T]GA
7598i	192 G T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCCAGATTTACCTTGAGAAATGAAAATTATTTCTTGAGGATGCCTTTTA ATATTTGATCCCAATTATGTGAGAGATTTCCCTGATATGTTATCTTATTATATTTTCCCGTATTTTCCCT CCTCAATGCAGA
7598h	144 C T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCCAGATTTACCTTGAGAAATGAAAATTATTTCTTGAGGATGCCTTTTA ATATTTGATCC[C/T]ATTATGTGAGAGATTTCCCTGATATGTTATCTTATTATATTTTCCCGTATTTT CCTCAATGCAGA
7598g	142 C T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCCAGATTTACCTTGAGAAATGAAAATTATTTCTTGAGGATGCCTTTTA ATATTTGAT[C/T]CCATTATGTGAGAGATTTCCCTGATATGTTATCTTATTATATTTTCCCGTATTTT CCTCAATGCAGA
7598f	120 A G ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCCAGATTTACCTTGAGAAATGAAAATTATTTCTTG[A/G]GGATGCCTT TTAATATTTGATCCCAATTATGTGAGAGATTTCCCTGATATGTTATCTTATTATATTTTCCCGTATTTT CCTCAATGCAGA
7598e	83 C T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAA[C/T]CAGATTTTACCTTGAGAAATGAAAATTATTTCTTGAGGATGCCTT TTAATATTTGATCCCAATTATGTGAGAGATTTCCCTGATATGTTATCTTATTATATTTTCCCGTATTTT CCTCAATGCAGA
7598d	77 C T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAA[C/T]GCTAACCCAGATTTACCTTGAGAAATGAAAATTATTTCTTGAGGATGCCTT TTAATATTTGATCCCAATTATGTGAGAGATTTCCCTGATATGTTATCTTATTATATTTTCCCGTATTTT CCTCAATGCAGA

7598c	56 A G ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCCAAGCCA/GJAGGAAC TCAATGAATTAAGCCGCTAACCGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTT TTAATATTTGATCCCATATGAGAGATTTTCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598b	47 C G ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACA/CJG]CCAAAGCCAAAGGAAC TCAATGAATTAAGCCGCTAACCGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTT TTAATATTTGATCCCATATGAGAGATTTTCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598a	30 A G ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCCAAGCCAAAGGAAC TCAATGAATTAAGCCGCTAACCGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTT TTAATATTTGATCCCATATGAGAGATTTTCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7998c	116 A T ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCTTATTCAGACATCTGCCAGCTCTCTGTGTA ATACTTTATGAATGGGTAGTCTATCTTCTCAAGGTCCTCCCAAAATAT/TTCTTGAGGTTCTCT
7998b	94 A C ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCTTATTCAGACATCTGCCAGCTCTCTGTGTA ATACTTTATGAATGGGTAGTCTATCTTCTCAAGGTCCTCCCAAAATACCTTGAGGTTCTCT
7998a	75 A T ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCTTATTCAGACATCTGCCAGCTCTCTGTGTA ATACTTTATGAATGGGTAGTCTATCTTCTCAAGGTCCTCCCAAAATACCTTGAGGTTCTCT
8071	119 A G ---	---	AAATACAGAATTTTATTAAGAACTGTTTAAAGTAGAAAAAACCCCTGTCAAGAAAGACCCAGGTGG AAAAATGGTTCCTCAATAAAATGGAATTTAGGGCAACAAAAGCTAAAAGGCC/JG]CAAAAAGAGA AATAGCACCACTGTCAATTTGAACAATGGCTAGTTACTTGCAATTTTGGCAATTTGTTAATCACTGAATC TGGGTTTCTCTGAATTCACACAGAGCATGCACATACACAATTTTATCAT
8467b	93 C T ---	---	AAGGCTTTCCTCTAAACATCAGTCTACGGAGAAACTGGGAAATCCTGGATATTTGGCTTATCACTT TGACGCAAAATCCACTTTGCTGTAA/CJTG]GTCATCCGAACTCCCTTCAGAGAGCAAGCAAGCAAAA TTAAGTGTGATCTGGAGCTTATGCATGCAAAAGCTTGCAAAAAGTATTAAAGGAAAAATTACTG
8467a	70 A G ---	---	AAGGCTTTCCTCTAAACATCAGTCTACGGAGAAACTGGGAAATCCTGGATATTTGGCTTATCACTT TG/JG]CGCAAAATCCACTTTGCTGTAAACGGTCAATCCGAACTCCCTTCAGAGAGCAAGCAAGCAAAA TTAAGTGTGATCTGGAGCTTATGCATGCAAAAGCTTGCAAAAAGTATTAAAGGAAAAATTACTG
8498	84 C T ---	---	AGGTTTCAGGGTTTGGTTTAAATCAGGCTGCACACCTTTCAAAATCAATCTGACATCTCTATGTCA AACTGGCTTCAGCTAG/CJ]TAACTCTTCAATTAATCGAAAAGAAAAATTGCTTTAAGGAAAAAA AATCCAGTTTAAAGAACAAATTAACATTAGTCTTTAAATAAAGGAGGGCTAATGTTTCATGTTGCT TTATACATCTCTCTCTCAATACAGAACCCAGGAATGTAATTTTCTTAACCTCAG

WI-18562	29	G A ---			CTAAGGAAAAATTTAATGATGGAATATC[G/A]JACAAATATTCAACATCATTTAAAAACAAGTAG CTTCTCTATTTCACATAGCTTAGTTGGGATAGAAATAGAACTAATGTTTACAATGATCTTACATT TAGCATTAAATCAGAAACGA
WI-18618	51	A C ---			ATAGCAGACTTTTAAATCAATGCCAGAGACAAAGTGAGGCCGAGCTAAGAAC[A/C]JGCTCAGCTTCG TTACAATGAAGAAATGGTTTCCTTCGATGCAAGATAATTGTAAACCACAGTGTCTCGCACAGTTC AC
WI-18683	22	C T ---			TAAGCTGTTCAAGGACTGGACTC[G/T]GGTCCCTTTATTGAGACTGACAGGCCAGTGGGTCCACCCAAA CAAAATAAATTTCTCTCCCAAGCCTGCCTGCAGT
WI-18520	75	G A ---			GACTTTGGTGATTTAATTGCTTTTCCCTTAAATATAGAAATAGGTGTAATTTCTCCTTTTGTCTTTT ACTACA[G/A]CCGGAGTGGTAAATACTACTACTGCAACAAACACGGGATCCACTCTGCTTCAA TGCTCTTCCGTGAGAC
WI-18563	94	A G ---			AAATAAAGTTTTATTGGCACACAGCCAAAGCCACTGGATGACACATTTGCCACGGCTCATCTTGCAA TACAATAGCAGGGTTCACTAATGTGAC[A/G]GACATGGTGGCTCACAAAGCCAAAGATATT
WI-18582b	69	T A ---			GTCCTATTTCAATTTAGCTAGACCCATTTCATCTCTGTTTAATGGCTACATTTGTTTTCATTGTGAGAC [T/A]GTGCCATAATTTAATCAGTGCCTAATTGAAAGACATTTGGATCGTTTCCCAG
WI-18723f	94	G A ---			AACTTATTGATCTGACGATCAGCGATTAGTCTCATCCACATTTGACTGTGTAGATTTTGAAG TGGTAACAGGTACATAGGTAAACCAAG[A/T]ATATAGCTTATTTGGTGAATCTTCATCCT
WI-18723e	71	T C ---			AACTTATTGATCTGACGATCAGCGATTAGTCTCATCCACATTTGACTGTGTAGATTTTGAAG TGGT[C/A]ACAGGTACATAGGTAAACCAAGTATATAGCTTATTTGGTGAATCTTCATCCT
WI-18723c	96	A G ---			AACTTATTGATCTGACGATCAGCGATTAGTCTCATCCACATTTGACTGTGTAGATTTTGAAG TGGTAACAGGTACATAGGTAAACCAAGT[A/G]TATAGCTTATTTGGTGAATCTTCATCCT
WI-18619	44	G A ---			TTTATTACAATATTAGGTGGCACAAATAACTAAACAAGCTTCTGA[G/A]JACAGGAGGTAAACATTCTCA TAGACTTTGCAACTCAGCCAGAAAGTAAAACTCGAAATA
WI-18715	76	G A ---			TTATTCACAAAAGTGATATTGCAGAGGGTCTGGGGGCTGTACATGGCAGGGGCTTGGTGAGCTTTG TACATGGG[G/A]CTGGGAGACAAAGGGAGCCTCCAGGTGGAAAGGGTATTTTAAATAAAAAATAA TGGAGCTACAACCCACCCCC
WI-18535	107	G A ---			GTAAATAAAGTTTTATTGGCACAGCCACGCTCGTTTCAATCATATGCCATTGACATCTGCTGTGCCCT ACACAGCAGGGTGGGAGCTGCTCTTCACGGGAGAGCTA[G/A]TTGTTTAAAGCAGTGGTCCCCAAC CTTCTGTGTGTCOCCCGTG
D17525	107	C T ---			AGAGTGGTCAGAACACAGCCCGAATCCAGGCTCTATCACTTACTAGTTTTTCAGTTCTGGGCAGGTGAC TTGATCTCTTCGAACCTTCAGTTTCTTCATAAGATGGAAAC[G/T]GCTATACCTTACCTACCTCGTAAAA GTCTGATGAGGAAAGATTAACTAATAGATGCATAGCATTAAACAGAGTGCATAGCATACACTGTTT TCAATAAATGCACCTTAGCAGAAGGTGATGTGTCTACCAGGCAGACGAAG

DWU-133c	313 A G ---	---	TAATTGGCCACTGCCCTTATTATTACAAAACAGAAATGCTCATGACTTTTTATGTGTACCATCCT TTAATAGATCTCATACACCAGAAATTCAGATCATGAATGACTGACAGAAATATTTTGTGGGAGTCCT GATTTAAACTAAGACTGGCTTGTTGTTAAATGAATATGTTGAGTTTGAATTTTAATAGTAACCTC AATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-133b	236 T C ---	---	TAATTGGCCACTGCCCTTATTATTACAAAACAGAAATGCTCATGACTTTTTATGTGTACCATCCT TTAATAGATCTCATACACCAGAAATTCAGATCATGAATGACTGACAGAAATATTTTGTGGGAGTCCT GATTTAAACTAAGACTGGCTTGTTGTTAAATGAATATGTTGAGTTTGAATTTTAATAGTAACCTC AATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-133a	199 C T ---	---	TAATTGGCCACTGCCCTTATTATTACAAAACAGAAATGCTCATGACTTTTTATGTGTACCATCCT TTAATAGATCTCATACACCAGAAATTCAGATCATGAATGACTGACAGAAATATTTTGTGGGAGTCCT GATTTAAACTAAGACTGGCTTGTTGTTAAATGAATATGTTGAGTTTGAATTTTAATAGTAACCTC ITCCAAATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-36	102 C T ---	---	ATGAGATCCTTTAAATCCTTCATGAACGTTTTGTGGTGGCACCTCCTACGTCACAAACATGAAGTG TGTTTCTTCAGTGCACTGGGAAGATTTCTACCCTGACCAACAGTTCTCAGCTTCCATTCGCC CCTCATTTATCCCTCAACCCCGCCACAGGTGTTTATACAGCTCAGCTTTTGCTTTCTGAGGAG AAACAAATAGACCATAAAGGGAAAGGATTCATGTGGAATATAAGAT
DWU-387	169 G T ---	---	GTGTATAAATGCAACTGTTGATTTCTCAACATGGCTCACAATTTCTATCCCAATCTTTCTGAA GATGAAGAGTTTAGTTTTAAACTGCAGTCCCAACAGTTCACTCATATATAAAGCATTTATTTTA CTCTTTTGAGGTGAATATAATTTATATTACAATGCTG/TAAGGCTTCTTTAATACTAAGTATTTTCA GGTCTTCAACCAAGTATCAAGTATAACACAAATGAAGTGTCATTATTCAA
DWU-447b	172 --- ---	---	ATTTTAGTGTCTTTGGCTTAAATAATCATTCGAAAAGTATTTCTGAAGCTGCAAGCTGCCAGTCAGAT GGGCTGTGGCATTAAATCACTGTAATTAATTAGTTTGAATAGACACAAAGCTTAGCTAATCAA CCATTATTTTTCATTTGTTGTTCTAAGAGGATTGANAATCAGTTTAGTTTAAATGCTTTCTGTTAG GCCCTTCTTCTTACAATGAAGAGATGATTTCTCTAGTTTATGGTTA
DWU-447	85 A G ---	---	ATTTTAGTGTCTTTGGCTTAAATAATCATTCGAAAAGTATTTCTGAAGCTGCAAGCTGCCAGTCAGAT GGGCTGTGGCATTAAAGTACACTGTAATTAATTAGTTTGAATAGACACAAAGCTTAGCTAAT CAACCATTTATTTTTCATTTGTTGTTCTAAGAGGATTGANAATCAGTTTAGTTTAAATGCTTTCTG TTAGGCCCTTCTTCTTACAATGAAGAGATGATTTCTCTAGTTTATGGTTA
DWU-476	63 C G ---	---	GTAAAATTCAGTTTTTCCAGTTCCTCTTTTGTGCTGCTCTCAATTAGCGTTTAAAGGTGAGTCGAT AAATCAACTGTCCATCAGGTGAGGTGCTGCCATACCAGCGGTTCTTCATGATGAGTAGTGGGCTATGCA GGAGCTTCTGGGAGATTTTTT

DWU-505	67	A T	---	---	TCATACTAGGGCAGTATCTCCTCTAGCTAGTGGCCCATACAGAAAAATCTATCACCATACAAAAATTA[A/T]TGCAGTATTATGTTTTAAAGCACAGGTGTACCGAAACTGTGAAAAAGTCTGAATTTATGGGTT CTATGCATGCAATTTTGCCTAACCTAGAGAAAGAGTTTGATAAATTTTACCAGCTTTGAAGATGGAT TAACTTTGGACTTTGAGCTTTAAACTTTTAA
DWU-512	131	A G	---	---	AAATCCAGGCATTTCGAATCTGTTTTTCATGATTTATAGAGGGTTACACAAAGTGCCACTTATTAA AGAGCTTCACAGTGAAGATGGAGAAAGTGAACCTGCTTTGAATATCCAGATGTGTTGGTQ[A/G] TGCATATGGCAGTGAGCAGGTATGTGTTTGCCTTTGCTTGCCTGCACTGAAAAATTAATGCTATCAAGAGC AACTATGAACGGTTTTTTTATCAAGATGCTCCAGAGTGAAGATGCCGAG
DWU-525	97	A C	---	---	AACTGCATATAGATAATTATCCAGGATGTGGCTCAATCTTTTCAGCTGTTTCTATACTGTTTGTGA ATATACAGTTTTGTAAACCATATGATTGA/CJAAGAAGAAAGTCTATGCTTAGGCCAGTCAGTACA CCCAATTTTAAAAAATAACATATCTTTCCTTTTCCAAATATAGTTGAACAAGATTCCCTAAAAAT CCACCAGGATTATCTCTAAATCTAGTCTGATTGTC
DWU-59	94	C T	---	---	CATTCTTTGTGAAGGTAATGGACTCAACAGGGGAAGAAACATGCTGAGAATGGAAGTCTACCCGG CCCTTCTTTGTGAACGTCACATTTGGC/CJGAGCCGTGTTTCCAGTCCAGGTGGCAGACTCGTTTTTG GTAGTTTGTTTAACTTCCAAGGTGTTTTTACTTCTGATAGCCGGTGATTTTCCCTCTAGCAGACATG CCACACCGGGTAAGAGCTCTGAGTCTTAGTGGTTAAGC
EST11	68	C	---	---	CTTGATCATGGGTGGGAATTTTGTGTATCTGGGCTTCATGGGATGCATAAAATTTTCCAGTTGGTAAAG CAGCAGGTGCCGAGGGTCTGGATCAGAAAAAAGGCCA
WI-19856b	63	C T	---	---	CACACTGGCATCTAGGCTTCGCCCTGCATTGCAGAGGAGAGCCAGGTCCTCCTGGAGAA/CJTG CTGCGTTCCAGAGCCCAACACCCGGCTTGCACCAACAGAGCTGTGAGGCAGGAGGTGGGTAAAGACGT AGCTGTAGACCCAAAGCAACCAACCCCTGGGACCCCTGGGAGAGGAGCAGCTTTAGAACATGGAA AAGTGTGGTCATCCCATCATTAGACAAGACACATCCTACATAATAAAAAAGT
WI-18014	40	A G	---	---	TCCATTTACATTTGGTGGCATTTGTTGAATAGCTACAGAA/JGJGAATGAAAGTGCACCATCAGAGT GTAATTAGGTCTGTGTGACCCAGGAAGTGTCTGTAAACAGAGATTTCTCAAGGGCAAGTGGCTTCT A
WI-18036b	97	T A	---	---	TTCCAATGTAAGAGTCAAGTACCAAGTTAACTTCTAGAAATACAAAGAGAACATGATAAAATCTG ATCAGAGTGGAAAAATTTTAAATCTTTTCAAA/JA/JCTGACAGGTCAAGTAAGCTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18036a	27	T C	---	---	TTCCAATGTAAGAGTCAAGTACCAAGTT/JCAAACCTTCTAGAAATACAAAGAGAACATGATAAAAT CTGATCACAGTGGAAAAATTTTAAATCTTTTCAATATCTGACAGGTCAAGTAAGCTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18046	72	C T	---	---	TGTAAGGTGACTTCTATAAGCTTCCTAAACTGTCAAACCTTTCATTACTGAGATTATTCAGGCCAAT GTGTC/JTGTGGGCTGAGATTGATTATCAGCTGGGTAAAGTTAACCTGTTCTCTGTTTCA

WI-18063	105	G A	---	---	AGGCTTTAACTGATAACAAATTTGCCCTTTAATCACATACAAAAAAGCTCGACATTTTCATCCCTTCCTTCG CCATGTTTCTGATTTGATGTAACATTTAAATTTGTGATCTTTAACAATATACGTAGCTGCA
WI-18078	86	A T	---	---	AGTTGAAAGATCAGAGAGGTTATGTTGGTAGTAGCTGAACCTCAGATCAAACCTGGTCCAGTGTG TTGTTTTTTCAGCATCAGATGTTGCCACTAGCCAAAGTTGATCTCTGCAGTATCTACATGTGGT
WI-18091	90	T C	---	---	CCAAAGCTCACTCAGTATTTAATCATCTGCTAAATTTTCATCTTTGTTAATCCATCAGACACTGTGGT TTTCATCTCTAGAAAGTTTGACTTTCGTTGGCCCTTTTATACCTTCCATATCTCAACTGTTAAGC
WI-18119	38	T C	---	---	GCAATCTGTAAACAGTTTGGTAGTGGTATTACAGAGGATCTGTTGTAATAATGGATTGGAGTACTTAC CACTATTTTCATCTGCTCTGAAATAGTTCACTAACCAAACTACTGACAACAGTTTAAATTTTGGTTCTT
WI-18142	66	T G	---	---	TTCAGATAATTACAATTGGAAGGGGACCAATAATCCACTTTTAAATCGAAAAATATCTATATAC T/GCCCCAATAAATCACTACAGTAAATAAGCTTCAAAAAGCCTTAAGACACCAAAAGAGGAAAA
WI-18178	68	T C	---	---	GCATAGGGTTGAGGGGTGTACAAGAGGAGAACAGATTCAGTCCATGCCTGGAGGTTAGTCTGGGGG GT/C/CGCGGGATGGACACACAGACACACATAGATCTGGCATCTGATAGCAGGGCATACAG
WI-18244	35	G T	---	---	TCAATCTGAAAAACTTGCTGTAAAGCCAGCATGGGTGTG/TGGGAGGTGATTATGGCTGGGGAAGATG GGCACTCACCCGACAGCAGCATCTAGCACACAGTGACAGGACGTTGAGGTGGCAGAGGGCTTT
WI-18245	115	G A	---	---	ACAGATGTCAGTTGTTGAATTGGCCCATTTAAAGTATGGGGCTTTCTTGTAAAAAGTCATCCAAA AGGCTTGGCAAGAGTTTGTCTATACAAACGAGGGGACAGAGAAACATGA/GA/CTGGGAGTAGGCTCT GACAGAGGTGGGGCTG
WI-18261	26	G A	---	---	GATTTGAAGGGATTGCTTTAATTTAACTG/A/TTGAAAAAGCGTGATAGAGGAACCTGTTTAAAGATAAACAA CTTATAAATACTCCCAATTGTAAGATGAAAGATTG
WI-18268	88	C T	---	---	TAGGAGGGAAAGAGGAGGTGGCTGGCCCTCAAGACATGAGAAACGGGTGGCTTCCAAAGC TTCTTACTTCCCCCATAGATCT/CCTGACAAATGTCTGCAGAAAGCCCTCCAACTGGAAC
WI-18299f	107	C A	---	---	TCACAAAGTCAATCTCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTGGTTTGCCAATTTTTT ATCTATTTGGGTCTGAGAAATCCACAAATTTTGA/GA/TTCTTTTGCCAAATTTATGACATATTCG CAG
WI-18299e	101	A G	---	---	TCACAAAGTCAATCTCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTGGTTTGCCAATTTTTT ATCTATTTG/GA/AGTCTGAGAAATCCACAAATTTTGAAGAAATCTTTTGCCAAATTTATGACATATTCG CAG
WI-18299d	77	G A	---	---	TCACAAAGTCAATCTCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTGGTTTGCCAATTTTTT T/GATCTATTTGGGTCTGAGAAATCCACAAATTTTGAAGAAATCTTTTGCCAAATTTATGACATATTCG CAG
WI-18299c	67	T G	---	---	TCACAAAGTCAATCTCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTGGTTTGCCAATTTTTT T/GATCTATTTGGGTCTGAGAAATCCACAAATTTTGAAGAAATCTTTTGCCAAATTTATGACATATTCG CAG

WI-18299b	52	G A	---	---	TCACAAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCAATTAACTTG/G/ATTTGCCAATTTT TTTATCTATTTGGGCTGAGAATTCACAAATTTGAAGAATTCCTTTGCCAATTTATTGACATATTTCTG CAG
WI-18299a	48	C T	---	---	TCACAAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCAATTAAC/CTTTGGTTTGGCAATTTT TTTATCTATTTGGGCTGAGAATTCACAAATTTGAAGAATTCCTTTGCCAATTTATTGACATATTTCTG CAG
WI-18307	76	G A	---	---	TCAACTTGTACCAAGTTTAGCAGCAAGAGGATACCTTCCCTTAGAGACTTTCAGTGGACTTAAACTCAG TTTCCGCTG/G/ATGCTATGTAAAGCATCCACGATGGTTTATTGTACTCTGCAATCTGCTGGTCAC
WI-18324	72	C T	---	---	TTTGGTATGAAATCTTTCTCTGACATTTACCAATCATCACTTAAACTCCGGGGGTGGGGTACTGATT TATC/C/TTTAGATCCAAATAAAGCATGCAGAAAGTG
WI-18350	48	T C	---	---	ATGAAAGTCACCTTCAATCATAGGGTCAAGAGAAAGAAATGTTTTCAGAT/C/TAATCTATGAAAA GGTGTATCTGCTTGCATTTAAGAAACACACAAAGTCA
WI-18395	77	G C	---	---	TCTTGACATGATCTGTGAAATAACGTGATTGTGGTTGAATTTCCCTGGAAAAATTTGAAGAATAAATTG ATTATTCAG/G/C/TTGTGCATTTGGTTTATACATATCTCTCTCTCTTAATGCAAGCTATG
WI-18398	62	G T	---	---	TGCAGTGGCAAGACACTCTCTCGAGGAAAAAAGAAAAAGAAAAAACAACCTCAAGGGTT/G/T/
					GATAACATTGCCAGTATAACCATTAATTCAAAACAAGCAGCAGAAATTTGGAGGATAATTTGTT
					CTCGTTGGTATTTCTCTCATCC/C/ATTCCTTTTCGCTCTTTCTAAAATTAAGAAAAAGCAATGGAAAT
					TTAAAGATCATCTAAGAAATAAGAACTTACATATGTAAACATTTAACTTATCAACTTGTACAAAGTC AATGAAAA
WI-18396	21	C A	---	---	AAGATGGGAAAGAGGAAATC/C/ATTTTCTTACTAGAGATTTTTCCTTTAATCCTTTTCAAAAT
WI-18409a	20	C A	---	---	TCAAAGGATCATCAAGGAGCAGGTGCAGAAAGCTCTGGGGCCAGAGGCCCCCAAGTGCTA
					AAAAAGGAAAAAGAAAGGATGGAGTAAGAGAGAGAGACAGAGAGGAAACAAAATAAGTTTCTGG/C/T
					JTTGGCTGATCTGGGTGATCAGGTGGACACTATTATCCAGAAAGGGAACACACAGAGAAAAAAGG
WI-18442	62	C T	---	---	TTTATAGTGGGAGAGAGGA
WI-18452	38	G A	---	---	TTGATGTTAATACTGTCTCTGGAGATCGGCTAAAAT/G/AAAGCATAGTTATTATTAGCTTTGG TATAATCTCGACAGATTTAAACAAGTAAGACATATATCAACCCCTCATATTTTCCAAACCA
					ATATAAGCTGGAGACTGTGGAGGTGAGAGGCAGTGGGACTAGCTGTTGAAAAGAGAGAAATGTAGC
WI-18489	102	A C	---	---	AGTAGTAAAGATGAAAGACTGCAAGGATTCAAACA/C/CGTTTATGGCAATAGAGGTGAAAAAGAAA AGGCCATATAAA
					CTGGTGGGAGGAAACAAATTTGGGTATATTATACATAATGGAACACTCTTCAGAAATAAGAAAGGAA
EST5b	93	A	---	---	CAAAACCACTGAATCACACAACATGGACAAATCTCAAAATCATTATGCTGATGGAAAGAAACCAATTCA TAAGAATACACAGTACAT

EST5	93 A	---	---	CTGGTGGGAGGAAACAAATGTGGTATATTCATACAATGGAAACTCTTCAGAAATAAGAAAGGAA CAAACCACTGAATCACACAACATGGACAAATCTCAAATCATATGCTGATGGAAGAAACCAATTCA TAAGAATACACAGTACAT
EST6	48 C	---	---	TTAGCTACTTTTCAGAAATGAAGGAGAAATGCATTATGTGGACTGAACCGACTTTTCTAAAGCTCT GAACAAAGCTTTTCTTTTCCATTTTGCACAAAGACAAAGCAAGCCACATTTTGATTAGACAGAT
EST8	158 A	---	---	GGACAGGAACCTCTATCCCGCTGTGGTGCAGCAGCGGCTGATGGACTGAGGCCCGCAGGGGACTGGGCC CTCTCTCAGGGGCTCTCCAGGACCCAGAGCTGTCTCTGCTTTGAGTTTCCCTAGAGCTGTGCGGCCA GATAGCTGTTCTGAGTTGCAAGCACGATGGAGATTTGGACACTGTGTGCTTTTGGTGGGT
WI- 18740c	104 G	---	---	TCCTCATTGTTGGGGATGATGAGAAAGAAATGATTTGGGAAATTAAGTAACAACGACCTAGAAAAGT GAGAAACAATCTCATTACCATCATGTATC/C/GJAGTAGTGGATAATTCATTTTGATGGCTTCTATTTT TGGCCA
WI- 18740b	96 C	G	---	TCCTCATTGTTGGGGATGATGAGAAAGAAATGATTTGGGAAATTAAGTAACAACGACCTAGAAAAGT GAGAAACAATCTCATTACCATCATGTATC/C/GJAGTAGTGGATAATTCATTTTGATGGCTTCTATTTT TGGCCA
WI- 18985a	105 C	T	---	CCAAAGCTCCTGTTGCTCATAAAGAGTTTGTGGATGGGAGAGATCCAGACCATCTTGGGGCA GCCAGGCCCTTGCCTTCATTTTACAGAGGTAGCACAA/C/JTGATTCACAAACAAACCCCTTCCCC TTTTAAATGATTTCTGTTCTAATGCCATAGATCAAAAGCCCTCAGAAACCAATTGTGTGTTCTCTT TGAAGCAATGACAAGCACTTACTTTCACGGTGGTTTGTGTTTCTTAT
WI-18746	114 G	A	---	GCCAGAGCTGAAGTCTCTTTTCTCTCTCGGCTGGAAGAACATCAAGATACCTTTGCGTGGATCA AGCTTGTGACTTGACCGTTTATATTACTTTTGTAATATTTCTT[G/A]TCCACATCTACTTCAGCT TTGGATGGTTAOCG
WI-19112	212 G	A	---	CCGTGTTACACACACACAATGGCAAGCATAGTCGCTGTTACGGCCCGAGGGGAATATGCCAAGG GACCCCTTAATGGAACACACAGATCAGTAGTGC/TATCTCATGACAAACCAAGAAACCGACGACAAA TCTTTTGGGAGATTTCTTCTAGTGGCTTAGAAACATGGCTTTAAGAAACACGCGTATATCTTTGAG GGTGACAAGGC[G/A]TCTCTCAACACAGTTCCATACCAACTGCTTTGCTCTAG
WI-19092	232 A	C	---	TGGTGGCTGGCTAGCTAGTTTCTACAGAACATAATTTGCCTCTATAGAAGGCTATCTTAGATCATGT CTCAATGGAACACACTCTTCTTACGCTTACTTGAATCTTGCCTATATAAAGTAGAGCAACACAC ATTGAAAGCTTCTGATCAACGGTCTGAAATTTTCATCTTGAATGCTTTGATTAAACTGAATTTTC TTTTAAGCTAACAAAGATCATAATTTT[C/C]ATGATTAGCCGGTAACT
WI-19057i	175 G	A	---	CCCATTTATTATAGCCAGTGTGCTCAAGAGTAGAGGAGCGTCTACTGGTCTTCAACTCCTTCA GTCTTCTGACGGCGGACTTTACCGTGACAGCGGAAGTGGTATTGTACGTCAGGCACCGCAGCCACTG TCTTCATGACGGAACACAGTGGCCAGATCCCCACAGCTC[G/A]TCTCTCACTCTGTTTGGCCACA

WI-20103	168 C T ---			TGGGACTTCCAACCTCAGAGGATGTGGGAATCCAGCTCCAGCTCAATGATACAGGATAAAGCTGGATGGCT AGGATGGACAGGCTGTGGATATGGGAGTCATGGGTCAAGTCTTATCCAGATGGCTCCAGGTACAG TGGGCTTCTGGGCTGGAAGCTGGGTCTCCCA/C/TTCATTCTGCTCAAGCTTCTTGAAGGAGC TGGTTTGACTTCAACTTGTAGAGCCTAGCCTCATCTTTCAGTCAACTGGGA
WI-20441	111 G A ---			GCCTTACCCATTTTGCACATATACATATGCACCACCTTTCAGTGGCAACATATATATCCACACTA TAAACATACCACATTTATAATCTTGTAGGACAAGAAATGGA/G/ATTTGAATAGTACCCCCCAA CATATACAAGAAAGTTAGCATACTTACCCCGTTTTTCACTACATCAGAGGCAAAATAGAAATCTTT TAAGAAATCTCAAGACTGGCTCATGGCAAAATGAATATGCTAAATTTGGGGG
WI-19911b	116 A G ---			TGGTTACAAAACCTAAGCCCATATACAAAATTAGGAACACATTTAGATGCCTCTTTTGAAGAACGT TTTAGTCTTTTAACTGAGTTTAAAAAAAATAACAATGCAATTTTAA/GJACACTGTTTTTGAAA ACTTAAAGTGCAGCAATA
WI-20613c	165 A G ---			GTCTCAAGGGGGAGAAAACCTGGTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAACA GATACGTAGTACATCTGTAGTATTAAATGGCATGGGAGGAGGAGTTAGAAAAACATCTAAAC AGTCTCTTAGAAGGCCAATAATAAGTTGGA/G/AAAGGGAGTTTCCACGACGACGAGTGTGAGC TGC
WI-20613b	156 A C ---			GTCTCAAGGGGGAGAAAACCTGGTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAACA GATACGTAGTACATCTGTAGTATTAAATGGCATGGGAGGAGGAGTTAGAAAAACATCTAAAC AGTCTCTTAGAAGGCCAATAATA/G/AGTTGGAAAAAGGGAGTTTCCACGACGACGAGTGTGAGC TGC
WI-19984	47 A G ---			CAGTAAAGAGTGATTCAAGTTGCAGTAATACACTGACAGGTAAATA/G/ATTAACATTAGAAAA GCAAAATCTTTTAACTTAAGGACAGACTGAACCATCAGGTATGGGTCTGAGATCAAGTAATACAGG TAGGCAAGAGTTTTTCCACACTGGAAAAATGAAGGCAGTTTCCAAATACTGTGAATTTACAAACAT TGGGGGAAGG
WI-20122	135 T C ---			GCCAGTTGGAATATGGCTATACGAACCAAGAGTGTATACAAAATGGAAGTGGTCATCAGGCAATA ATTGTTTCTTGGAACTCTGCACCGACTGTCCATGTCTGTGGGACTTACACATTCAGATTTGACAGI T/CJTGA AAAACCAACTGGAGCTGCTTTTCCAGAATGTTCTGTTGTCTTCAAATAGGAATCCATG TTATTTCTTTTGGCCTTAAGCTCTTATATCTTTCAAATGACCTAAGCTGA
WI-18846a	49 G A ---			GAGTGCCATACCTTCTCCAGGCCTCTGCCCAAGAGCAGGAGGTGCCTG/AAAGCTGGGAGCGT GGGCTCAGCAGGGCTGTCCACTCCCATCCCGTAAGACCTCTTCCCTTCTCAGCAGGCCAAACATG GCCAGACTCCTT
WI-18959	123 G A ---			AGCAGTGGCCTTATTGCATCCCAACCAACGCCCTTGAACAGGCTGCCCTTGTGGCAGCAACGGC ACAGCTAATTTCTACTACAGTCTTTTAAAGTGAATGTCGAGAAAGAGGACCC/G/ATGGGAAGCCG TCTGGCGCCTGGCAGTCCGTGGGACGGGATGGTTCTGGCTGTTGAGATTCTCAAAGGAGCGGAT GTGCTGGACACACAGACTATTTTAGATTTTCTTTTGGCTTTTGAACC

WI-20146	31 T C ---			---	TGAGTCTCTGTGAATTCATTGAGCAGTTAGCTTCATTTGAGATAAAGTCAAAAGTCCCAAAACACTAGCTCTGTATTAATCCCATCATTAATGTAAGGCTCATTTGAATGTGTAATCAATACAGGC
WI-18922	74 G A ---			---	TAGGAATTGGTTTACGCCCTGAGGCAATTAGACACTTTTGGAGATGGCATAAACCCTGTCTCACCTGGACTTAAGC[G/A]TCTGGCTCTAATTCACAGTGCCTTTTCTCTCACTGTATCCAGGTTCCCTCCACAGAGAGCCACACAGTTCTC
WI-18763b	53 A G ---			---	TTCTGTGTGTGGGGTCAACCGTACAATGGTGTGGGAATGACGATGATGTGA[G/A]GTATTTAGAATGTACCATATTTTTGTAAATTAATTTATGTTTTCTAAACAAATTTATCGTATAGGTTGATGAAACGTCA
WI-18763a	38 A G ---			---	TGTTTTTGCCAA
WI-18771b	75 G A ---			---	TTCTGTGTGTGGGTCAACCGTACAATGGTGTGGGA[G/A]GTGACGATGATGTGAATATTAGAATGTACCATATTTTTGTAAATTAATTTATGTTTTCTAAACAAATTTATCGTATAGGTTGATGAAACGTCA
WI-18771a	57 A G ---			---	TGTTTTTGCCAA
WI-18820	70 T C ---			---	CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACTGCTCTCGGAGGATGCCCTAGAAGATGTTGGG
WI-18742b	51 C T ---			---	AACAGAA[G/A]AAATAAACTGAGTTAAGGGGGACTTAAACTGCTGAATTCACCTGTGGA
WI-18882	94 C T ---			---	CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACTGCTCTCGGAGGATGCCCTAGAAGATGTTGGG
WI-19970b	167 G A ---			---	GGGAACAGAGAAATAAACTGAGTTAAGGGGGACTTAAACTGCTGAATTCACCTGTGGA
WI-19970a	126 T C ---			---	GGGAAAAATTTGAGACGCAATACCAATACTTAGGATTTTGGTCTTGGTGTGTTGATGAAATTTCTGAGGCC[T/C]TGATTAAATCTTTCATTGTGATTTCCTTTTAGGTATATTGCGCTAAGTGAAACTTGTCA
					GTCA
					ACAAAGTCTGTAGCCCCCTCACTTCTCTGTTTTCACCTTTTGCCAAATGA[C/T]ATCGGGTTGGTTT
					TCTTGATTAATTAACGGTTGTGGTTTCTTTTCCACGGAGGTTCAAGTAAAGCCGCTGCAGGAGA
					GTITACC
					GTGTGTCAAAATGGGGTCTGCTCCTGCTACCTTGACCCCTCCCTTTCTGCTTCTCTCTCTCATCA
					TCAITCCCAACAACATCCTCTGCCA[C/T]ACACAACAACAAACGTAAGTTTCATTTGGGCAAAAATTGA
					GC
					TATAAGCCCGAGTCACAGGACGGCCTGTCTGECACACAGACAGGGGCTGCCTGTGGAGCCTGCCCAAC
					GGCCCCGGCAGTCAGTCACGGGGGAGGAGGCTGCCCGTTCTGCCAGTTCCCTCACTGCGGGAGOC
					AGCAAAAGGCCTTCTCACTGGGTTGGTCAAAAG[G/A]TAGTCACCTTGGCCTGGTGCATCCACAGAGGA
					TGTTGTTCAACCCAGAAATCTTTAAACGACTGACCTTCTTAAAAACAGA
					TATAAGCCCGAGTCACAGGACGGCCTGTCTGGCCACAGACAGGGGGCTGCCTGTGGAGCCTGCCCAAC
					GGCCCCGGCAGTCAGTCACGGGGGAGGAGGCTGCCCGTTCTGCCAGTTCCCTCACTGCGGGAGOC
					ACCAAGAAAGGCCTTCTCACTGGGTTGGTCAAAAGGTAAGGTAGTCACTTGGCCTGGTGCATCCACAGAGGAT
					GTGTTCAACCCAGAAATCTTTAAACGACTGACCTTCTTAAAAACAGA

WI-19067d	202 T G ---	---	TATTGCTGCTTGCTACTGCTGACATTACGGCAGAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGC ACATCCCTCTGCTCCCGAGAGACTGCTCCGCCATCCACAGATGATGATCTTCAGTGGGTTCTC TTGGGCTCTAGGCTCTGGAGAATGTTGTGAGGGGTTATTTTTTTTAAATAGTGTTCATAAGAAAT/
WI-19067c	153 G C ---	---	GACATAGTATTCTTCTCAAGACGTGGGGGAAATATCTCATTATC TATTGCTGCTTGCTACTGCTGACATTACGGCAGAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGC ACATCCCTCTGCTCCCGAGAGACTGCTCCGCCATCCACAGATGATGATCTTCAGTGGGTTCTC TTGGGCTCTAGGCTCTG/CJAGAATGTTGTGAGGGGTTATTTTTTAAATAGTGTTCATAAGAA ATACATAGTATTCTTCTCAAGACGTGGGGGAAATATCTCATTATC
WI-19067b	151 T C ---	---	TATTGCTGCTTGCTACTGCTGACATTACGGCAGAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGC ACATCCCTCTGCTCCCGAGAGACTGCTCCGCCATCCACAGATGATGATCTTCAGTGGGTTCTC TTGGGCTCTAGGCTCTG/CJGAGAATGTTGTGAGGGGTTATTTTTTAAATAGTGTTCATAAGAA ATACATAGTATTCTTCTCAAGACGTGGGGGAAATATCTCATTATC
WI-19067a	57 C G ---	---	TATTGCTGCTTGCTACTGCTGACATTACGGCAGAGGCAAGGCTGCTGCAGCCTCC/CJCTGGCTG TGCATTTCCCTCTGCTCCCGAGAGACTGCTCCGCCATCCACAGATGATGATCTTCAGTGGGTT CTCTGGGCTCTAGGCTCTGGAGAATGTTGTGAGGGGTTATTTTTTAAATAGTGTTCATAAGAA ATACATAGTATTCTTCTCAAGACGTGGGGGAAATATCTCATTATC
WI-19106	247 T C ---	---	TTATCCAGCCCTACCTTGTTAGTTATTTAGGAGACAGTCTCAAGCACTAAAAAGTGGCTAATTC AATTTATGGGGTATAGTGGCCAAATAGCACATCTCCCAAGTTAAAGACAGTGGATCATGAAAGT GCTGTTTGTCTTTGAGAAAGAAATATGTTTGAGCGCAGAGTAAATAGGCTCCTTCATGTGGC GTATTGGGCCATAGCCTATAATTGGTTAGAACCCTCTATTTTAA/TCJTG
WI-18944	147 A G ---	---	CAAGGCAAAAAATATCAGGAGCTTTTACACACCTACTAAAAAGTTATTATGTAGCTGAACAAA AATGCCAGAAGGATAATATTGATTCCTCACATCTTAACTTAGTATTTACCTAGCATTTCAAACCC AAATGGCTAGAAC/A/GTGTTTAATTAATTTCAAAATTAAGTTCTACAGTTAATTATGTGCATA TTAAACAATGGCCTGGTTCAATTTCTTTCTTCTTAATTAATTTAAGTTTT
WI-18952	232 G A ---	---	CCCATCCCTGTGAAGGAGTAGGCCACTTTTAAAGTGAAGGATTGGATGTTTCATAATACATAAA GTTCTCTGTAATTACAACATAATTATTATGCCCTCTCTCACAGTCAAAAGGAAGTGGTGGTTGGT TTTTGTTGCTTTTTAGATTATTGTCCTCATGTGGGATGAGTTTTTAAATGCCACAAGACATAATTA AAATAAATAAATTTGGGAAAAGGTGAAG/AJACAGTAGCCCCATCACAT
WI-18932d	177 C T ---	---	CACACCTCATGCTAGCCTCAGGAACTGGAATAAGCCTTCGAAAAGAAATTTGCTTGAAGCTTGTA TCTGATATCAGCACTGGATTGTAGAACTTTGCTGATTTTGACCTTGATTTCAAGTTAACTGTTCCC CTTGGTATTGTTTAAATCCCTGTACATATCTTTGAGTTCAAC/TCJTTTAGTACGTGTGGCTTGGTCA CTTCGTGGCTGAGGTAAAGACGTGCTTGTGGAAGACAGTCTGTGGCTTG

WI-19042	193 A C ---			TTTGTGAGTGTGCTCTGGCAATGCCTCAGTAGCATCTCAGTGGTGTGAAGTTTGGAGATAGATG GATAAGGGAATAATAGGCCACAGAGGTGAACCTTTGTGCTTCAAGGACATTTGGTAGAGTCCACAG ACACAATTTATACGCGACAGAACCTTCAGCATTGTAATTATGTAATAACTCTAACC[A/C]GGCTG TGTTAGATTGATTAACTATCTCTTTGGACTTCTGAAGAGACCACTCAAT
WI-18984	208 A C ---			ATTGGCCCTGTACAGTTGCTTATTATAAATCATTAACACACTACAGGTGTGAATGGTTAAAA TGTAAGCCTCCAGTTCATTTTCAGTTATTTCTGAGTGCAGACAGTATTTCCGACTGTATTAAAT GTAACCTATTATGAATCAGAAGCAGTAGACAGATGTTGGTGCATACAAATATTGTGATGCATT TATCTT[C/C]ATAAAATGCTAAATGTCAAATTAACACTGCGCAITGTTGACT
WI-18851	90 T A ---			GCCTCAATTGGCGATTGATTGAGTGCCCAATGTAAACAGGGTGGTAGTTGTACTCATTTTGAAT ATACCTTTTCTTATTGTATTCTT[A/G]TAAATAGGATCCTGGAAATGAGACCTGGTGGAA
WI-18821b	76 T C ---			TCAACTGCAGTGTGCTTCCCTCCCTATAGGGCTGGAATCTGTCTAGGAGCCCTCTCTCGGAGGCC ACAGAGGCT[C/G]GGGGTAGCCATTGTGCAGTCATGCCCCGGGGAACTTGCCAACTTCGTGTCAG GTGCTGTGT
WI-18821a	69 C T ---			TCAACTGCAGTGTGCTTCCCTCCCTATAGGGCTGGAATCTGTCTAGGAGCCCTCTCTCGGAGGCC A[C/T]AGAGGCTGGGGTAGCCATTGTGCAGTCATGCCCCGGGGAACTTGCCAACTTCGTGTCAG GTGCTGTGT
WI-19021a	20 C G ---			ACTCCTCTGCTGTCTCAT[C/G]ACTGTCTTTTGAACCAGGAAAGTCACAGAGTTTAAAGAGAA GCAAAATTAAACATCCTGAATCGGGAACAAAGGTTTATCTAATAAGTGTCTCTCCATCACGTTG CTACCTTACCACACTTCCCTCTGATTTGCGTAGGACGTGGCATCTACTACGTACGTGGCATAAC ACATGCTGTGAGCCCATGTATGCTGGGTAGAGCAAGTAGCCCTCCCTGTC
WI-18908	70 G C ---			TGGAAATTCCTTTCATCTGGAAACCATCAGAAACACCCTCACACTGGGACTTGCAAAAAGGTCAGTA TGG[C/G]TAGGGAAACATTCATCCTTGAGTCAAAAATCTCAATTCTCCCTATCTTTGCCACCC TCATGCTGTGTGACT
WI-19037b	155 A G ---			CACGGTTCCTGCATCGTTACAGAGCGCTTCTGGTCTAGCCACGCCCTGTATACCGCGCAATA TCCCCAAAGCTTTGGGTCTCAAGTCATGCCCGAATTTAGATGCTGGTCAATTTCTGGAGAGGGTC CCCTCCCTTACGAACACA[A/G]AAACCCAGCCACATGACTAGCACGCTGAGCTCTGCAGGGACCA GTGCCAGGCACTGGGGGTGGAAGTGTGGTGACACAGTGAATGGAGGTGG
WI-19037a	47 C A ---			CACGGTTCCTGCATCGTTACAGAGCGCTTCTGGTCTAGCCACG[C/A]CCTGTATGACCGCGCAA ATATCCCAAAGCTTTGGGTCTCAAGTCATGCCCGAATTTAGATGCTGGTCAATTTCTGGAGAGGG GTCCCTCCCTTACGAACACAAAAACCCAGCCACATGACTAGCACGCTGAGCTCTGCAGGGACCA GTGCCAGGCACTGGGGGTGGAAGTGTGGTGACACAGTGAATGGAGGTGG
WI-19064	66 T C ---			TTGAGGAGGTGGGTGAAGTCTCTTGGCAGGGAATTTGTGACACTGCATTGCTGGGCTGTGTCTCQI/ CJGGGCTCTTCTGGACCTTGCAACCGTGGATACAGGCCCATGGTATTTGGTCTCTGGGAGGG TGGGTGAATAAAGC

WI-18972a	112 A G ---	---	AGGCTGTGGCTTATGTACCCAAACAGAGGGGTCCTGAGAAAGTCTGGCTGCTGGGATGCCCTGGCC CCCTCCTGGAAGGCTCTGCAGAGATGACTGGGCTGGGGAAGCAG[AG]TCTTGTCTGGCCATGGAGCC TCATTGCAAGTTGTTCTTGAACACCTGAGGCTTCTGTGGCCACACAGGCACTACGGCTTCTCTCTCC AGATGTGCTTTGCTTGAGCACAGACAGTCAGCATGGAATGCTCTGGCCA
WI-19016b	184 C A ---	---	GTTTGCAAACCAACATGTGCTCTTTTCAGTCATTCACCTGTTTAAATATGACATGGTAGAGAAGATAAG GTTTATGGCAGGTAATTTTGTAAATGTGATTAACGGAAGTTCAAAGATTAGAAATACATCTGTGTC CTGAAACCTTAGATACATAGCCGACTGTATACAGAGGTTCACTCAAC[CA]CTCAACACTATTGAC TTTTGGGCTGGATAGTCTCTGTGTGGGGGTTGTCTGTGCACTGTAG
WI-19016a	161 C T ---	---	GTTTGCAAACCAACATGTGCTCTTTTCAGTCATTCACCTGTTTAAATATGACATGGTAGAGAAGATAAG GTTTATGGCAGGTAATTTTGTAAATGTGATTAACGGAAGTTCAAAGATTAGAAATACATCTGTGTC CTGAAACCTTAGATACATAGCCGAC[CA]TGTATACAGAGGTTCACTCAACCTCAACACTATTGAC TTTTGGGCTGGATAGTCTCTGTGTGGGGGTTGTCTGTGCACTGTAG
WI-20096	21 T C ---	---	GGTTTGGGGCATTATTTCT[CA]GATAGAGACTGGCACAAAGCTTTGGGCTAAGGACACCCGCCGCC ACCTCATCTAGAAACAATCTCTCGCCAGACTTG
WI-19591b	156 C A ---	---	TGGGGCAATTTTAAACAAACAGGCAAAATATCATATACCTGAATATAAGGTAACCTCAAGCCATG AGTATAAGATTAAAGGAGTTACTTTTATTTGAACAGGAAGTGGCATAAGCAACTCAGTGTGCCCC CTTAGGTGGGAGCTCTCC[CA]CTACCACTCCCAAGGATCATTTTGGGAGAAAAA GTGCTTCTATCTGGCTAGCTGTGTTATCTAGGGATTGCACCTTCTTACACGG
WI-19591a	45 T A ---	---	TGGGGCAATTTTAAACAAACAGGCAAAATATCATATACCTGAATATAAGGTAACCTCAAGC CATGAGTATAAGATTAAAGGAGTTACTTTTATTTGAACAGGAAGTGGCATAAGCAACTCAGTGTG GCCCTTAGGGTGGGAGCTCTCCCTACCACTCCCAAGGATCATTTTGGGAGAAAAA GTGCTTCTATCTGGCTAGCTGTGTTATCTAGGGATTGCACCTTCTTACACGG
WI-20310	125 G A ---	---	TCCTCAGCTCTGTCATCCTTGTCTGAGGGTTCTGTGTTACGGGCCCTCCAGGCATGGTTCTTCAT TTAGGTAGGAACAAAGGCCAAAGAACATACAAGCCAGCTCTAGAGGCTCC[CA]TCAAGAA CTGGACCTTTAACTACAAAGGAATCTTGGATGAATTTTATAGGGGGCTTCAGGAGCAGGTAGC AGAGCCAAAGTGCACACTCAGGCCATCTCTCTCCCAATGCTCTCCCGGGGG
WI-20860	224 G A ---	---	CTCTCCCTAAGGAGCCTTGGCTTGCAGCCCATTCAGCAGGGATGGAAGTCACAAGACATGAGT GGAGCTCATGCCCTCCATGAGGAGCCCTTAGTATGCTGACATCTGCCCTTATCTGCTCTCTCT CCCCAGTCTGTACACTTGGCAAGCAGAGTGGTGGCAGACCCAGCCTTGAGAGCTCTTGTAGAAC GGAAGGAAGGGCGGTCAT[CA]GAGGTATGGCTCTGGCTCTCTGGCT
WI-19359a	39 T C ---	---	GACGTGGACAAAGGAGGTTTAAATGAATACCTTTGTTTGT[CA]TATGTTCAAAAAAGAGATTAAAT ATTTTGTGACTGCATCTGTGAATGAAGACACTCAAAAGCCATGTTTCCAACTTAGGTTAATAATAA GGCTATTTGTCCACCCACTCTTGGGCACTTGTGCAATATCTGGGCTCAAGTGGAGGCCAGGTG GGAACAAGGCCCTCAGAAAAACAAAGGACATGCAGCCTCCCTGAGCCAGTTCTCT

WI-19766b	93 A G ---			TGGCCTCAATGACTGGTACATTGGAGAAGCTGTGCAGCAGCATCCTTTCTGTGGTGGCAGGGCAGG AGATGAACCATAGGAGCCAAAGTC[AG]GACAAACAGAGAAGGACACCAAGCCTGAAACCCCTC CGGACAACAGCAGAGTTACAGCTGAGGGATGTCCTGGAGTTTCTGACCCATGAGAGGCCOCCCTC ACCTCTTCACCCCTCCTACCAACAAGCTCTCCGGCAGTCATGGACTTAT
WI-19766a	31 G A ---			TGGCCTCAATGACTGGTACATTGGAGAAGCT[GA]GTGCAGCAGCATCCTTTCTGTGGTGGCAGGGC AGGAGATGAACCATAGGAGCCAAAGTCAGACAACAGAGAAGGACACCAAGCCTGAAACCCCTC CGGACAACAGCAGAGTTACAGCTGAGGGATGTCCTGGAGTTTCTGACCCATGAGAGGCCOCCCTC ACCTCTTCACCCCTCCTACCAACAAGCTCTCCGGCAGTCATGGACTTAT
WI-20512d	126 C G ---			CTTCTCTGTTGGCTTGCAATTGTGGATTGGAAAAACCACCTTGGAGAAGGGACTTTCTCTGCAA AACCTTAAGACTGGTTAAATTACAGGGCCTAGGAAGTCAGTGGAGCCCTTGACTGA[CG]AAAGC TTAGAAGGAAGTGAATTGCTTCTTGAATATGGATTTAGGGCGGGCGTGGGTGGGCTCACGCCT TATTAATCCAGGCACGTTGGGGAGGGCCAAACGCGGGTGGGATCACCTGA
WI-20512c	59 T G ---			CTTCTCTGTTGGCTTGCAATTGTGGATTGGAAAAACCACCTTGGAGAAGGGACTT[GT]CTCTG CAAAACCTTAAAGACTGGTTAAATTACAGGGCCTAGGAAGTCAGTGGAGCCCTTGACTGACAAAGC TTAGAAGGAAGTGAATTGCTTCTTGAATATGGATTTAGGGCGGGCGTGGGTGGGCTCACGCCT TATTAATCCAGGCACGTTGGGGAGGGCCAAACGCGGGTGGGATCACCTGA
WI-19599	230 C G ---			GGGCTTAAATTCCTCTGTTGGGACTGGTCTCTCCAGTTTACAGCAAGGATCGACCCCTTTTC ATAACCCCTTCTACATTGGAAAGAGCACACCCTTGATACAGAATGGCTCCGTGAAGTCTTTTAAACG GACAAAGGTAAATCACAGCTAACAAACGTGATGTTGGCTCACACGTAAACCAACCTCTTTTCA GAACAGAGAGCGTTAAAGTAAAGGGCA[CG]TTCCAAGAGTAACACTGCTA
WI-20679	82 T C ---			TGTTTGAATAAAAATTCATGGTCTTAATTGAAGTGTATGTTACTTTCTTTTAGAATATCCTTTT TTCATTAAATAT[CT]CTAAACCACTCTATGTTTCAACCTCTGTTTAACTAAGATATGGGT TTTTGGAAAGGCCACAGTCACCACTCCATGAAGTGGCGAATGGTCTTGTGTTGGAAAGCTCTC CAGGGTGTCTCCAGAAA
WI-19909a	29 T C ---			CCAGAAATAAGCCTGAATATCTCTTCT[CT]CTTAAAAATATAATTTTCTCTTTGCTCTTCCAA GTAAATCTTAAATGAACCTGTCTAGTCTATTTTAACTAGGCAATTATAACACTACCTAGGGGG TTTTTCTTTATACCTTGTCTGTACTGTGGAATCAACTAA
WI-20341	221 G C ---			TTGAGAGGCTGAGAGAAGGCTGTTGAGACATTGTAATAGTCTTAGGGCATGAGACATTAGGAAG GCCACAATTATGAGTAATGAATGTGGAGGCTGATGAGAAGCTACTGCTCCATTGTTTAGCAGGA GGCAGGAAAGTGATCTGGGTCTCTGGCAGCAAAAGCGTGTGTTAAATTTGGGTGACGTATGC ATCCCCATGCATTGGTTT[GG]ATGTCCTCCAGTGAGCTGTGGGCAAGTCT

WI-20113	60	T C	---			TTCTGTACATGGTAAGTGCTCAGTATTACTGAGTGAATGAGCAAGACCTGAAATACTGT/CJGGA AACAGTAAAGCAAAATACCACACAATTAGGAGGAATTTATTTTCAGACATAGGATATTTAAACAT CACTCAATACTGGAGCATGATTCAGCAATAAATCTATTCATATAAACCCAGGTAGATAAATGTCACA GCTTTAAATATAGTTAAGTACAGTTGATCCTCGTTATTCATGGATTCCGTATT
WI-20895	107	G C	---			TGATGGCAAGTACAAAGGCTCTGAAAGAACAGAGTAACAAGAGCAGCGCAGTGCGCGTGTGGC CACTTCCACCAGGAGAACACTTGACTTCATTAAAGGCAAA/G/CJTCTTACTCTGTACTTTTCCTC CCACATAGTTTAAACCAATAGAAAGGCATTCTATTCTCACACTACTGCTCTCTAAGGTCCTAGGAA TATACTGGTACTATAGGCAAAACAGATGCA
WI-20721	72	T C	---			CCTGCAATCACAAAAGTGAACACTAGTTGATATTTTGAAATCATACTTGATTTAACCCACTTCAGAAA TTCTAT/CJAAAACACTAGCAACTTCCTTTTATCAGA
WI-19415c	161	A G	---			CTGGATTTTAATATTTCTGGCTAATAACCAAAATGTAATCAATAAAATTTGGTCAATATCTCCACCTC ATTTCTGCTAACATGTTTTCGAAGATTCCCTAAGTAAGGTAATTGACGACTGAGACTAGTCCGGCAAA GTCATGAGACCCCTTAGCTGATCTCAT/GJAAGTCCACCTCATGAAGGAGATGATTCAACATCTCAA GCTAAGGTATAAAGTGTGGACATACAAAGGCTTACAAGTTTACACTTCCTG
WI-19348c	103	C T	---			GCTGCTCACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTACGATGGGCCATGCACCTCTG GCGGTCGATGAAGAGACTGTTGGTCATGGCGGTGA/CJTCTCTCCAGGCTCATATGGATGTCTT CGAGTTGCACAGGGAAGTCTCTGCTTGTAGAAGCTCTCC
WI-19348b	98	G A	---			GCTGCTCACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTACGATGGGCCATGCACCTCTG GCGGTCGATGAAGAGACTGTTGGTCATGGC/GJAJGTGACGTCTCTCCAGGCTCATATGGATGTCTT CGAGTTGCACAGGGAAGTCTCTGCTTGTAGAAGCTCTCC
WI-19635	98	A T	---			ATTAGTTCGTGTTGGGCCACATTCAAAGCCATCCACACAAGCTTCTGTAGGCCATTGTAAACACAATG TTAAAAGGTACAGTAAAAATACAGTATTAT/AJATCTTATTGTGTAGCACGGCTGTGAGGCTCAT GTTGAATGAAGCATCCTTAGGCAGCACGTGACTGCATGCAGATATGTGTGCTGAAAGAACTTTTGCCTT T
WI-19641a	46	A G	---			TCCAATTTTCAGAAACATGTTCCATGTTTATTGIGATAAGCAGTAG/AJATATTATAGTCTCATGTTT TTAATTTATGAATAACGTCTGATTCATTTGATTTTGTATTACAGAAGATGTCAGGGCTATCTCATTC AGTTATTAAATAATGGATCAGAGTAGTAAGTCAAGAATAAGTGCATAATGIGGTTTAAATTTTAAAA AATCTCAGAAATGAGGTAGTATTTTAAATTTTAAATTCATCCACCCACTTG
WI-19642b	52	C A	---			ATATAGGTACCATCCATGGTTTCAAGCATGGCCTGGACACATTATCCCCCT/CJAGGGTAAACCAG GACTATTGCATGAGCATCTTTAATACGTATTTTGTATGGACACAAGTTTTCATGCTATTA
WI-19673b	180	C T	---			TCTGCCATGATCACATTTGTATGAAGAACAATGATGGTCACTAGTAGGTAACCTTCTGTGTCATTGCCT TACTCTAGTGGGTGCTAGTGGATTACCTACCCCTGCTTTTGCATCACCAGTAAATCTAATAGT GAAAGGCCAAATGATGCTCAGTATCACTGTGAAAAACATTTTCTCTTGGACCAAGCTGAAAGAA TCTTGAGGAGCCTGAAGGCTTCAAGGTTCCACAGCTCAAAAAACACAGCCC

WI-19673a	35 G A ---	---	TCTGCCATGATCACATTGTGATGAAGAACAATGATG/GATCAGTAGTAGGTAACCTTCTGTGTCATTG CCTTACTCTCAGTGAGGTGCTAGTGGATTACCTACCCCTGCTTTGTCATCACCACCTGTAATCTAAT AGTGAAGAGGCAATGATGCTCAGTATCAGTGTGAACAATTTTCCCTTGGACCAGCTGAAAGAA TCTTGAGGAGCCTGAAGCTTCAAGGTCCACACGTCACAAAACACAGCCC
WI-19724	35 A G ---	---	TTTATTTGGGAACAACAGGATTGTAATTTGGGTAJAGJCTGAGTCACGGTGGCCCTGAGTAGTGTC CTAGAAAGCAACACGAGATTTGGTTTTCTCTT
WI-19307	196 T C ---	---	TCCTCTCCCCCACTAGATGGTATTGATCACTCTGCCCAACAATGGTACCCCTTTCAGCAAGAATG CAAGCCCTCTTGGATTGCCCTTCATGAGAAAATGGTGGCTGGGATGGAGGTGACATTCCTTGGTGT GGTGAATGCAAGAAGAAACAGGCAATGTATCCATAGAGGCCCTTTAAAGAGACCCG[T/C]TGG AAATGGGCCATGGTCTAATTTGGTGTGAATAAATAACCTCTTTGGCTG
WI-19269	85 A T ---	---	CTTCCCTCATCCCTCTTCCACCAACACATCCCGGAACAAGTGTCCAGGATCCCTGCCCACTGGC CATTTTGGAGTGTGTCJATTTGGGTAGCAATGTGGAACCAACCCAGGGCCTTTGGGAGAAAATGG AGGGGTTGAGGAGTCCAGAGGGGCTTATTGAGGGCCTTTGCCACTTGTCTATAGCGGAGCTCG ATCTCTCATCATCTGGACAGGTGGAAGCGAATCTTCCCGGGCGTAGGCA
WI-19946	122 C T ---	---	CAATGGACTGAATGAGTGCCTGGTGGGTGGGGACACACACACCTTCAATACACGTCAAGGTGG CTTCCAGTTTTAGAAAACAGAAATCTGCATCTCAGCTGAGACGCACAGAGAGGT[C/T]TCTTCTGTG ACCCAGAGCACTCACGAGCCAGGTCTGGTTTTCAAAACTGCAATTAACCTGCGCCAGAGAGTTCA CGTAGGCATCTTTAATAAACTAATCCAGCAAAATGTGGGTACGGTTACTAA
WI-19956	141 G A ---	---	CACAGCATGGTGAATAGCATCAGATTGAATGAAAAGTTTGTAAATGCAACCATAAATATATA ATAAATATACATCAAGTAATTTAGACACACATTTTGGGCCAAGTTTGGATCTGTCTGGACCT CAATGT[G/A]CTCTCGGAGAGCAGCCACGTTAGCAGCAGATACCTTACAGCTTGTGATCTACTCAA GTGATGGCCCAACAGAAGCTTCTGAATCCTCTCTGGGAGGTAGCTGACAAG
WI-19076	40 G A ---	---	TTGGTTGGATACCTTGTGGAACAAAAAGCAGTTTTTAAT[G/A]GATTCAAATACCTTTTAAAA GTATTCTAGCACAAAGATTTTCTGTAACTAGATTATGTTGTAACCTTTTCTAAATCTTGTAGGAG TGTCGGTTGTTAAGAACTAGAGCTTATCCTATTCCAAATCTATCTTGGCTCCTGAAAACTGCAGA AAGGCATTTGAAAGCTGTTTCTTAAAGATATGGGATTTCTTTTATCTT
WI-20218	26 T C ---	---	CCACACACTCTGGTTTTATAAGCTAT[C]JAGGACAGAGCAGAGATGGAACCTGAAAACAGGGTAG AAAATAACATAAATTGGAGGGGAACAGTGGGATGCAGAAAGAATGACAACAGCCACATGTGCCCA GTCAAATACTTTTAGTCCCTGCAGCAGAAAGATGCCAACCAAGTCTCTATCTGCTGGGGATCCTGCC ATGGATGCAGGAGAAAA
WI-20295g	154 T G ---	---	CAACCTTTTGACAAGGGGACGTGAATTTCTGATGAAAGTTATCTTACCAAGTTTAAATTCATAATTG GGAATTCCTCTTTTAAATATCTCAGGCTTGAATGGGAGGGCTGGGCTCTACCCCTTCTCTTCCCA TCCAGTCTATTGCCAGAT[G]CCAGAGAAAGCGGGGAGCCAGCTCTCCAGCATAGCCACTGTGG GTCGGCTTCACTTCTGTGACTCTCATCTGCTGGGACTTGTCTTTGGGG

WI-20361a	192	G A	---			CTGGAGTGTGACCTAAGTGACATTTTTTTTAAATGCCAAATACAGTAATCTCCAAGCTTTTAAATGG CITATGCAAGATGACAGAATATGTGAAATCTGATTTGCCAGAGTTACACTCTGCAGCTCCAAAGCTA CAACAGTGCCACAGCTGAGAGTTTCCCTATATCTCTACTACTGTGACAAATTTAGC(G/A)ATCCTTC AAATGGGAAATTCCTAACTACAGAGACAATGGGTCTCTACAGTAGGCCCG
						GAGCCAAACCCCAAAATAAAACAGAACTCTTTTGTAAACTAAGTCATACCTACTTCTTCT TCAGAAAT(G/J)TCATAAAACATCATCTTTACAACATGGAGAGCGAGGTAGGCCATAATTTGTTCA AATTCATCTTCTCAAAATTTAAAATTTGTTTAAATCCCAAGGTGCCTATTGAATCTTCAAAATA AACTGCCTATCAGGTATCATACCTGCAAAATGCTTCTAATATCTCTTGATTAT
WI-20572	75	A G	---			CATGACAAAAGACAAAGATCAAGGAGTAACATAAATTAAGTTGAATAATAGTATACAGCAATC TTCACTTTTTAAGAAATGTGAGATCCTTTGTTGGTTTTTATTCCTTAAGTACAAAATGCTAAAAC G(A)GGAGCCGAGCTCTCCGCATTCAGG
	133	G A	---			TGACCTCATACTGGTCTGTTAGAACACAGCCACTAGAACAACTCCAGTCTTTTTCAGTCTGTTG CTGTACTTCAG(G/J)TTAAAATCTGGGAATGAGCATGCAGCAATGCTCCACAGATGAGGAAGAAA AGCTGTTAAAGGAACCTCAGGATGTTGTTAGGAAGGGGAGTGATGCCAGGCTTCACCCAGACTAT CCAGAAGCCATTCATGGGTATTTGGTCTGCATCTGTGAGACACTGAGCT
WI-20593	79	A G	---			TTCTTTGCCAAGCCTGTTCTCAAGTTATTCAGAACTGGGTATACCTTGTCCCTCAT(C/J)ATGTATCT TGTCCTGCTGCTTTTAGTTAGCAAGGTGATGAATACCTTTAAGTTTGTGTTCTTTTCTCGT GGTATCAGTGAATACTGATCTATCTCTGGCTAGGGTCAATTTACAAAATGCCATGGAAGTGGC AAAAGGCCACGTTGGGATAAAATCACTCACCATCGAGCCACCCAGTATT
	57	T C	---			TGACAAGGGAGAGAGGGAATTCCTACTATTGCAAGGAATCCTCACTTAAGCTTCAAGTGAGCCAC AAGCACTTAAACCCCATGAACCTTCAGCTGATCGTCCCTAGCCAGTCCAATCTCTACGAGGAAGTGG CATATGTTCTTGCCTGGTGCACCCCTGAGCTGAATTAATCTCTCCATATCCGGATGCTCAATTACAGT ACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCACTA(G/J)GTTCTTTT
WI-19066i	239	A G	---			TGACAAGGGAGAGAGGGAATTCCTACTATTGCAAGGAATCCTCACTTAAGCTTCAAGTGAGCCAC AAGCACTTAAACCCCATGAACCTTCAGCTGATCGTCCCTAGCCAGTCCAATCTCTACGAGGAAGTGG CATATGTTCTTGCCTGGTGCACCCCTGAGCTGAATTAATCTCTCCATATTC(J)GGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTCTTTT
	184	C T	---			TGACAAGGGAGAGAGGGAATTCCTACTATTGCAAGGAATCCTCACTTAAGCTTCAAGTGAGCCAC AAGCACTTAAACCCCATGAACCTTCAGCTGATCGTCCCTAGCCAGTCCAATCTCTACGAGGAAGTGG CATATGTTCTTGCCTGGTGCACCCCTGAGCTGAATTAATCTCTCCATATTC(J)GGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTCTTTT
WI-19066g	184	C T	---			TGACAAGGGAGAGAGGGAATTCCTACTATTGCAAGGAATCCTCACTTAAGCTTCAAGTGAGCCAC AAGCACTTAAACCCCATGAACCTTCAGCTGATCGTCCCTAGCCAGTCCAATCTCTACGAGGAAGTGG CATATGTTCTTGCCTGGTGCACCCCTGAGCTGAATTAATCTCTCCATATTC(J)GGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTCTTTT
	148	T C	---			AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTCTTTT

WI-19066e	147	G C ---	---	TGACAGGGAGAGAGGAAATTTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAAGTGG CATATGTTCTTGCG[G/C]TTGGTCAACCTGTAGCTGAATCTCTCCATATCCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAACGGCTTCAC TAGTTTCTTTT
WI-19066c	100	G A ---	---	TGACAGGGAGAGAGGAAATTTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCG[G/A]TCTTAGCCAGTCCAATCTCTACGAGGAAC TGGCATAATGTTCTTGCGTTGGTCAACCTGTAGCTGAATCTCTCCATATCCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAACGGCTTCAC TAGTTTCTTTT
WI-19066b	87	C T ---	---	TGACAGGGAGAGAGGAAATTTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAAC[C/T]CTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAAC TGGCATAATGTTCTTGCGTTGGTCAACCTGTAGCTGAATCTCTCCATATCCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAACGGCTTCAC TAGTTTCTTTT
WI-19066a	72	C T ---	---	TGACAGGGAGAGAGGAAATTTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCA[C/T]TAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAAC TGGCATAATGTTCTTGCGTTGGTCAACCTGTAGCTGAATCTCTCCATATCCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAACGGCTTCAC TAGTTTCTTTT
WI-20660	105	G C ---	---	TTTACAGCGAGTTTTCCTGCTCAATAAGTATGAATCTAAATAGATTAGGGTGAAGAAAATGTG TGCTAAATAAATCTCCCTTTTGAATGATATTTG[G/C]TTAATAAGGGAAGCATTAAATATTA CAGACATATTTACAAGGTTCTGAACATGAGTATTCCTACTGTTTCTGTACAAGATAGAACAAA AAGCTATCCACCCCGCCCCAAAATACTGTTTAAACAACACTATGTTTAAAGA CTGCTGCCAGCTTCTCTTTGGCCCTGCTCCAGATGGCGGTCTCTGGCAGCCCTCCCTCAGTCTTCC TCCACCCGCTCTTCTTCCAGCCTGCTGCATGTCATGTCACCCCTGGT[C/T]TTCGCTCCATCGGC TTGAAAGCTCTGAA
WI-18768	120	C T ---	---	TTCCCCAGGGTCTGTATTGCAAGCTCAATGT[G/T]ATTAACTTCTAGTTGCTTGTCTTGTG GTCCTTCTCCAATGATGCTTACTACAGAAAGCAATCAGACACAATTAGAGAAGCCTTTTCCATAAA GTGTAATTTAATGGCTGCAAAACCGGCAACCTGTAACTGCCCTTTTAAATGGCATGACAAGGTGTGC AGTGGCCCCATCCAGCATGTGTGTGTCATCTTGTGATCTACCTGCTCC
WI-19087	37	A G ---	---	GAAAGCCAGAGATTAGCCCCGATTCCGCACTGTCAACCCAGGACAGAA/[T]GCATGGACAAGGGA TGAGCTTTACAAAGATGATGCACCTTTGGAGATCAGAAAAATTCATATTAAAGCAAGTGATACAAACA CAGTGAATTTGGGAATGCT
WI-18790	49	A T ---	---	AGGAGGCTGTTCCAGGATCCTGCCAGCAGCCT[G/A]GTGGCCAAAGCCAGACACTCACCCACCTT CCCCAGTGGCCCCGTGGATCCTGGTCTAGGCTGGACAGGATTACAGAAAGACACCCAGGCTGCACA GAAAGCCAGATGGACCTGAGTGTGGTCCACAGCCCCCTACACTCAAGGCTGAGAGGGCCTCAGGAA AGTCA
WI-18987	35	G A ---	---	

WI-18919	26 C T ---				TGGATGAAACCACAGGATTCCGGA/C/TGCCAGACCCCAATTTTATACATTCACATTTCTCTACAGTG TTGTTTGTGTTGTTGTTTATTTTATACATTTGGCCATACCACAGAGCTAGATTGCCAGGTCT GGGCTGAATAAA
WI-18741c	64 G A ---				CTTCTGTCAAGGCTTTGGACATCTCTCAGTCATCAGACAGAGTATCTCTGCTTAGACCTC[G/A] CTGGAGTTCAAGCTTGAATTATATATGCAAGTTAATTTTACAAGCCGTGATGAGGCTACTGA
WI-18741b	38 G C ---				CTTCTGGTCAAGGCTTTGGACATCTCTCAGTCATCAGACAGAGTATCTCTGCTTAGACCTCG CTGGAGTTCAAGCTTGAATTATATGCAAGTTAATTTTACAAGCCGTGATGAGGCTACTGA
WI-18741a	23 T G ---				CTTCTGGTCAAGGCTTTGGACAT/G/CTCTCAGTCATCAGACAGAGTATCTCTGCTTAGACCTCG CTGGAGTTCAAGCTTGAATTATATGCAAGTTAATTTTACAAGCCGTGATGAGGCTACTGA
WI-19179a	170 G A ---				TCAGAAAGCAGACATGGCATCTGTTCTGCTTGTGTTGGTTGTGTAACCTTCACGAGACCTGAATT TTAGAAATGCCAGTCTGCCAGAGTGAGTGAGTGAATTCCTCTTCAGGTAAGATAGGCTATCTC AACACTGCTGAGTGATTATATAACATATCAACCA/G/A/TAGCAATTAACCCATTTTATTCCTGTCTT AGTGTCTGAAGATGCTCACCAGTTTCTGTGTACAGTAAGGCAGCATGCT
WI-19212	46 T A ---				CCAAAGTGCATCCATGTTGATTTCTGATGAGACTAGAGTGACAG/T/A/GTTTTCAGAACCCAAATGT OCTCAGGTAGTTGGAGCATCTCTATGAGATGGGATATGAGATGGCCTATGGAAATGCAGCTGC ATAATTAAACACATTATCAAGTCTCTTACAAATTTATTTCCGACGATGTCAGCTAAGTAGACCCA ATGGGAGAGAAATGCCTGCTTCTTCCCTCTTTCTGCACTGCCATAT
WI-19183	210 G C ---				CTGTTGAAGGCTTCTCAGGCAACTCCAGCTTAAAGCCCTAGACAGGTAAAGCACACACATTGGATG GCAGCATGGTTTCTTCCCATTTATGGGATGAATATGTGTTAGAATAAGGAACAAGCATATT CCTTTGCCAAGACGCTCACTTAAGAGGCTTTTGTGCTGAGTCAAGCAACACACTTGCCTGCTGCC CTTGGAG/G/CT/GCATTTGACCTGCTCTCACTGGTAAGGIGACTTGGTGGC
WI-20014b	214 T C ---				TTGAAATCCAGTCTCCTGGCCCCCAGGCAGGCTGTCTACCATAGAAATGTCTCTACTGGGTC GTTCTGGCTTTTGTAGAAACTTGGTCTGAGATGTTCTTCCCTGTCCATTACCATTCGATGTTCTTT TGTTCAAGAGCAATGTTCTTGTATTCTGAAACTGGAACTGAACCAAGTTTGCCTTCTCCTAGTCACC AAGCATACT/T/C/JTCTGGCTCCCCAAGTACTTAAATGTTCTCATCTGT
WI-19041	198 T C ---				GTCTCCCAGAGTGTCTTGACCCCCAGCCCCGTCTGCTGCTGTAAAGGGATACAGAGAAGCTCCCCG TCTCTGATCCCTTCCAGGGGGTGGCTTAGTTGGACATGCTGGGTAGCAGGACTCCAGGGGTG CACGGTGAGCAGATGAGGCCCAAGCTCATCACACCAGGGGGCCATCCTTCTCAATACAGOC/T/C/G CCCTTGCAGTCCCTATTCAAAATAAAATTAGTGTGCTCTTGCCTGCTGT
WI-19135	20 G A ---				CAGTTACCTGCTTTGCCCTC[G/A/JAAAGTGTCAATCAATTTGTAAATTTAGTATTAACTCTGTAAAGT GTCTGTAGGTACGTTTATATATAAGGACAGACCAAAATCAACCTATCAAAAGCTTCAAAAAC TTGGGAAAGGTGGGATTAAGTACAGACACATTTGGCTTACAGTAAATGAACGTGATTTTATTAACT GCTTTGGCCCATATAAATGCTGATATTACTGGAAACCTAGCCAGCTTAC

WI-19236	54	G A ---	---	TACACAGAGGGTCGCACCTTGAGCTCTGAGGGTGGGTGTGGAAGGGGGAAGG[G/A]GATGGAGAC CTGCTCCCCAGCTCTTCTGTAGCCGGTTTACATGGGAACAGGGTTAACATCTGTGTAGGGGAGGT CACCTTACCTTTTTCATAGGGAAGAGTGTACACCTCTCGCTATCTCAGGGGAATGGGGAAAAG AATCTTCAAGGGCAAAGACTCGTGGGAGGATGCTGTGTATGTATACT
WI-19144	222	G C ---	---	GTGCCAGTCTTCCAGAAAGCAAGGACTGCCCTTCATTACGCCCTTGTGACCTCCAGCCTTCTTAAGG CTCAGCCACAGGGACTCTGGTGGCTGCCAGCTTGTGAGCTATCTATCTATATTCATTTCATAGCCAA ACAGGAGACCCCTTTGCAGGACTTGCACACAGGAGGCTGTAGCCAGGAACCCCTCTCTTCCCTGGT CTGGCTCTGCTGGAGCGG[G/C]TGGGAACCAACACCTTCAGTGTGGTG
WI-19139b	110	C A ---	---	CCCGTCTAAGGGAGAAAGCTAATGTTTCCACAAGACTGAACAACGTGTATTTACACGAGGGTAGAC GGCAGATGCCCTGACAGAGAGTGGTGGCAGACAACACTAG[C/A]ATTTACGGGTGTGGGCAC ATGGGTGTGCCACCTGGACGTGTGCAGCATGTGGCGTCTCTGTGGAAGCCCGTCTCTCTTTGG GGGGCCGCGAGATCTAGCATCTCTGAAATCCTGGCTGTGAGGCTTTGAAG
WI-19139a	66	C T ---	---	CCCGTCTAAGGGAGAAAGCTAATGTTTCCACAAGACTGAACAACGTGTATTTACACGAGGGTAGA[C/T]GGCAGATGCCCTGACAGAGAGTGGTGGCAGACAACACTAGCATTTTACGGGTGTGGGCAC ATGGGTGTGGCACCTGGACGTGTGCAGCATGTGGCGTCTCTGTGGAAGCCCGTCTCTCTTTGG GGGGCCGCGAGATCTAGCATCTCTGAAATCCTGGCTGTGAGGCTTTGAAG
WI-18910	112	T C ---	---	GGCTGGGACCTTTAGGAAGTGAAATGCAGGTGAGAAGAACCTAAACATGAAGGAAAGGGTGCCT CATCCAGCAACCTGTCTTGTGGGTGATGATCACTGTGCTGCTG[C/G]GGCTCATGGCAGAGCATT CAGTGCACGGTTTAGG
WI-19235	173	A G ---	---	TTCAGGAGGTGGAGTTCGTCAGCTCTCCTGCTGTGATGTGGAAGCTTCTGATATTTGAAGAAACA CGAATGTCTGTAGCTTCTCTTCACTGCCCCAGTATGCTCTGTATTTACAGCGATGCCCTCTGT CACTCATGCCCTGCCTAATGTTTCACAATGGTGGAA[G/G]CTTCATGTAAATGATCAGGACCCACC TCCAGTCTCTGAAAGTGTACAGTGTCCAGCCGGTTCTGCAGCCTA
WI-19222	179	C T ---	---	CGTTTCCCCTAACTCACCCAGTTTAGTTTGGGATGATTTGATTTCTGTGTTGATCCCATTTCTAA CTTGGAAATTGTAGCCTCTATGTTTCTGTAGGTGAGTGTGTTGTTTCCGCCACAGGAAGT GGCAGCATCCCTCTCTCCCTAAAGGGACTCTGCGGAAC[C/T]TTTCACACCTCTTTCTCAGGGAC GGGGCAGGTGTGTGTGGTGTACACTGACGTGTCCAGAAGCAGCATT
WI-19117	134	A G ---	---	AAATAATGCAACGCAGGAGGAGAAAGAAATGCCTAAGACAAGAACATCTCTCATAGAACATTG ATCTGTTTACAGGAAACAACTTGCCTTGAATTTACACAGTGAGACTGTACATAATTGCATGAA A[A/G]TAGCTATTTTTTCCCTAAGACATTTTTCATTCATGATATTTTCAAGTTTTCATACTGTACA CATTTCTTAAACACATGATACCCAGCAGCACTGAAATGAATGCCGAATTTG

WI-19134c	263	CT	---	CTCCTGTTCTGACCTGACAGGGTGACACAGCCCTTTCACACTCTGCTCCTATCTTCCTGGGTAGA TGCCCTGGTGTAGGGCTAGTACTGAATGGTCTTCCATCCCAAGCAAGGGGTGCAGCCAGGGTCTCAG GCCCTTCAGAGCCAGGGCTAGAGATGCACGGTGCTAGAGCCAGCTGCACATCTCTTTTCAGAGCAC TTCATCCACTTGCTCCTCTACCTCGGCACTGGTGGGAAAGGG
WI-19134a	162	TC	---	CTCCTGTTCTGACCTGACAGGGTGACACAGCCCTTTCACACTCTGCTCCTATCTTCCTGGGTAGA TGCCCTGGTGTAGGGCTAGTACTGAATGGTCTTCCATCCCAAGCAAGGGGTGCAGCCAGGGTCTCAG GCCCTTCAGAGCCAGGGCTAGAGGATTCGACCGGTGGCTAGAGCCAGCTGCACATCTCTTTTCAGAG CACTTCATCCACTTGCTCCTCTACCTCGGCACTGGTGGGAA
WI-19224	112	CT	---	GGTTTCACCACTTTCCCAAGGAACTCCGATGAAGTGTCCACAAAAATGAGCGAGTGAACCAAGA AGAGGATGACATTAGATCCAGGAGATACACAGAGGAGATAATCTCTCAGGATGCCCTGTGAAGA AAGATCCCTGGATCCAGGATGATTATAGGACAAGTTTTCATAATCCAGCAGGCCAGAGACTTCC AGGAAACTCATCAAGGAGGTGAAAATGATGGATGACTCCTCCAAGATGAAAA
WI-19201	179	TC	---	GCAGCTCTAAGGACCACTGGCCATTAGCTCTTGCTTTTGATGGCATCTCTTCCACCTTGCTCTC CTTTGCTCCTCTGTGTAGTGTGGCAGGTATGACAACTCATCCAGTGGAAACACAGCCTCACACTGCC CTTCGGCCCCCACACTTTGCCCTGAGGTGCACCGAAAGGACTTCCTGGGGATATAAATTCAAAAA GTGTGATGTGCTGCTCAGAAAGGTGAGACTCCATGTCTGCTGGCTCAA
WI-19034	45	TC	---	GAAATGGCTCCACTCAGAGCTACCCCGGTGATGAGGATAGGGGAATTCACCTCTATTACATTAAG GCAACAGCAGTTAGTAAAGGTTTTACAGTGTCTGCTGTTGAAAGTGCAATATAAATTTTTTG CTAGCCCATGATCAATCGACTTCTATTGTTTGATATACACTTCAGCATTTAAGTTCTGTCGAATTGAC ATTGCTACTTATAAACTTAGTCCCTAAGTCTCTTATGCTGTGCTATATA
WI-19102	25	CG	---	TGTTCTGAGTCAAGTGAAGAGTCGCTTCACTCAGGATTCATGATGATGATCATGATGATGATGATCA TGCGACGTATATTTCTTTGGAAACAGATGAAGCAGAGGAACTCTTAATACITTAATCGTTCT TGATTAGTATCGTGAGTTTGAAGTCTAGAACTCTGTAAGTTTTGAACCTCAAGGGAGAAGGTAT AGTGAATGAGTGTGAGCATCGGGCTTTGCAGTCCCATAGAACAAGAAATGGG
WI-18548b	65	AG	---	AAAGGAGGGAGAACTCTTTTACATAAAATGCCCTTGATCATCTCCAGTCCCTCAGTGGGGAAT/ GJAAAAGCATCTNTCAAGTCTTTTGCCAACTTTGGCTGC
WI-18548a	62	GA	---	AAAGGAGGGAGAACTCTTTTACATAAAATGCCCTTGATCATCTCCAGTCCCTCAGTGGG[GJAJA AAAAAAGCATCTNTCAAGTCTTTTGCCAACTTTGGCTGC
WI-18700	97	TC	---	GGCAGCAGCTTTTAAATTTGAACACTTTCTCTTGAGGACACACCTTCAGTACAGTTAACAAATGGT TACACTGAAATCTGCTGAGAGCAGAGCTTT/JAAGATCCACAAATTCGAAAGGCCACTGCTGGCTCA CTTCTCACA
WI-18501	121	CT	---	CAGAGGGAAAAAGTTTATTAGTCAGCCACAGAGGAACAGAGAAACAGACACAAGGAGGTTCTGTGT GCATGGAGGAAATCAGGGGCGCCGNACAGCTGAACCTCGCAGGACAGAGGGGGG[CJTGACAGCA GCGCATGCCACAACATTC

WI-18017	87	C A	---			ACAAAAGAAAATGGAATAGGTTTGGAAAACTTATCTGCATGTACAAAAGTAATCCCGTAGATAA GGAGAGGCAACCCNGGAACA[C/A]ACTGCTGGATAAATCGTTTCATTAATAATATATCTCTTTGCAT CAGAGCTGGTGGAAAATCAT
WI-18148b	101	A G	---			TTATTGGGTTCTTCGATAACCTCTCTTTGGGACTATGAGATCATCACCAGATGTGAAACGAAAGCA GTGATTTTCAGAAACCCNTCGATTCTGAATATCC[C/G]TGGCGGCATATGCAAGGAAGATGA
WI-18254	64	T C	---			TATACGGATCATGTATTTGTGTGACCACCACTACCACAGTCAATTTGTAGAGCAGTTAAATCACT/C GCCAAAATCCCTCTTGGCTTCTTGTAGTCAGTCTCTCCCAACCCAGGNACITGGCAACCTGTTT TCGGTTCCTAGACATTT
WI-18265b	117	C A	---			CAAATGGGTGGACTGAGTGATAAAACGCATATTGAGAACAAAGACGGCCTCTGGCCNCTCTGGGTCC AAGGCTGTAAAGGTCTCAGGATTGCTGCTAAGTGAGCCATGAACCTGGCTG[C/A]GTTTTCAACCTTTC CTTGGGTGGTTTCTTCAG
WI-18295	40	C T	---			ACCACACATTTGTTGAGAGCCCTATTGTGGAGAACAAACAG[C/T]TTGGGAAGTAAAGGTTGATTACT TCCTCTCCAAGGATGATATGTTAATGAATTCCTTTNCCTTAGCTTCATTCTTCATATAATGCCAAA
WI-18459b	64	T C	---			GGGCAAGAGACAGAGATTTAATTGAATAAAACTCCAGGCTGTGACACGGGTGGGAGACACAAAT/ C/GAGTAATTAACACATAATATTTTANATGACAGTGAATTAATAACGTCCTGGGTAAAGCCAGAG GGGAGGAGGGCGTCTTCA
WI-22585	56	A G	---			TTTATTTTAAATTTGCATCCTGAGATAATAAAATTTTATCTGACAAGTGAACAATG[A/G]CAGAAGC AGCAGTGAAGTTTCGGAGAGGCAGGTATCCTTCATTTGGCACAGCTGTATATAGATTGA
WI-21155	36	A G	---			GGGCTGTGGAGTAACAGAACTTGATGGAAAATTTGG[C/A]GTCTGTAGAAATGATTCTAAAGCTTTC AGACAAATGGCAGA
STS-F02766b	88	G A	---			GCCTTTGCTCTTTGCTGTCTCAGAGGCCCTCAGATGGATACGCAACTTCCTTTTGAACCTTTTAT TTTCTGGCAGGAAGAAG[A/G]GGATCCAGCAGTGAGATCAGGCAGGTTCTGTGTGCACAGACAG GGAAACAGGC
WI-19888a	98	C T	---			GGCAGATTCAACCCATAACAGAGAAAATACTCCTTATTGGAAAACAGGTTTTATTTTATATGATG AAAATATTTTGGAACTAGAAAGTAGCAGTG[A/C]TTGGACACCGTTGTAAGATATTAATGCCACT GAACTGTTCAATTTAAATGGTAATTTTCATGTTATGTATTTTACCTCAATTAAAGAAATGGAACATGT CTTAATATTGTAATTACATGAGANCATATTTATGTTGGAAGTGAACACAAAG
WI-21485	82	C T	---			TGAGACCATCCTCCTCAACAAAGAAATCAGTCAGTTACGACCTAATTTTCCACACTGAAGTCTACG CAATTTTCATGCAG[A/C]TTGTGCACACAGTACAGTGCACAAATCCAGAGGGCAACACATTTGTAATT CATATCATCCGTTTCCAAA
WI-20601a	125	T C	---			TCAGAAATGCTTTCCACTGCCCAACCAAGAAATTAATGAATGCNCTTACAATTGAGATGACTT GAAGTTAAAGAAAGGTACCTCCTTGAGGTTGCATGACAGGATTAGTCTCTCTGTTT/CJCTGGT GCAAGTTTGAACCAGTGATTATGTACCATTTGCATCAGAGCATCTGTTCCCTGTCAGATCCCCACTAG

WI- 20561b	94 T C ---			CGTTGCTATTAAAGATGGCTGTTTATAAGTATAAAGCAGTTTGAGCAACACTGATTGTGCAATTATG TACTTCAGATGAAAAATCCTTACATGT/C/GGAATCAATGTCTTTTAAATTTTCAGATAAAGAAATTT NCATTTGAGGAGACATACAATTGTAA
WI- 20561a	25 A G ---			CGTTGCTATTAAAGATGGCTGTTTAA/GTAAAGTATAAAGCAGTTTGAGCAACACTGATTGTGCAATTA TTGTACTTCAGATGAAAAATCCTTACATGTGGAATCAATGTCTTTTAAATTTTCAGATAAAGAAATTT NCATTTGAGGAGACATACAATTGTAA
WI- 20116e	69 T A ---			GCCTTCATTTCTGTCAACCCCTGTCCACCAGTTATGTTGGCCTTCAATATATGGCGTTAGAACAT A/T/AJATAAATCTATATCATATATTTATACACACAAACACACTTCTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGGCCTCTCCCATGCCACTTAAATGNGCACAGGTTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI- 20116c	59 T A ---			GCCTTCATTTCTGTCAACCCCTGTCCACCAGTTATGTTGGCCTTCAATATATGGCGTT/JTAGAA CATATAAATCTATATCATATATTTATACACACAAACACACTTCTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGGCCTCTCCCATGCCACTTAAATGNGCACAGGTTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI- 20116a	22 C G ---			GCCTTCATTTCTGTCAACCCCA/C/GJCTGTCCACCAGTTATGTTGGCCTTCAATATATGGCGTTAGAA CATATAAATCTATATCATATATTTATACACACAAACACACTTCTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGGCCTCTCCCATGCCACTTAAATGNGCACAGGTTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI- 20466b	133 G A ---			AAAGATTGCAGTCTGGGACACAGTTTGGAAACACTATTATAAGTTGCACATATTACAAACAG NTCCCAATGGTGAACCTGGTATTCTAAGATGAAGCTTAATGAACATAATGAAGTGAATAAACGC/ G/JGTGAACATAATGTTTAAAGTTAGAGCTTGCTCAAGTCAGTACAGCTCTTAAGATAATAAAT ACAGTAACACTACTTTTATTTCTTGTCTTTTATCCCTTTCAGGTTGATT
WI-21444	39 A G ---			CTGGGCAGCAAGTAACCAITTTAAAGAAATAGTCTCAAC/GJAGTCTTTTTTTATGGGGTATTTC GTTGTTAACAAAGTTAAATACTATTGGAACATAATCTTTGATTTTATCGAGGAAGAAGAAATCT ATAAGATTGACTTACTCATTTGTTGACTGGTTTTTTGAAGCCTTACTGGGG
WI- 21034b	148 T C ---			AGAATGGACAATGATGCAGATGATTGTGAGCATTTTGATGAGAAAGTGGTATTAGAAGGATACAG CATAAATTTAATTGTAAACATGCTTATCTAGCTAACCTAATCTGTTCTGTAGAATTACTGGTCATGG GAGATTGGATAGAT/C/GJCCCTAACCTATCTCAATTTTAAGTAATGTAGCAA
WI- 22091c	205 G A ---			GGCGTGTATTGATGCAATGTCCAACCAAGTCAAGCTATCATTTGAATCCAAATATTTCCAGTAGAG ACATGCAGAGCAATGTCAATGTAAACATACAGCATATTACCTCCCCCTTAAGTACTCATATAATTC ATTACTGTGTCTGTAGCTTTTAAAGGTTTAAAGTTTAAAGTGTAGCATTAAGTGGTATTACTTGAGGGCA ACA/G/AATTACGGCTTAACAACACACACTAAATCATGAGGCTCAGGGATTG

WI-21805a	45 A T ---			CAACTGCTGTGAGGCTTTCAC TAGCTGATTATAATCCTATATTATJAAAAAAAAAATCTATAGTCTG CAGTCTTTTGACATAC TCTCAAGGGTGGATATGTGGTGAATGACAGATCCATCAATATGTGTGGTT TTGTTGCTTTTGTAGCTTAAC TGTCTGTTT AGNAATCCAGAGGAATATGATTGAGGCCAGAGTTA CATTGGTTCATAAAAAITCGAACAGTTGAAGGCTGTTTTGTTAATTGCTG
WI-21778b	155 T C ---			AAAAATCCATAATATTGAAACCCCAAGTTACAGAGAAAGTTCTGTAAC TTTTATTGAATTATTGAC TCTGCCCGGTGCTGTTGCTGCTTCAAC TCCAGTCTGTAATGCOOCTGTGTAGTGGGGTCCCCAG GTCTGGGCTTCTGAGGTCCTCJGGTAGAAGGAGGGCAGGTGGT
WI-20907	241 A C ---			TGAGTCAGTGGTCAGATGGGGCAGTTGGCTCAGCTGAGTCCCTGACTCCCGGAAACACTGTGCTCT CAATGATCTAGAGCTCATCTTGGGGTACATGAGGGCAGTTGTTGTTCTAGTACCCATTTAGCCC ATGGCTCTCAAGCCAATTCACACTGGGAAAAACACACCCCTACAAGATGCCTATCCATTTGAGTTG ATACAGGTTTGTAGCTAGAACTAAAAACATTTTTTA/CJAJAATTAICIA
WI-21449b	222 C T ---			AACAGCAGCAGTCAC TTTCCAAAATGCAAAAAAATTAACAATTTT TAGAATAAAAATTATAATGTTTA TAATCGGGGTCAAGANITGAAGGTACAACAGAAATCAATCAACGACACTGGAGGGCGGTGGAG AAGCCAAAGCCCACTGGTCAGGGGTCCAAAGCTGACAAGAGTCCCAACCTGAGAGGTCTCCACAOCC AAATCATACCCCTCAGCTTCCAC/CJTJTGACAGAGCCAGTGTCTCTGGGTTAG
WI-21558a	157 G A ---			GC TTAACAGGAAGCCTGTGGACAGGCGAGNTGGGTGGAAACCGACTCCAGCCTGGAAAAACCTGCCCTC CCATCCCCCTTAGCGCTTCTGGCCTTCCGGCTGATTTCTTCGACAGCAGTTCTGGCCAGGGCAAGG AGCTGTGGTGGGGGGCAGTATG/AJAGCCAGGGACTCCCTTCCACAGATGAGGCCCTAGGGCTGCAA AAGGGCCCCGTGAAAGAGAGATGTGTGTC AAGGCTTTATGGGTCTCTCCACOC
WI-22187b	178 G A ---			TTTGCTGTGGAATCCATGAGAGCCGGAAGCATGCTTGGGGCCGTGGCTAGCAGAGCTCATGNGACCA GTCTGGGCCCTGACCAATGGGTGATTACATTTAAAAACCAACCAAAACAAACAAATACCAAGA ACAGATCACTTGCATGGACATCAGTAATCTATTGGTAATGGTG/G/AJAAATTTTCATGAAAAATTTCC CCTAAACCATACAAAAACTGTCTCTCTTACCCCAAAAGTGTGGAGGAAAG
WI-22187a	110 C A ---			TTTGCTGTGGAATCCATGAGAGCCGGAAGCATGCTTGGGGCCGTGGCTAGCAGAGCTCATGNGACCA GTCTGGGCCCTGACCAATGGGTGATTACATTTAAAAACCAAA/CJA/CAAAACAAAAACAAATACCA AGAACAGATCACTTGCATGGACATCAGTAATCTATTGGTAATGGTGGAAATTTTCATGAAATTTCC CCTAAACCATACAAAAACTGTCTCTCTTACCCCAAAAGTGTGGAGGAAAG
WI-21609b	146 G A ---			TCATGAATATGCAGCCTCCATAATCTTCTCCCTTGTAAACAAACGTGCAGTCCGTTCAACAGCTGTAAA AACAGCCCCAAACCAAGACATCAAGAGGCAAGACAGTGGCAGTGAGAGGGAGCCCTGTAAAG GATGTTTCAAAG/G/AJAGGGTCCCGGCTATGTGGCCACTGGATGTAGGCAGTGAGCTGAGTCCAGGC TTTCGGTCTGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG

WI- 21609a	42 C T ---	---	TCATGAATATGCAGCCTCCATAATCTTCTCCCTTGTAACAA[C/J]GTGCGAGTCCGTTCAACAGCTGT AAAACAAGCCCAACCCAAAGACATCAAGAGGCAAGAGTGGCAGTGAGAGGGAGCCTGT AAGGATGTTTCAAGGAGGTCCGGCTATGTGGCCACTGGATGTAGGCAGTGAGCTGAGTCCAGGC TTTCGGTCTGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG
WI- 22512a	104 T G ---	---	ACATTCGAGCCAGTTTTTCCATATTGCTCCACTGCCTAAATCCCTTGGTGCCTCCCTAGGGCTTCA GGGTAAGCCCTGACATCATGTGCTCTTGTGATCTG[J/G]JACCTCACCCATGTCTCCACCTNAGTTCC CACATTTCCCCACGCTTAAGGGCAGGCAGCTACACTTGACTGCA
WI- 21028b	139 A G ---	---	ATCGGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAATTTCTGTCCCTTTTAAGGGCTCA CAACACTAAAGATTTACATGAAGGGTCTGATGATTGAGCAATCTAGGGG[A/C]TATGTGACAG TTT[C/A/G]TGCACTGGTACAGAACACACAGGGAGTTTCACAATTTTTTATACAAATGCTTGGGAAT CTAOGG
WI- 21028a	121 A C ---	---	ATCGGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAATTTCTGTCCCTTTTAAGGGCTCA CAACACTAAAGATTTACATGAAGGGTCTGATGATTGAGCAATCTAGGGG[A/C]TATGTGACAG GGGTTTCATGCACTGGTACAGAACACACAGGGAGTTTCACAATTTTTTATACAAATGCTTGGGAATC TACGG
WI- 18829d	58 A G ---	---	ACAACATGCCTGTTACAGGGGGGAAAAATCCTAGGNAATAACTTATGTGTACTTCTTG[A/G]TTTCA TCATACAAGACAAGCACAAAAAGCACCCCATGCCTCTGAGGAACATTGGACCATGACCCCTTGAAA AA
WI- 18829b	35 T A ---	---	ACAACATGCCTGTTACAGGGGGGAAAAATCCTAGG[J/A]AATACTTATGTGTACTTCTTGATTCA TCATACAAGACAAGCACAAAAAGCACCCCATGCCTCTGAGGAACATTGGACCATGACCCCTTGAAA AA
WI-20964	87 G A ---	---	AGCCAACTCAAGGCCAAAAAAATTTCTTAATATAGTTATTATGCGAGGGGAGGGGAAGCAAAAGGA GCACAGGTAGTCCACAGAATA[G/A]GACACAAGAAACCTCAAGCTGTGAGGTCAATTTGTAAATTA AAGAACTACTAAGATTAGATGAACACACACTCAGAAATACTTAGGAGAGCTGAAAAAAGGAAGAAC AGATGTTAACAAAAAATAAAGGCTGCTGGGGAACCTGAGTCCATGTTAAGCTTG
WI- 20059a	59 T A ---	---	CTCTGAACATAAGGGCCGTGAAGGCATGATTGGTTTGGCACACAGAGTGGATAACCAAT[J/A]ACAT TGGCTGGAATGAGGTGGTCAGGAAAAATAANTGCACAAATCTAACACCATGTTGAAATCATGTCTGA GTTCTGGAGAAAGTTAAAGTGAATAATTACAAAGACTGACATGCAACTCTTTACCTTACATTATT CATCTACAGACTATTTTCTCCCTTAGGAGATGAGGAGTATGGCCCTTAGGT
WI- 22130b	165 C T ---	---	TGTTTTGAGGGCTGTAGCAGACTACATAATAGCGGGTGAAGCGGCTGCCTTCCCTCTCCTGACAC CAGCAAGGGGGAGGCACCATCACCGGCCCTGCCCATCATGCATCCCAATGATTACTAGCAGTAGGAA GCCAACGGAANAGGACCCCGCGGCTTGCT[J/C]JTGTTTAAATCCAGGTTAAGCTATACACGTTTAA ATACATGTCGGAGGTTACATGGTCTCATGCACTCCCTGTGATGGGAATGAC

WI-21661	117 GC	---			GCCTAGTCTCCACCCCTTTAAATGTACTCTAGGTACAAATAAACATTATACACATATAAGATCAGT CTTTCCAACTTTAGAATGTATAAATAAGAAATGACATTTTAAATAAAATA[G/C]TTTAGTCACAGTC ACACAAACTACCTTCTAAGGAAACTGTCCAGTGAAGCCGTTAAATTTGTGCTTTCAGCTATGAAG GA
WI-21980a	25 TC	---			TCAGTTAAACACATTTCATCAAGGA[T/C]AGATTAAATATGTCAAGTGAGCATAAAGGGAGATTAA TAAACCAGAAATGTGTTTCTGGGAACCAAGTTTCAAGTGACTCAGGATAAGTTTATTAAATTTTCAT GGGTGAAGCCCTGGGATAAAG
WI-21636	71 AG	---			TGCTTGATTAAATGTGGTGTTCACATTATCCTATTTCACAGATGGAACAGAAAATACCAGCTTTTTT AA[A/G]TAGCAATATCTATTATAATAATATTGAAATAACACCATAATAATATCAGCTAAGGA AGTAATCTAATTGTGTGATTTTGAGAGGGAGAAAACATTACCTCTAGAGCTGAGGCTATTGTGC TCATGCAAACTCCAAATCTGAAGGTGGTAGAACTAGGAAGGCACAGGGATTTC
WI-22457a	112 GA	---			TTGCTATAATTTCCCTTAAAAATGCAAAAGAGTACATCACAGCAGAGTATAGCCAATCAGCTATTAGA CAACAGATAACATACCTGGACACGGTTTCAGGCATGAAGGATACAG[A/C]CAGTTAATTAACATAAG GAACAGAGTCCCTGCATTCTCTGAAGCATAGGATGGGGAACAGTAATGCAGATTAAATACCTGGGGCC AAAACCCAGTGAACCTACCCAGCTGAAACACTGAAGGATCTGGGTAAGGA
WI-21524b	97 CT	---			GCCGTGAGGGTTAGCGTATAATGAAAGGTGTAATAGCCTGATGACGACCTTCGGGTCATCTTAT AATGGTTAATAACAGCATTCTGTCTACCC[C/T]GATGATGCTCTCTCTGCAATGGACTATTTGCC CAGTTGCAACAGGGCTAAGATTGTGCACTATGACAAATGAGTTGTTGATTGTTGGAGTTGCGGTGTC CTGTGAGAAAGATTCTTGACITTTCTCCAAGTTACTTCTCCAGGGGATG
WI-21524a	35 AC	---			GCCGTGAGGGTTAGCGTATAATGAAAGGTGTAAT[A/C]GCCTGATGTACGACCTTCGGGTCATCT TATAATGGTTAATAACAGCATTCTGTCTACCCCGATGCTCTCTCTGCAATGGACTATTTGCG CAGTTGCAACAGGGCTAAGATTGTGCACTATGACAAATGAGTTGTTGATTGTTGGAGTTGCGGTGTC CTGTGAGAAAGATTCTTGACITTTCTCCAAGTTACTTCTCCAGGGGATG
WI-22652a	32 GT	---			TTACCTTCCAAACCAGGCCACTTTGGAGAAAG[G/T]AAGAGATGCTATTAAATCAATAAGCCAAAGAC AATAGGGACTACCTGGGTAGACCAAGATGGCAGTCACCATACACCATCATCTCTGCCACAGAACC TTTGACATGCTGCCCTCCTACTCTCGGCACTCACTGCTTAATTGGGACCTGAAGCTTCAGCATCCCTT CTTTAGGG
WI-21703d	197 AG	---			CAACAGGCTCATGGAACAGAGCCCTAGGGATCCAGGAGCATAGGAGGTGGTGGTGGGAGGGCTC TGATCCCCCTTTCTCAGCAGCAGCACCATCTTCAACCCTCCTGGGAAAGCAGCATTTGGAGCCTACACCA CTTGTGCTTTTCTCACCAGGGTAAGAAATGCAGGTTATTTGCAGAGGGGAGTGAGTCTGGGAA[A/G]G TGGGCAGAGCACAGCTAGGGGCAAGGACTTAAGGGAACCTTGTGGGGGAAGAG

WI-21703c	134 A G ---	---	CAACAGGCTCATGGAACAGAGCCCTAGGGATCCAGGAGCATAGGAGGTGGTGGCTGGCAGGGCTCTGCATCCCTTTCTCAGCACAGCACCATTCTCACCTCTGGGAAAGCAGCATTTGGAGCCTACACCAAG/CTTGCTTTCTCACCAGGTAAGAAATGCAGGATTTGCAGAGGGAGTGAGTCTGGGAAAGTGGCAGACAGCAGTAGGGCAAGGACTTAAGGAACTTGTGGGGGAAGAG
WI-22663c	139 G A ---	---	CCCTTGTCAGTCTGTCCTCGCTTCTCACTGCACCTGGCGAGGTAGCCGGCTCGCTAATCTTATTCOCAGTCTCGTGAACATGGCTCAGTCTCCCGGCTCAGTGTGGGTTGCACCTGGTGCACCTTACAGGC/GA/GAAGAGCTTCTCATTTGCTGAGGGCTTTTCTCGAATCCGTGTGAATGTGGGT
WI-22663b	55 C T ---	---	CCCTTGTCAGTCTGTCCTCGCTTCTCACTGCACCTGGCGAGGTAGCCGGCGCTC/GCTAATCTTATTCCAGTCTCGTGAACATGGGCTCAGTCTCCCGGCTCAGTGTGGGTTGCACCTGGTGCACCTTACAGGCGGAAGAGCTTCTCATTTGCTGAGGGCTTTTCCGTAATCCGTGTGAATGTGGGT
WI-22663a	38 C T ---	---	CCCTTGTCAGTCTGTCCTCGCTTCTCACTGCACCTGGCGAGGTAGCCGGCGCTCGCTAATCTTATTCCAGTCTCGTGAACATGGGCTCAGTCTCCCGGCTCAGTGTGGGTTGCACCTGGTGCACCTTACAGGCGGAAGAGCTTCTCATTTGCTGAGGGCTTTTCTCGAATCCGTGTGAATGTGGGT
WI-22668	99 A G ---	---	TCCTTTATCTGCTGCCTGCCTGAGTATTCGGGAATCCTACAAGGATTTGAGGGAGCCCTTGGGATTCCAACCTAACAAATTAGTTTCTGTAATATT/GJTTCTAGTCCATTTAGATTGTGTAATGATCTAAATGNGTAACCATTTAATATCAAAAGTATAACAGCATTTAAGTCAGCTTTTCGAAGAAACTTTTATT
WI-22631a	52 T C ---	---	AAGATATAGTGGCAGGACAAGATTGGTCACGAAATCCCTGGCTTCAGTTCGAT/CJAGCACCATTTCGAAATTTAGGCAAGGTATTTAACCTCTCAGGCTCATTTTCTCTTTGTAAATTTGTATAATGGACC
WI-20258	157 G T ---	---	TATGTACCATCATAGGGTACTTGGACAAATCAACTGAAATTTTTAATCCACACTTTCACGAGGGGACAGCCCTGCCATGTGTCCTCCAGGCTCACAGCAGCGCGGTACTCTGCTGGTGGTTGGTGGCAGGTGGAGATGGTGACGCGCATTTGGAAACCCGTAAAGCATGACAACGGAGGCGCGGGGTGTTTCAAG/GTJGCGGTTGACGAGGTGCATGGCTGGCAGCGGCGCTCTACAGAAGGAGGGAGCGCAATTCACAGCCCTCTTGACGTAGTTTCCGGGGAAAGTACC
WI-22714	212 C A ---	---	ACTACACATATGCTGATTTTCAACAGTAAATAACATTTTACATTTGTAGAGAAAAATCTAGGGTCTACTAAATAATCTAGTACTTGTTCCTCTCTCTGCTAATCTGACAGGAGTGTGTGGGAAACGAAAGTCTGAAAGGATTCAAAGGGGGCTAGGATTTGCCACAGATCCTGTAAAGGAAAGGATGAGGTGAGCTTACCAACCCCA/C/ATJGAGTAGGGGCCAAACATCCTTAACAAGCTAGTTGCT
WI-22734a	44 G A ---	---	TGGGGCTACTTTAGATGGGATGGCTCAGGGTCTGGGAAGGCCT/GA/JTCTTAGAAGACATTACCCAATGATGAGAGGCGCAGTCGTGGAAGCCATAGTTTGGATGGCGAGACTTTCCGGCAGAGGAAATAGCAAGTGCAAGGGCTGAGGGAGAAATGAACTTGGGCTTGTCTACAGGTTGAAGGGCGCGGNTGGCTGAGGTTTAGTGGATG

WI-22724	117 A G ---	---	TGATATGATGCTGAGATTGCTTCCAAATATGCCATAGTAAGTAAAGCTTGTAAAGGGT[A/G]GTTATTCTATTTT CAAATCAAGATTGTCAAAATGTATAGTAAGTAAAGCTTGTAAAGGGT[A/G]GTTATTCTATTTT TGGGATAIGTTGGGAATT
WI-22750	48 G A ---	---	TGTAACCTGTGTTTCTGAAAGTTGAGGGAAGCTGAGGCAGCTAA[T/G]AGGCTCATACAAAGGT TTGGAAGACCCATTCTGACTACCTAAGGAGAGTCAGCATTCAGACCATTCGACTGTGCT
WI-22775a	60 A G ---	---	TGCTGTTCTTTAGTTTCATGACGTTTATCACAATGTGCTACTGTTTCCATTGTTTACATC[A/G]TAGTA GGAAAGGGGAAATAAACTCCCTAAGGGCAGCAATAATTTCTGCTTTTGAATCCTTCATTCAGGCCAAA TATTTGTTGAGCACCAAGGGCCAGATGGGAAC TGAGGTATGTAGGTGTTGGGAGCCAGGAAAGGAAG GGT
WI-22808	143 C T ---	---	CTTAGCTAATGAAACTGGCTATGTGGACTATGATAGACCAAGAAAGCTACCCAAAGTCCCTGAGGGAG CCTAGTCTCTCTAAATGCAGACATGTACCCATGACAAGGGCTACAGCTTGGCTTTAGCAACCAGGA GGATGAAGA[C/T]AGCAAACTGATTAGAGAGTAGGTATAAGAACCCAGGAGAGTGGGGTCCCAAAT ATC
WI-21016	207 G A ---	---	TCTCTGTGCTTTGAGCCCTCATCCCCACCCCTCCAAAGCCCTCATGCCACCACACCCGTGCCACATT CCCCATCTCCCTGCTGCTCCCATCTCAAGTCCAATTCGAAGGCCAGAGCCCTGGCAGCTTTTCTG GGAGACAGCATGAAAGGAGGGGAGTGGAGATGGCAGAGATGGGTGGAGCCAGTGCCTGTGGGTG CT[G/A]TTGGCGTGGTGAATGTTGGGGCCAACTCCTGAGGCCAGAGTTCA
WI-21031	31 C T ---	---	TTGAACACCTGACCTGACCTCTGACATGTGG[C/T]CTCTGGTCCCAATTGTCTCCAACGGTGGCACA TCTTCATCTTTGTTATATATCTGCAGGAACACTCAGTCTCTTCAGCAGCCGAGAAACACACACA
WI-21314	122 A T ---	---	CCATATCCAGTCTTCTTTGAAGCTTTCTATTGACTTTTAGGGTCAGTTATTATCCCTTTATCACTAT GACTTTCATTTGATTTTATTTGTTCTCCATTCTCTGTCAAACITTT[C/A/T]TTTGTATTATAA ACTGTTTCTAAACTTCACCTTAATCTCTATCTGTATTNCTGTAGTCCCTGAACTTCTTTTAGAGG
WI-21186	95 G A ---	---	AGCGAGCATCAGAATCAGCTAGAGGGTTGACTAAACAGAGCTTCTGGACCCAAACCCAGAGCTTCT GATTCAGTAGGCCTGAGGTGGGGCTTAC[G/A]AATTAGTATTTCGAAGACCTTCCTAAGTGTTCAG ATGCTGCTTGTCCTCCGGGAACACACTTTGAGAAGTATTGTTCTAAATGTTCTCTCTCTTTTAA GGAGAGACAGGAATCCAGAGAACTGCTAATTAAAGCATAATGTATTGAAT
WI-21187a	94 A G ---	---	CCAGATAACTATAAAGCAGAAAAATTAGCTTTGAAATCAAAATACATATTAGTAACACACATT CATTTTATAACACACATAAAGACACC[A/G]GNTCTCAGTAATGCTCTAGTCCAGGGTCTCAA AGTATGGCTTCAGACAGCCCCATTTCATCACCTAGGGGAATTGCTAAATGCAGATTCTCAGGCC CTACCTACTGATCTACTGAATCAGAACTCTGAGGGTGAGACCAAGCAACCTGT

WI-21190	39 T C ---			TTTCCACATACCAATGCACCTGTTGTATAACTATT/CJGTGGGGTAAGCCCTCTTTGGAGAC CAGTGACATAGACATGATCCCATTTATTAACAATAATTAATAATCTGTACTATTACTGC TTAGTTATCTAGTGTATTGAGAAAGGAGAGTCAGCATAGTTTATTTCCATGTAATAAAGCTT AACACA
WI-19937d	186 G A ---			ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCANCTAACTTGAAGGAAA GAACTATTGCACAACCAACATTTACATATCTGATTTAGACAAGCAAAAGCACTTCATGTTGCT GTAAGGTTCTCTATGGCAACAGTGATGACATTTGGTGTCTCCTCAGCAAGTC/GA/JTCCAAACCTTC CAAAAGAAGCAGTCATTTGAAAATGCTGACTTATGCATTGCCTCAGGAAGAA
WI-19937c	185 C T ---			ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCANCTAACTTGAAGGAAA GAACTATTGCACAACCAACATTTACATATCTGATTTAGACAAGCAAAAGCACTTCATGTTGCT GTAAGGTTCTCTATGGCAACAGTGATGACATTTGGTGTCTCCTCAGCAAGTC/JGTCCAAACCTTC CAAAAGAAGCAGTCATTTGAAAATGCTGACTTATGCATTGCCTCAGGAAGAA
WI-21117b	227 C T ---			GAAACGGGGTGCTAAACAAAGAAAGTCTCAGATCCCACTGAAAATCTGTTTCACAGGCTC TCTCAGAAAATGCAATATGTACCAATTTGCATGTACAATTCAGAGCCTTCAAATACATTCGGGG TCCAATCACATACCTCAGGTTCCAGACTCCTAGCTCCCAATATTCCTACAGTTCTGAAGANTTAGCAGT CCTCTCATTTCTACAGTCTGATTT/CJTTCCTACTGAATCTGGGTGGGAG
WI-21122a	42 C T ---			TCACTTTGTATCATAATCCCTGTAAAGCTAAAGTTATTCA/CJTJTAACAGGAACCTCTGTTTTCC TTATTCAAATGTCAACAGCCTGACGCGTTACTGTACATATTGCTAGCAGGAGACAACCTGGAATACT AAACAAATACTGGAATTCACATTACAGACAGACGAAACCAACATGGGATGCCACACATAACTCCT TTGTAGGTTTCACAGAGAGCCTATTGTGGGTGCT
WI-21254	53 A G ---			CAGTTTGGTACAGGAAGGGCCCATGAATGTGGCGGGAACCTATTCCACAGGAG/AGJCAAGGAGAAG CTGTTCTCTGG
WI-21054	23 G T ---			AAGGAACTGCATGGGTACAAAT/GJTCCAAATCATACTTAACAAGGTGGGAAACGGGTCAATTCT TGGCCTGCTCCAGAACAGGGGCGAGTCTATGCACCTCTG
WI-21059b	181 T C ---			GGGACCAGGGTAACACCATTAGCAATATCCGTTATCAGCCTTATTCTTCCCACTGAGCCTGGCTGAA CTACAGCTGCCAGCATTTCTGGGCTTGCAATTTCCAGCTTCGTACATCTTAATTTCAAGCTGAAA AATCCTGGGGAAGAGACATACCTCACTGAAGTCATTTCTCTATTCT/CJATTGTAGCCAGGGCAAAA TGAGATTAGGGATTAGCTCAGCCAGAGTTAGGGTGACTATCCTTGCCCTAAT
WI-21059a	63 C T ---			GGGACCAGGGTAACACCATTAGCAATATCCGTTATCAGCCTTATTCTTCCCACTGAGCCTGG/CJTJ GAACTACAGCTGCCAGCATTTCTGGGCTTGCAATTTCCAGCTTCGTACATCTTAATTTCAAGCTG AAAACTCCTGGGGAAGAGACATACCTCACTGAAGTCATTTCTCTATTCTATTGTAGCCAGGGCAAAA TGAGATTAGGGATTAGCTCAGCCAGAGTTAGGGTGACTATCCTTGCCCTAAT

WI-20442	37	T C ---				TCCACGTGAAGGAAGAAAAAANGGGGGGGCTT/CJTAAGGTGGCACAATTTAAGAAAAT ACCATCCATTTTCTCAGTCTAATCTGAATCCATACATTAAACAAAAGTCAAGTGATGAGACGAA CA
WI-21235	43	T C ---				GTGACAAGAGGTGAAGCAAGGGACAAGGGGCGAGGGGCGAGT/CJCTCGGGCGGATGTTCCAGGG CAAGCTACGTA
WI-22012a	57	T C ---				ATCAGAACTGCAATCTGCACATGAAAGACCTGGGGGAATGCCTACATCTGGAAATTC/CJATTAC ATCAACGTTAAATTTGTCCGACCAGTTCTTCAATGCTGATCATTGATAATGACAGATCCAACAT GAAACTCCTGAAGCAAATGAATATTTACCTTGCTTTCATGCAAAATTTAGGACCAAACTCAAAGG TTTCATCCATGCTGGGACACACAGATCTAAGGAATTTGACAGGGATCTCT
WI-21149a	167	G A ---				AGGACCTGCTCTCACACGTTCCCTCACCCCCACCAGCTTTGGCAAAGATAGTTGACTAAATACCCT AAATAGTGGCTTTTAAATTTTAAACAATGACCTTATTTATCTTTTAACTTAACTGAGTCTTATATA CAGACCTGCCCAACTGGAAGCTTTTACAC/GAJTGCTTCAGAATGGCGAGTATTGCACAATGGTT TGGGGCAGGTTCTGTGGTTAAACATGGGATGGAACCCAGGCTCTACCTG
WI-21376b	188	A G ---				GGTGCAACTTGGAAATAATGGTTTAAACAGGATAAGCATTAAAGGAAAACACTTTCAATGTGTC TTCCATTTGATGAATTTGTTTCTCTCTTTATCCCGCAAGTGGAGTTTCATGTCCTCGGTGAACCA GACAGTGAATCTGTCCAGCCCAATCTGCAGCATTAGGGATGAGTTCTC/GJGAGTGATTTCT GAACTGAGCAGCACTCATGTCTGCATGGGGAACCTCTGGGAGAAGAGCCT
WI-21382d	125	C G ---				CCATTGCAGTCCAGAGATGAGAACTGGACAGAGGCAATCATGAACAGAACGGGAGTCAAGAGA AGGGGTTCTAAGATGGAGAGTGGGGGGGTTTGGATCCAGTGGGATNGGCTTCC/CJGJAGGT GCAACCCAAAGGAAGTCTCTGGAAGCAGCACCACTGCTGATGGGGAGCAGAAGAGCTGCCATCCTC AGTCAGGGTCCGAGTCAAGGTCCGAGGAGAGCTGCTGCTCCATAGTCTCGAC
WI-21437a	201	G A ---				TCCCTGAGGTGGAGTCTAGCATAGTCCCTCCCTCAAGAGGGACAAGGGGTACAGGGGCAGAGC AAAAATCCAGTCTGTTCAACCGGAGACIGCCTTTGGGATGGAAGTTCTGGAGCTCCCTCCATT CTATTCTGTGGGCAGGAACATGCCAGGGCTGCTGTTAAATGGCAGGGGTACCTTTACCAGGGGQ /AJCAGGCATAGTGTGGCCCTGCTGCTGGGGGCCACCCCTGGGAACAGT
WI-21202b	156	A C ---				CAAAATAGAAATCTTTGTGAGTGGATTGACTTAAATTTTATTTCTGTATAAGCTAAATATGT/CJTG GTTTTATGAACATGATTTTATAAAATGGTCACAATATATTTTAACTTAAGTAACTGATTTATTGA AGGAGGAGAGAGTTGACCA/AJGJCTCTACATGCATAGACAGTCTCTAAAGCGTATCTCTCAAAACATG A
WI-21202a	61	T C ---				CAAAATAGAAATCTTTGTGAGTGGATTGACTTAAATTTTATTTCTGTATAAGCTAAATATGT/CJTG TCTGTTTTATGAACATGATTTTATAAAATGGTCACAATATATTTTAACTTAAGTAACTGATTTATTGA GGGAGGAGGAGAGAGTTGACCAAGTCTACATGCATAGACAGTCTCTAAAGCGTATCTCTCAAAACATG A

WI-21627b	153 A G ---	---	---	GCATGAAAGAACTCCAATCAGACCTTTATTCAATAAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTCCAGTATCAACTTGAGTACCTCATTATGGATATTTATGCTAGGAATGACAA CAGTAAGGGCATTGCAAA[A/G]TCCAAAGTCATCTAATAATTAACCATATTTTACATAATTTGTAGG GACAGTATACTAATACTCTACAATAAATAAGGGTTTAAAAATGTTGCTTA
WI-21627a	106 A G ---	---	---	GCATGAAAGAACTCCAATCAGACCTTTATTCAATAAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTCCAGTATCAACTTGAGTACCTC[A/G]TTATGGATATTTATGCTAGGAATGA CAACAGTAAGGGCATTGCAAAATCCAAAGTCATCTAATAATTAACCATATTTTACATAATTTGTAGG GACAGTATACTAATACTCTACAATAAATAAGGGTTTAAAAATGTTGCTTA
WI-21399a	75 C T ---	---	---	GGATTTGAGTCCCAACTTGATCTCAAAATTCACCTTCTTGATGTAAACAAGCTCATTCCTCTAAAGTT TCAGTTTC/[T]TCACCAGTAAAGGAAAGGTTGGACCAGACATGTTGGACCGTAATTGCTTGGTAA CTGCCCTCTGCATTTGCTCTGAGGTTGTGTCCCTAGGACTAGGTAGGATCTCTCTTGCTTTCTGCC TTACCTAGGCATAGTGCTGATAGCAGGGCTGAAGCCCAATTCATACTTGT
WI-20329a	68 A ---	---	---	CGATGCTGCTAAGATAGGAGGTTAATTCCTTACATGGTGAGTGGTCACAGAGACAAGACATCAAT C[G/A]TCTGTTAGCAGCGAGAGACACCTTTAAGTTCGCCCAAGAGTACAAATCCCCTATGAGAC AGCAGTCTGGCTTCTTAAACACAGTAAACCAATCAAAAGAAAGATTTAGAGGTTTCAGACATT AGGAACAANTGTGGCCAGAGATACCACAGAGCCCTTGAAGGAAAGGCCCTCACT
WI-21249	155 T C ---	---	---	TTCTGGCATTCAAATGTACATGTAATCCAAATTTAACAGATCAAAATGTTACACTAAGTTTCACCT TAGTATCTAAGTATCCAATCACAATTGTATCTAAGTTTCACCTTTAAGAAACATTATAAAGGTAATT AAAACCTAGGTGTATACTTAT/[C]ATGGAACCTAGTTTATTCNNATTTAACTACTGTTTCATTGCGTA AAGTATGTTGTCCCAATTTTCAGCTGTTTTAAGGAAATTATAAACATTGAGA
WI-21504	147 C T ---	---	---	TGACACAGCATCAATTTTCATGAATACTTTGAAAGGGCCATTAGAAAAAATAAGAGCCAAATTTGGGTC ATTTGAGAAACATTTTCAGCACAATTACAGTGGGGGCACGGCCGTTCCGCTCCAGCTGGGTTTTOCC AGATGCAACAAT[C/T]GCGGTTCTGGCTTCTCCACTGTGGGGATGGGGATCGCGCCTTCGGAGCTCT CAGGG
WI-21242	115 A ---	---	---	CTGCACCCAGGAGGACAGCTGCTGGCAGGGACTAATAAACCTTCCACCTGGCCATGGTGGTGGTGT CTCTATGGACCGAGGCCCTGAAACCGGGGCAGGGAGGGGCAGAGAA[C/G/A]CACTAGCTTGGGGGTG GGCACAGCTTCAGACCCCTT
WI-21475c	181 A G ---	---	---	TAGCCCTTCTGCCAACATCTGGCAATNTAGGCTGGGGTGGACGTTGGCCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGGCTCCAAACCCAGGCTTCTCACTTGTCTTACTAAGCACAG CAGTCTGAAGCTTGGGACCTGGGCAGTGGCTCTTTGGAGAAAGGC[A/G]AAAGCCACAGCAGCAAC ACTTAGGAGCAAGACCCCTTCCCGTTCTCCACCCTATTTCCTCCCTTGAAG

WI- 21475b	117 A T ---	---	TAGCCCTTCTGCCAACATCTGGCAATNTGAGCTGGGGTGGACGTTGGCCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGCTCCAAACCCAGGCTTCTG/TCTTGTGCTACTAAGCA CAGCAGTCTGAAGCTTGGACCTGGGCAGTGGCTTTGGAGAGGCAAAAGGCCACAGCAGCAAC ACTAGGAGCAAGACCTTCCCGTTCTCCACCCATTTCTCCCTGGAAG
WI- 20893d	207 A G ---	---	TGTTGTGTTCCAGCCACATCTTCCAAAGGAACCCACCCAGCCGTTGTCAGGCTTGTGCAGGG CTGTCTTCGGCGTTAAAGTCTACTGAGGAATACAATATTGTCAGTAACTCATCCGCACTCC AGCGTCAGGCCAAACCTTCCGTGGACCTGGGNAACCTGCCATTTCTCTCTTTTACAATGCAGT TTC/A/GIACATAACATTGGTAGAGTAAACAACAACCAAGCCTAAATG
WI- 20893c	179 T C ---	---	TGTTGTGTTCCAGCCACATCTTCTCCAAAGGAACCCACCCAGCCGTTGTCAGGCTTGTGCAGGG CTGTCTTCGGCGTTAAAGTCTACTGAGGAATACAATATTGTCAGTAACTCATCCGCACTCC AGCGTCAGGCCAAACCTTCCGTGGACCTGGGNAACCTGCCATTTCTCTCTTTTACAATGC AGTTCAACATAACATTGGTAGAGTAAACAACAACCAAGCCTAAATG
WI- 19941c	71 C G ---	---	GAGCTCAAGGGAAGACOCCTTACCCAGATAGGGACTAACTGGAGGGTGGAGGAACAAAGGTGAAA GGTATTC/GGGTCTGTGAGACAAAGCAGGGGGCTGAGAACACAGAGCAAGGTGGGTTTGGAG GGAGCACAGCAGGGTGCAGGAAGGAGATGGGGGACATTTCCATTCCAGTGCATGTCCCTTAAAT AACTGGGTACAGGACATTNTGGAAGGAGAACCAAGGACAGAACAAAGCG
WI- 21552b	166 C A ---	---	TGGGTACATGGACAGATGTATATGTTATGGGTTATATGAGATATTTGATACAGATACACAATGTG TAATAATTACTTCAGAGTAAATGCGATCTCTTCCCTCAAGCATTATCCATAGTGTACAAAGAA TCCAAGTATACCTTGATTATTTAAAATGTACAAATTAATTTATTTGAATTTAGTTACCCCA ATTGTGCTATCAAAATATCAATCTTATTCATTCTTTGTAACATTTATTTGTA
WI- 21552a	66 G A ---	---	TGGGTACATGGACAGATGTATATGTTATGGGTTATATGAGATATTTGATACAGATACACAATGTG /AJTAATAATTACTTCAGAGTAAATGCGATCTCTTCCCTCAAGCATTATCCATAGTGTACAAAG AATCCAAGTATACCTTGATTATTTAAAATGTACAAATTAATTTATTTGAATTTAGTTACCCCA TTGTGCTATCAAAATATCAATCTTATTCATTCTTTGTAACATTTATTTGTA
WI-21512	54 C G ---	---	TCCTCGTACTTCATGCTCCCTCCCTGCCCCAGAACCTTACAAAATATTTCTGTG/GTAGAGAGGGA AAGAGCTGGTGCTGCTGAGGGAACGTCAGTCCGGGGAAGGCACTCGTGGTCTGTGATCTGTC TCAGTGATGGGAGGTCCTCACTCGCCCCACAGGACGCTCGGGGCCAGAGATGAGAAATGCTGTAA TCCAGTACAGGGGCTGCTGCTGGGGTCCCAACAGCTCTCTTTGGGGG
WI- 21513b	192 G A ---	---	CACATAGTTTCTCAAGAAGAGGATGAACCTGAAACTCCCTCAAGGAGGACAAAGCAACTTTCCATT ATTCTTAGTTTAGACCAGAATCTTTAATTTTATATCTCTCTTTAATACTGTCAAAATACACCAATA CTTAGAGGAAATAATTCACAGTATACCAAAACATTTTAAGATAAAGAGGCGAGTGA[G/A]AGTAG TATCTCTACATACCACAGTATACAATGATGCTCTCTGCGAGTTTAGGAAC

WI-21514b	133	C T ---	---	TTGAACCTCTGAAGGTGGCTTATGTCCTGACTCCTCTTAGGACTGGTCATGAGCTGACAAGCATAGAGCAAAAGTATCTCAACATTACAAAACCCCAATCTTCAAGAAAGGAGCAGCATATTACCATGGAGC/TACAGGACTCCAAAGGACCTCAGAAAGCATTAGCCAAATCTCTTATGCAGGAAATAAATGAGGANTTTAAGGCTCAGATGGGTTAAGGGTGATTGTCAAGGGTCATAAGGAACT
WI-21514a	100	A G ---	---	TTGAACCTCTGAAGGTGGCTTATGTCCTGACTCCTCTTAGGACTGGTCATGAGCTGACAAGCATAGAGCAAAAGTATCTCAACATTACAAAACCCCA/A/GTCTTCAAGGAAAGGAGCAGCATATTACCATGGAGCCACAGGACTCCAAAGGACCTCAGAAAGCATTAGCCAAATCTCTTATGCAGGAAATAAATGAGGANTTTAAGGCTCAGATGGGTTAAGGGTGATTGTCAAGGGTCATAAGGAACT
WI-22020	27	C G ---	---	ATGAACATGTTGCAGTGGGATGAAT[C/G]TTATCATGATGCTAAGTGAATAAGCCAGACACAAAAATCCAAATGATCATCTACCTGTATGAGGGTACTT
WI-19576a	113	A G ---	---	TTCATCGGTTCTTAATACAGTACAATCCTTTTGTGAACAAAAGTCACACTGGCAATGATTATTACAGATCCAAATAGACTCAGGCTTCAGACATAAAAAATTTAACATT[C/A/G]TCTAGTTCAAGTATTAGTACAGAAINTTAACATCTGCCAGATGTACACAATTTGGTAAAAACTACAGCTTCTCTCCACGGGGA
WI-21695a	141	A C ---	---	ATACACAGGCCACAATTCAGGATGGAAAGGAGTGGGCACCTTGGAAGTGACTACACATGGCAATAAGCAGCCTATCTCTTACCAACCCAGAAAGTTCTTGGGGCATGTGATGGTAGGCCAGACCCCTTTCCAAAGGAAT[A/C]TACTACACTAAGCCTACACTGTACTGTGAGAGTCAATGTGGGAACAAGGCCACAGGCAGTGGGAGGAAATGTGATGACTTCACTGTGTTCAGANTTCTAAGGCCAGCAT
WI-21574a	235	C T ---	---	AAOCCAGAAATTTAGGTACTTTGTATTATGAGGAACTCACTATACTAGGAAAGCAACTTATGAGTGTGTAATATTGATCTAGCAGCACTTCCACTGATCCCTGGCAGGTGACAGCTCTCAGTGAACAGCGCTCATCAGCTAAAGTGAGAGGCTGTCTATTCTCATTGTGAATGTCCCTCAGAGTCACTAGGGAGCCATTGGCAGGCCAGGGAACCTTACTGCTACTTCTCTCTGCTGTCAGGTGGGA
WI-21644c	151	T A ---	---	TGACTGCCAAGATTTAGGCCCAACTTAGGAGCAAGGTCACTTAACCTTTCAGGAAGCTTGGGTGTGACCCACTGCATAAATGGATTTTCACCATANTATTAAACAGACTCAAAGTGATACATACAAGCTTGTTTCATAAATAAGGGAIT/AJTTCAATCAAGATCCATGGAATGATGCAGTTTAAATGTGTCTCAGCTTGCCCTACTGACCACTTTCCTTTCTAATATGGCAACAGCACAGCAAGTC
WI-21614b	55	G A ---	---	TGCTTTAACCTCAAAAGTCCAAATAACATATAGACATTTTGANTATAGCTATC[G/A]TTTTAACAACCTCATTATGATCACTGTGCAATTTTCAGTCACCTAAATACGGAAACCAGTACTATTAATAAACA
WI-21615b	151	C T ---	---	TTTACTGTGTGGGTTTGTGGGACTGAACATTAACCATACGTGATTTCTAAGGTACTAGGGAGTTGGAAACAGTACTACGGGTCATGGTATTTTGGGCAGTTGGCTGTGTGTGGG
				GACCGAGAAAAACTGCAAGGCATATGATGTTTGTGCAAGTATCACATGACTATTTCAAGCTTATAGA
				GAAACTTGCAAAAAAGTACAAAGATGGCTATTTTAAATTTACATACATATTAAGATAAGGATGGACT
				CTTCACTAGTATTATC/TJAGGACACAATCGACGGATGTAATCTATTTGANTTATACCATAGGCCCTTATCTATATGGCCAAAGGGAAAGGTAGGATGGGTACTGTGGAACGGGA

[illegible]

WI-22082b	67	CT	---			CAGGACTGGTTGCTGCTCCCAACTGCACATAAATGTCCTTTTGTGTTGAGTTATTGGTTGTGTG[C /JGTTTTCTTTTGCATAAGAAATATGTCATTAGTCCAGAGGCTCTTGCTTTATCCGGATGACGG AGGTACACGGGGCTCGCTCAGTCCCGCCGAAGACGATTCGCTGAACCTGGGACGAGTCTACTC CTCCCCACAGGAGCCACGATTCAAACTCCTCTTTGCTGCAACCCTCT
WI-20993	139	A	G	---		AACACAAACTCCATGCTTTCAAGATTCCACACCCAGATCACTAAGACATATTAATAATTACAGCAAT TAAACAGTGTAGTTTGGTACAATAACACATATAGCAATGATACAAATTAGGGGAAAAACCCCTGG GCTTCT[AG]TAACAAGTGAGTATACATTAAAGACAGATTATGCAGATGGCTTCAGGATTAAATTTGA TTAATTTAGAGAGAGCCTATTTTCAGGTCTTCTAGCTCATCCACACACATCACC
WI-21723b	125	A	G	---		AAGCGATTTTATTAAATTGATTGGACATACTGTAGGTCAAAATAATTTTCTGAAGATAACAATTA TGGACTTTAAAGCTCGACATAAAATTAGTACTTCAAAAGGTTAGTCATATTCCTCA[AG]CAACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAAACTCGGAAATC ATT
WI-21723a	82	G	A	---		AAGCGATTTTATTAAATTGATTGGACATACTGTAGGTCAAAATAATTTTCTGAAGATAACAATTA TGGACTTTAAAGCTC[AG]ACATAAAATTAGTACTTCAAAAGGTTAGTCATATTCCTCAACAACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAAACTCGGAAATC ATT
WI-22132	99	T	G	---		CAACAGATGCTTGAGCCAAAAAGCAACATAGGCAGAAATACAATTGAGAAATATCTTCATGTTTC AACCTTTAATCTGACTTGCTTTTACTATCCTTT[AG]CCCCATTTCTTCTTAATCTCTTTGCTTTACAA TATATTACCTTCTAGGTATCACCTCATCCTATAGGAATGCTTCTAGTTAATGCTGCTGCCCAACA ATACTAACCCATTGAAGGATACTAAGAAACCTTTAAATGGGACAGTGGG
WI-21006a	106	A	G	---		TGACAGATCACACCACATTTTGTGTAACTTTTCTCCTTCAAGAGTCACCTTAGCTTAAGCCAGAA GATTCTCTTAAAGAACACATACACATGTGCACACAC[AG]GAGGCAAGTACAAAAATGTAACC CCACCAAAGTGCATGTGAATGAAAGTGCAAAAAGGCTTCATTGCAAACTCTGAGGATCATCTCT CTGCTTCAGGAAAAATAACAGAAAGGTCCTAACTGCCCTAGGCCT
WI-21761b	138	C	G	---		CTGAGGCCTGCTCTAACTTCATNTGACGGAGCGAGTTTCTGCTTGGAAATAACTGAAAAAGATTCAAT TTTCTCTTTGTGTACAAAGGATCAAAATATTTTCACATCTTCTCTGCCAGTTAAACGTGCGGTGG CT[AG]CAATACACACCAAGCCAAAGCGTAACCTGGCTGCCTCAGGAAGGCTGGGAGGAAGTGCCAG ATGGTA
WI-21079c	166	G	A	---		AATGAAAAATGCCACCCAGAGGTTAACAGCTTGCCATGCACTGTGTCGCGCAAAATCAAGTTGT TTTAATACCAGTGTGCAGCTTTGATTCCTCCATGAAATTAAGCTGTGTGCTCAGTTGTTTACATAA CTCAGGCCACCCCTGAAATATCTGCTAGTGGG[AG]AATTTACAACCCACTGAACATCTCAGCTCAA GCCAGATGACTATCACCTACATCTGCCAGGTAATAGGCATGGCAAT

WI-21079a	50	G A	---	AATGAAAATGCCACCCAGAGGTTAACAGCTTGCCATGCATGCAACTGTG G A CGCAAAATCAAGT TGTTTAAATACCAAGTGTGCAGCTTTGATTCTCCATGAAATTAAGCTGTGTTGCTCACTTGTTTACA TAACTCAGGCCACCCTGAAATATCTGCTAGTGGGAAATTTACAAOCCACTGACCATCTCAGCTCAAA GCCAGATGACTATCACCTACACATCTGCCAGGGTAATAGGCATGGGCAAT
WI-22129a	45	T G	---	TCTGTAGATTTAGCCATGCCATATATTTAACTTTTAAGGAAAAGT G JTATATAACAGTCATTGCT TGGTAGAATCCAGTCTGTCATTAAGTTAGCTCTAACAGTTAACATTGAAGCTTATACCTTATATTTA AATGTTAGCAATCTCTACTACATTTTCAATATAAATAATTTGGTTGCAATTCAGNAAGGGCA TTAACCAACATGGGACTGATCTGGGGCTTCCACCTGACTAAGGTTTTA
WI-21941	79	A G	---	TGGAGTTAAGTGGGCTCTGCTATTTCCOCAAAGGAGCTCGGAAGTGTGATTCAGGGCGAGAGT GAGGGCAGAC A G GGATGAGGCTCTTCTGTAAGTCCAACAGACGCTCACAGATGCTGGGAGGCT GGGACTGCCAGGTTGGAGCCTCAOCCAGAGAGCCTCACTGCATTGACCCACACACCACCTCAOCC CAGCACAGGCACACGCGAGGGCACACGACACACGNTGCACCTCAOCCGC
WI-18916b	42	C T	---	AATGGCATCCCTGTGATACCAAAACATCTTCAGCAGCTCAGC C T GGCTTCCCAC TCTTGGTACCC GGTTAACTGCCAGGNGGTGACAGTGTATGCCAGGGCTGGOCCACTACTGCACTGGACACAGCCTCAOCC AATGCCACCTTCATA
WI-18916a	35	G C	---	AATGGCATCCCTGTGATACCAAAACATCTTCAGCAG C C CTCAGCCGGCTTCCCAC TCTTGGTACCC GGTTAACTGCCAGGNGGTGACAGTGTATGCCAGGGCTGGOCCACTACTGCACTGGACACAGCCTCAOCC AATGCCACCTTCATA
WI-19828c	200	A G	---	TTCCCTTCTCCCCAAGAAGTGGGCAGAAAAGCTTTGTTAACTCCTTTTACAGATGAAGAAAAACAA GATCAGAGGTGCTAAGTGTGTAGCCTAGTGCCAGGNTCTCGGCCCAATCTGGGTTCTCCCCAAG CCCATGCTTCTCCACTTCTCACAATCTTACTCTTCTGACCTCACCACCACCCCAAAAT A G CTTTTAACTCTGGAAAAGAACCCAGCTGCACACTGGGCACACTTGACCT
WI-21863b	47	C T	---	CACAAGAGTCTGTACAACCTTAGGGACACAGCCCTGGCCCTG C C T G AGCTGCATGCCACCCCTC ATATCCACCCOCCATCCOCCAGCCTCCTGCCOCCGACACCCOCCAGGCTCCCTGCTCTGTTGAAGTATTTT CTCCAAGGCAGGAATGAGTCCTTGATCCAACCACACAGCATCT
WI-19860	51	C G	---	TTGACCTAAAGCCTAGCATAAAATTAGCTAAGTAGAATGTTTCCAAAGATG C G CTGCATCAGTAT CTCCCATCCACATAATTTCTGTTTGATTTTGCCATTACCCCATAAATGGTGGGATCTACCTCCOCT CCTTGCAAAATTGAGCTGGNCCCTCTGATCCTGTCTAAGGATCTGAAGCC
WI-9889b	80	C T	---	ACCCAGCTCCTCTTACCCTCTGGCTTTCAGTAGGCTTTGGCTAATGGCCANTGAACTGCAGGGCAAG AGGAGTGAGGG C T TACAGCATTTATTTCCCTCTTTTCACTCCCTGTTAGCTTTGGTAGTGGCTGTAT TTCTCTACTGATAGTTCCCTTGGCCACAGTCGTAAC T T G C

WI-19891c	172 C G ---			TGTTGGTCTGAGAAATTCACAGCTTACTACAAGGAAGCTGAGAATTGCTTGTGGCCCCCTCCCCCGG ACTCCTCTGTCCTGGGAAACGTGGCTTTGNTCCAGACACAGTGTCAAGTCCAGCTCTCCTCAGCGG AGCTCCCGATCCCTCAATTTGCCATCTGCTGACTC[C]G[GTCTTCCGGGGCGTGGGGCGTCTTGT CAGGCAGCGGGGGGAGGAAGGAAGGAGATCCAGGGTCTGTCTG
WI-20155a	81 C T ---			GCACCTGTAGGGGTGAGCTTCCATGGTTCTCCAAGCAGGGGTGTACATTACCTTAGGCTGACCAT TCCCTTGGGGGG[C]TGGCAAACCTGCTTTGAGGAATNTCCCCAGGAGGAATAAACTAGAAGACGC ACCTGCTATTACCATACTATGGAGATAACAGCTAATGAATGGTGGCAGAGCTTGGCCGTGTGA GTCCCCAGGGTAAAGTCTCTCTCTGTCAGTCCAGTCCAGAGCAGACTTCTC
WI-20270b	91 T G ---			AGCCATACAAATGCATTGCAAGAAACAAAGCAGCTGTACAGGAGTGGGGACGCGTCAAGTGACAAAT ACATTTCATGTCAGGATAAGGAGCA/TGACACACAGGATTTATACACGGTGGCAGCGGCTATAGGCA CGATGATACAAAATATAAAGTATATTTCCATCTATATAAATACACAGCTGGGTGGGAAGGATGCT GGTGATCTTGTTTCCCCCGCAGAGGGCTGGGAGGCGAGGNGGGTGGTGGAA
WI-20270a	53 G A ---			AGCCATACAAATGCATTGCAAGAAACAAAGCAGCTGTACAGGAGTGGGGACGCG[A]TCAGTGTAC AATACATTTCATGTCAGGATAAGGAGCATACACAGGATTTATACACGGTGGCAGCGGCTATAGGCA CGATGATACAAAATATAAAGTATATTTCCATCTATATAAATACACAGCTGGGTGGGAAGGATGCT GGTGATCTTGTTTCCCCCGCAGAGGGCTGGGAGGCGAGGNGGGTGGTGGAA
WI-20622	130 T C ---			CCACTTTCAATATTTACAAATGCTCAGCAGCAAAATATGAAAAGCTTCAACACTTTCCCTTTGTA ACTTGCTGCAATAAATGCAACTTTAACAACATACAAATTTCTCTGTATCTTAAAGTTGAA[T/C] TACTAATTTTATGATGTTACTCATATTTTATTCATATACATCTTTAATGACATCATTTGCCAATACATA CATTATTTCTNTAACTTTATTTTACAATAAGCCCAACATCTGTCATGCAG
WI-20768b	190 C T ---			TTCCCACTCAAAACTCCCAACCCCAACCTTCTGGAAGGCGAGGGCTAACAGGACCTCCTGCCTGCCTGC TCACGACTGATTACTTTCAATCCAGCTGCAATGCAAACTGAAACTCATTTCTGTATATCACCACCTTA CAGGAGAGGTCTATTTCTGGGGCACCCAGAGNTCAGCACACATACTGCTGGGA[C/T]CAGGGACTC GTAATTCGCTTGGTCCAACTCCTTCTATGGGGTTAGCTGCCCTCATTC
WI-20768a	71 C T ---			TTCCCACTCAAAACTCCCAACCCCAACCTTCTGGAAGGCGAGGGCTAACAGGACCTCCTGCCTGCCTGC TCA[C/T]GACTGATTACTTTCAATCCAGCTGCAATGCAAACTGAAACTCATTTCTGTATATCACCACCT CTACAGGAGAGGTCTATTTCTGGGGCACCCAGAGNTCAGCACACATACTGCTGGGACGAGGACTC GTAATTCGCTTGGTCCAACTCCTTCTATGGGGTTAGCTGCCCTCATTC
WI-21909	153 A T ---			TGTTTGGCTTTGGCCAGGTACTCTACTGCTTTACATAAAATATCTCATCTGTACATCTAACGGCAA CTAAGTATACGCTTACATCTGCTAGTGGCACCTAAAATAAGGATATTTGTTGTCATCTTTAAAGAAA TGCTTAAACATACCAAAG[A/T]AGTGGGAATCAATAGAATAAATATTTAAGTCTTACAAAGCGGTAC GACACTAAAGTAATAGGATACCACCTAAATTTATATTTCTATGATGGAAG

WI-22202	128 A G ---	---	---	TGTTGCTTTGGTTGTTTCTTGGAAACATATTGGAACACATTGTTTTCATAAAGCTGTCTGACAGT GGCACAATCCCATCCATCTTCAGGCCCTTTAATAAGGTCATTATGAATCTGAATTTCT[A/G]TTAAT ACTCTGGTGCATTTCATCTGCAAAAGCAACTGGCACAACTCCCTTCCGGTGCAGCTCTCGG AGAACATCTAATATTGAGTCTAGTCTGTGCGGAACCTTCTCCAGCTCAC
WI-22189	70 C T ---	---	---	CCAAGGATGAAATTTCCACATTTATTTNCITTTATGTGAATAGAAAATGGCAGTGAAGTGTCTCTATG AACTGAGCGAGGAATGGGCATGGCGCTGGGTACCGCTGGACGCTTGCTTCCAAAAGTACAC TATGTGTGGTGGAGACAAAGGGT
WI-22283	109 T C ---	---	---	GGGGAGGCATCATAGAAAAAACCCCTCAGCCAGAAAGTTAGGACATTGTGATTCAGCCACTAAACGA GCTGTATGACCTTGGTCACTAGGCCCTCGCAGGCTCTGGTTG[C/T]TCATTTGCAAAATAAAACCCA GACCGGGTCATCTTTCAGTCCCTCCAGCTCTATTATTTATGATTTGCTCTTAGTCTTTATGAGCCA TGTATGATTTATCAGTCTCCCTGATGCACTCAACTCCAATGATGCAAAAG
WI-22290a	136 C T ---	---	---	GACGTCTCTGAGGGCTCTGCCAGGTGGATTAGGTGAAGAGAGGTTTATGGGCCCTTAAGCACCG GCCAGTAGTGGGAATGCCATGCCATGGGTAGTGGGATCTGGGGGGTGCAGACCTTGCTTTT [C/T]TTCCAATCTCTCTCTTAGCCAGAACTTTCGAGAGCCCCCTTNAATTTCTTCCCTCTATTCC CCTCTTTCCCAATGTGCTAAGTCCCAATTCAGACCCCCCTCCAG
WI-22292	53 A G ---	---	---	CCAGTGAAGGGTTACAGCCATAGTAGGTTCCCCATTGCTCAGTACCAGAA[G/G]TTTGAGTAC GGTCGTTAAAAATACTATTCTGACCACAGTGGAAA
WI-22387	186 C T ---	---	---	ACCTTGCACACCTGCCATCCGGTGCCATCTCTGGCTGGCAGCATCTATACCCTCTGGCTCTGAAAG GCTTGTCAACCAAAATGGCAGCTGGGGCTAAGGCATATTTAAACAAAGCTCCAAAGGACCCCTT TCATTTGGGTCTAGCATCCAGCTCTCTCTCAGCAAGGCAGGATTGTGGT[C/T]CCTTGTGTTTCTG AACAGGGCCAGGGCAGCCAGGCATGCCATCACTGCAGCACTCAACCT
WI-22395b	127 A G ---	---	---	GCCGTTCCAGTATTGATAATAATTTGTGTTAATTTCTATACAGAAATGGTTCTTTCTTGAATATTT GTAGGGATGGATGAATTGAAAGTGAATTAAGTCAAGATAAGGGGGCACTCTTTAAT[A/G]AAG GAAATGTTACCAATCCATAGTGAAGAGTAGAATATGTTCTTTTAGAGTAGNTAGAAAGTCCCCAGG CTCCT
WI-22405	90 A C ---	---	---	TTTATGGCTCCTGAGTGCCTTACCCAGCTACACTTTACCTTGTATCTATAAAAGTGAATTTAGAGT AAATACATTGGCTGAAAGTCG[A/C]GATCAGGTGCTCTCCACCAAAAGCAAACTGCTGA AATGTGGCAAGTTTCTCAGTG
WI-22419b	67 T C ---	---	---	CCCTTCTGGACAGTTTGTCTTATGTGTTTCAGACAATCAAGNCTGCCCTCCAGGCACAGCCAGTGT [C/T]GTGATGGCATCAGCACAGGCTCCCTGCCCGGCCCTTGAAGCATGGCTGTGTGCAAGAT
WI-21342d	59 T C ---	---	---	ATTTTCCCCTTCTGTGTTTCGATTTTCCCTTTTGTGAGTAAATNAGCAATACACTGAT[C/T]TGGAA ATCTGCGATGATTAAATAACATTAAACAGTTTCATAAACACACCCCCATATCAGAGTATAAAGCAAGAG GTTGAAAAATATCCCTTAACCGAATGCAAAATAGGTATCCCTCAAAATTCACATTTCTCCTCTAGTT T

WI-21763b	154 A G ---	---	CATACCCCTTTTAGTGCCACATTGATCTTAGTTAACAGTCTTGAGTTCCTCTTTAGGCTTCAAGA TAATTGTGATTTTCATCGCACCCAGATACTTCCAAGTGGAGCCAGGCTCAGACTGTTCTCAGTCACT GCTCTCCACAGCTGATT[G]CAGACATTGCCTGTGCTTCTACCCACAGCAGCTGTCTAGTGCACCT GA
WI-21763a	135 T C ---	---	CATACCCCTTTTAGTGCCACATTGATCTTAGTTAACAGTCTTGAGTTCCTCTTTAGGCTTCAAGA TAATTGTGATTTTCATCGCACCCAGATACTTCCAAGTGGAGCCAGGCTCAGACTGTTCTCAGTCACT T/C/GCTCTCCACAGCTGATTACAGACATTGGCTGTGCTTCTACCCACAGCAGCTGTCTAGTGCACCT GA
WI-22440	64 A C ---	---	CAGTCCATTTGAGTCCCAGTCCAGGGTGCACTCTCCTTTATCTTGCTTAAGCCACTTGGGT[A/C] TCCATTCCAGCTCTGCACCTTCTCCAGTTTCTCATGTGCAGAGTCCCTGGAGGGAGGCTTTCTGG AAAT
WI-22449	74 T C ---	---	CAATGAATGTTGTGGCATATGATTTNCCATTGTGTGACAAATTTATTAGCTGGCATCCGAATACAGTAC TTCTTTT[C]GAAAAAATACACAATGGGAACGTGACA
WI-21965a	112 A G ---	---	CAGGTTCCACCAGAGGCTTTTATTTAGCCACTCAGGACCTGCTGCTTCTGCTCCAAGGCAGTGAACA CAGTCAGGCTCTTCTAAACACTGGCAGGACCTCCCCACAGCC[G]CCCCACAGGGTCTCTGTT TCCCAAGTCTGATGGATTGAGCAAGACCTTCACACATTCACCCACTACCTGCTGGAGAGGAGGCTC ATGAGGCAGCCTGTGGTGCCACGCTCAGTGTGACACACTGCCAATGTGC
WI-21687c	115 C G ---	---	CACCTGGCAGTTGAGTCAGATTGTAGGAAAAATTAAACCCAGATGGGTCTACATTTTNTTCAAGTTCA AACCACATGGTTTCCTAGTCAGAAAGTCTCATGGACTTCTTCTTAAG[C/G]TGTTCTATGATCAGAC CACCTCTAAATGTGGCTTTTACCCATTACAGGCTACAGTTGAATCAGGCAGGAGCAGCTGCTGGAG AG
WI-22374a	149 T C ---	---	AGCTTTTACAACAAAGCGAGGGTTTAAGGAGCCTGAGAAGAAATTTTCACAACTATTGACTATACAGAG TCTTCAATTCAAAAACAGTTAATAGTAACTTGGTGGCACATACAACATGCATTGAATACTCTGTAT TATTCAGTAACTAAAT[C]JAGGNTCCTGCATCTCTCTTCA
WI-22250b	132 C T ---	---	ACTTGCTTCAGGCAGGCATTTCTGGGATCTAAACTAGAAATCCTTGAAAACAAATAGTACCAGCCA CTTTGAGGAATGTGCATTCACTGTAGTGGGTTATTATGGGTCTCTGCTCTGCTGCTGCTGTTATG[C/T] GGANCCAGGAGTGGAGGAGGAGCCGTGGAATAGACAGGGGAG
WI-22250a	89 G A ---	---	ACTTGCTTCAGGCAGGCATTTCTGGGATCTAAACTAGAAATCCTTGAAAACAAATAGTACCAGCCA CTTTGAGGAATGTGCATTCACT[G/A]TAGTGGGTTATTATGGGTCTCTGCTCTGCTGCTGTTATG GGANCCAGGAGTGGAGGAGGAGCCGTGGAATAGACAGGGGAG
UTR-04932-2b	192 G C ---	---	GCAGCCATCCTCTCTCCAAACACCTCCCAGGCCACCTTGGGGCCAGAGCACCTCATGCCCCAGCAGCAC CTACGTGGCCCGAGTACGGACCCGCTGGCCCCAGGTTCTGGGCTCTCAGGACGTCCCAGCAAGTGGGA GCCACAGGTTTGTCTGGGACTCCCAGCCAGGGGATGAGGCCAGCCCCAGAACTG[G/C]AGTGTCTTC TTTGACGGGGGCCCGCTGCTCAGCTGCTCTCTGGGAGGTGAGGAAGGAGGT

stSG1019 3	136 GA ---	---	---	GGAACAATACTACCTAAGGACAAAATACTATTATTAACAAAAAGTCTCTAGTGTATATTGTGTAACACATTTCTGGAGCTGGTAGGAATAACCATTTTATTTTCTGTAGTGCCATCTATACAAAACCTTTTAC T[G/A]TTTGAAAACAGATTAAAGTTGCAAACT
stSG1020 2c	143 GT ---	---	---	AAGCTAACTTAGGTGAATGGTCCCACTCAAAAGTCTTTCCGAGGGAAGCTCAGTCCGCTTGGCTGGAGAGTCAGCCCTGGTCACTCATAACGGGCTCCAAGCTAAGCGTCAAGGAAGAGTCCCACTGCTTCTCGCTGTCA[G/T]CAAGACCCACAAGGCAGATGCCACTGCTGCTCTTCTCTTCTGCTACTTTCT
stSG1020 9b	75 AG ---	---	---	TCCTTTCTCTTTCACTCTCAGTCAGTCACCATGATTCAAAATAAACTAAATCTCTCTTAAGATCCCACTTTATTTTTA[G/C]TCCAATAAATGTAATTATCAGCTGCTGAATT
stSG1020 9a	34 CT ---	---	---	TCCTTTCTCTTTCACTCTCAGTCACCATGATTTC/TAATAAACTAAATCTCTCTTAAGATCCCACTTTATTTTTAACTCCAATAAATGTAATTATCAGCTGCTGAATT
stSG1021 8	29 TC ---	---	---	TACTAGACATGCAAAATGAGAAGATTACA[T/C]GTGAATATTTAAAGAAGTTATATTTGTTTGACATAATATGCATTGACCCGGGCATAATAAAGTTAAAGCCAGTTATTCIGA
stSG1025 2	108 AC ---	---	---	ATAGGTTTCAGGAACAAAATCATTAAATGGAATAATGAGAAGATTCTTTATTTTGGACCAATTTTAGGCACTTAAGAGTTTCTTTCTCTCTCTTCCCTTTGATCA[AVC]AGTGAAGATATGATAGGGAATTCAGAAATTCCTCTCTCTG
EST10915 0	123 AC ---	---	---	CTGTATTAATTAAGAAAGGCACATTAAATGAGGGACGGAAAAATCTACCTGTACACAAAAATTTCTGTACTTTAACAGCATCTCAATAAACCTTTAAAGGATAATGGTTACGATCATTTTAAAG[AC]ATTTTAAAGAACTGAGTTATTGGAC
EST11023 1	166 TA ---	---	---	TTTTTGTTAAACCAACCCCTGAAAGTTCCACATGTGAAATATAGATACAACAGTGAACAAAAATATGTGGCCTCCCATGTACATTGGTTACCTATGTACAAGTATCCTATACACAGTAAACAGCAGGGCAATTAGTCAATTAAAAAATAGTACATGTTAT[AT]GTGTAATAAAAAATTAATTTACAAAGGCTTTTCCACTCGTGGATTGTATCCITTTTGGAGGGAGGAGTAACTCTGG
EST14096 8	71 GC ---	---	---	GGGATGTATATTACAGATAACACAACCTCACAATAATATACCATCAGACATTGAAAACTAAGGCCATTCTGTGA[G/C]TTATTTTAAACCTGGTGTTTGCACATAATGATCTTAAAAAATAATGAATTACCAAAACCAAGATTCTCTCTTAAATGAAAAATTAATGCAGGTACAGGATAACTTTAGGGCTATATCTAATCTGAAG
EST22113 6c	125 CA ---	---	---	TGCAATTGTGAGAAGGCAGAGGGGCCAACCCCTGGACCTCATCTCTGTAGATGTGAGGTCGCAGGGATGCTTAAGTCTCTCTCTGGCAGAGACCCGAGGTGCAGAGATGATCTTCTCA[CA]CCCTTCTCAGGGTCGTGGAG
EST22555 7	60 GA ---	---	---	TCAAGCATGTGTAAGGCACCTGCCCCGCCAGACCCCTTCTAACTTCTGCACACTGGAAGGTG/AJAAA CCTGGGAGAGAGAAGACACTCCCTCCCTAGCTTCTACCTGGGACCCCTCCAAAGATGAGCATTCATCTTGGAGACCATAAAAAAGGACAAAAAGACCAGGGGCTCAGAG

EST22917 6	74 C T ---			GTAAACCTTGCAACGCCATGCTAAATGGAAGCCTGACTGACCAGGGGCTCTGGGCTCTCAATGCA ATAGAAAC/TTTGACATGGGGCCAAAGACTTCCAGACAAAGCACGCGAAGGGTAGAGGATATAG GTTAGCATCATCTGGTTGTGA
EST36458 6	65 A G ---			CAAGTTAGAACCATGTCATCAGCTTTTCATCCATGGTGAACCTTAACCCCTCAGGCTGTCTACTCA/AV GTTGGTTTCTAGCCTCACTCGCACACAGGAAGCTTGGAAATTTGGAGGCTCCAAAGTCACTCTCCA GAGGGGGAACCTTCAAAGAGGATTCACACAGTGAAGCAGATCATGGGCAAAAGTC/AVGCTATGG GGCCAGACTGAGGTTGGACCAACAGCACTCCAAAGCTGGGCCAATCCCAACCGCTGGTGAAGCCGC ACAGCACGGAGTAGCCAT
EST36745 3	56 A G ---			TGTGACCATACCAAAACCTATGCAATAAAGAAAGAAAAATCCTCACTTAAAAAACAACAAAA AACCTTTGCAATGCTATCATTTTTCAGGCTCTTTGAAGTGTGAATAAAGTTTCATAGCAATTTTGGGA ATTATGGTTTGAATAAATAACAAATGTGTGATCTCCTGAGACACATTTATAAACATTCTGGTATG T/ATTTATGTGAGTGGTCTCTAGTGGCCAAT
STS- R37410c	201 A T ---			TGTGACCATACCAAAACCTATGCAATAAAGAAAGAAAAATCCTCACTTAAAAAACAACAAAA AACCTTTGCAATGCTATCATTTTTCAGGCTCTTTGAAGTGTGAATAAAGTTTCATAGCAATTTTGGGA ATTATGT/TTGTTTGAATAAATAACAAATGTGTGATCTCCTGAGACACATTTATAAACATTCTGGT ATGTATATTGTGAGTGGTCTCTAGTGGCCAAT
STS- R37410b	139 G T ---			TGTGACCATACCAAAACCTATGCAATAAAGAAAGAAAAATCCTCACTTAAAAAACAACAAAA AACCTTTGCAATGCTATCATTTTTCAGGCTCTTTGAAGTGTGAATAAAGTTTCATAGCAATTTTGGGA ATTATGT/TTGTTTGAATAAATAACAAATGTGTGATCTCCTGAGACACATTTATAAACATTCTGGT ATGTATATTGTGAGTGGTCTCTAGTGGCCAAT
STS- R37410a	48 C T ---			TGTGACCATACCAAAACCTATGCAATAAAGAAAGAAAAATCCTCACTTAAAAAACAACAAAA AACCTTTGCAATGCTATCATTTTTCAGGCTCTTTGAAGTGTGAATAAAGTTTCATAGCAATTTTGGGA GGAATTTATGGTTTGAATAAATAACAAATGTGTGATCTCCTGAGACACATTTATAAACATTCTGGT ATGTATATTGTGAGTGGTCTCTAGTGGCCAAT
STS- R42778	74 C T ---			TATCGTGGGAAGTTCCAAACCTCATACTTATGCTGCTTTTCTACTTGCTAATATGGATGCTCTTGCCA GGCTC/C/TTTAAATTGTCTGTAACTGGGAAGAAACCTTCTACTCTCCACAAACCTGAA CAATCTGAAGAGATGCATAGCGGATTGGTGGCTTTCAGCAGCTGTGGGAGGTGGGACTGAGGAGCG ACTGCTAATCAGTATGGGTTTCCCTCCGGGATGGTGAATAATGTTCCGGACCTAGATA/C/GT/GACGA AGGTAGCACGACACTGTGAGTGCACTAA
UTR- 04350	125 C G ---			GAAATAAACTAAACCTGCAAGCAATCACTGTTAATAAGAATTGTTCTCTCTGTTT/C/GACAGTTG AAGTGGGTGTGAGATGGGCATAGCAATGAACAGTGGAGCAATGAGGTCTCAGAAATGCGGGCAAA CTCCTCTGTGAAAAATGTAT
siSG1026 6	55 T C ---			GTATAATTCAGCATAAGCCCAAGCCCTTTTAAATAACCAATACTATCATTTTATGAAATCTTTTACA AGAAT/GAAGCACAGTAGTACAATATTTAAGCATCTCAAGTCTCCATTTAAGAGTTGACTATC CACCTTTAGATATGAGGAAATGGTTTAAATGGACACAAAGGAGTCAGCCACGTTGGAAACCAACATAG TTTCATACCACGTTGAAACCATGTGTTTGATATGCAAAATACAGCAATAATTTTTTCACT/C/ATTTG TCAATGCCAATGCATTGAAAGGCCCCAGAAAAATGAGAAAGGATAACAAACCTTTTGATAAAAAGGTA AGAATTCTGTGTG
siSG1028 2	70 T G ---			
siSG1031 0	128 C A ---			

stSG1033 1b	116 T C ---	---	TTTAAAGCTACATGTCTGAAAGAATGATGCTGCTGATTGAATAAAGGAAGAAAGGATGCATTTCCGG GCTCAAACCTGTCTAGGAAGGCTAGACCTCAACACCAACACCTCCAT/CJGCAATTCCTCTTTGG CTACTATGTCTTTTCCCTGACTTCTGCTCTCCAGCTCTCTGGGCTGCTGCTTCCACCTGTTTCATCTGA CTTAGGACCCCTCC
stSG1033 1a	107 A T ---	---	TTTAAAGCTACATGTCTGAAAGAATGATGCTGCTGATTGAATAAAGGAAGAAAGGATGCATTTCCGG GCTCAAACCTGTCTAGGAAGGCTAGACCTCAACACCAAT/CJCACTCCATGCATTTCCCTCTTTGG CTACTATGTCTTTTCCCTGACTTCTGCTCTCCAGCTCTCTGGGCTGCTGCTTCCACCTGTTTCATCTGA CTTAGGACCCCTCC
stSG1243 b	225 G A ---	---	ATTGGCAATGGGAAATGACACCAATCATTTGATTACAGAAATGTTTTATAATCCTCCTCTTG AAATTATGTTAGGCGCCAGCATGTTAGCTTATGCTGCAATCCAGCACTTCGGGAGGCCAAGGAGA AGGATCGCTTGAGCCCGAGGTTGACACCCAGCTGGGCAACATAGTAAGACCCCATCTCTGTTTTT TTTAAAAAAGAAATTCCTGTTG/CJ/AAAGTATTTTCAGACCCAAAGGAGGT AACTGACGTATCACAGGGGCAAGTATCTCTGCATAAATTTGAACCTAGTTTGTCTTAC/CJ/CGCT TCACATTTTAGCATGGGCCAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGCAA AACTGACGTATCACAGGGGCAAGTATCTCTGCATAAATTTGAACCTAGTTTGTCTTAC/CJ/CGCT TCACATTTTAGCATGGGCCAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGCAA
stSG1345 b	60 G A ---	---	TTAATGTCATOCAGGGAGGGGCCAGGGATGGAGGGAGGGTTGAGGAGCGAGAGGAGTTATTT TGGTGGGATTCACCACTTTTCCCATGAAGAGGGAGACTGGTATTTTGT/GJTCAATCATTAAGAA GACAAAGGGTTGTTGAACCTGACCTCGGGGGGATAGACATGGGTATGGCCTCTAAAAACATGGCC CCAGCAGCTCAGTCCCTTCTCTGTCG
stSG1385 b	117 T G ---	---	TCGTCCTCTTCCAGTGTCTCTGCCAGAAGCATCCCATGATGTTGTGACCGCACAGCACTTTGTGCT T/CJGCTTTGAGCACTTGCCACTCTGGCTGGTGTGCTGCTGCACTGATTTGTACTGCTTGTGCTGCCC GATCTGGTTCCAGACAAGGCTGATTCAGAGACTCCACGTGGTCAAGGCTCTGTTTGTCAATCCCT TGGCTCCTCCACTTCCAGTTTGGCTTCTGCTCCTCAT/CJAGTCTCTCTCCATGTGGCAACAAGATGGC TACTGGTGGTCCAGGTTCAAGTCTCAGCTTGGAAATCCAGCAGCAAGAGATGCTCTCACTCCCA AAGTCCATAAATCAATCCTTGGGAAG
stSG1427	103 T C ---	---	CCCTGGAGTTTCTGAACATAGGAAGAGAAATGCAAGTATGTTAGGTC/CJ/GJCTCCCTTGCATGA AATGTGGGAGAGGGAATAAAGTTAGGCAACATTTAGCAATCAACAGAACCCCTTCCCTATCCTACC GCA
stSG1471	50 A G ---	---	CAAAACCAAAATCCTTCCACCATATATTACTATTAGTCTAAGT/CJTTTAAATCAAGGTTGAGA ATGACGAATCAAGAATTTCTTTCATACATAAATGCTTCTTCCCTAGTTCTGCAGATGGTA
stSG1483	44 T C ---	---	CACACCCACAAGTTTCAATGCTAATGCCAAGTATCAACTCTTGAGGACAAGGCAAAACCAAGTGTGCA /CJ/GJ/ATGTGGAGGATGTCTGTTCAGCTGTAGTTACTAATGCAGGAAACCCCAATGCAAGAGGAA AATGCCTGA
stSG1696	67 C G ---	---	

stSG1847 b	95 G A ---			TTGCAGACAACAATGGAAGCTTTAAACCTCTTCAACACAAATGCTACCCCTAAAATGAAAGAATTT AGAGGTTAAATAAAACAAGTGAGAGACC[G/A]TTTACTTACATCAGTTCGGTTTATAGACATTTGAA TCATATCTGAATGACTGACTTGTTCCTCAATGTGAAACCAAAATTAATAACTTGATCACTGTGCT TCAACACAACCTG
stSG1847 a	49 C A ---			TTGCAGACAACAATGGAAGCTTTAAACCTCTTCAACACAAATGCTAC[C/A]CTAAAATGAAAGA ATTTAGAGGTTAAATAAAACAAGTGAGAGACCCTTTACTTACATCAGTTCGGTTTATAGACATTTGA ATCATATCTGAATGACTGACTTGTTCCTCAATGTGAAACCAAAATTAATAACTTGATCACTGTGC TTCAACACAACCTG
stSG1897 a	83 A G ---			CTTAATGCCCTTCTCTCTCTCTGACAGGACACAGATGGGTAACATAGAGGCATGGGAAGTGG AGGAGACACAGGACTT[A/G]CCCCACCACCTTCTCTCCGGTCTCCCAAGATGACT
stSG2022 a	86 T C ---			TGCTTGAGGTTTCAAATCTGAGATATCTATGGCAAGTTTATAAAAAGTACATTGATCAAGGTACAA TTTTAACATTAAATACAT[C/J]ATTCATAATCTCATCTATTTAACATTAAACACAGGCCTTTGTGTG TGTTATTTTTTCTCCCTACAATATTTCTGACTCTGTAGGACAGTGGCCCTCAGTTGGGGGTTGAC T
stSG2076	104 C G ---			AAACGTTGTCCCAAAATTGTTTCAGTTTCACAAGTATAAAATAAGACTTCTGAAAAAAGTTTACA ATTAGTTATAAAACACTTAAGAATATATTTGACATT[C/G]ACATCACAGTGGGGCATTTT
stSG2108 c	71 A G ---			TTGAGCAACAATGATTGCGAATTGGGCAGCTCCAAACCAAAAAATGATT[C/G]AGGGGCTCCACAG GAGC[A/G]TAAGGGGAAGACTTTTATAGGACAACTGTAGAAGTAAAGCAAGCAGACGTTTGATTG GTTACAGTTACACAGTTGCTTATTGGTCTATCTTATTGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTGGGCTGTGCTGA
stSG2108 a	49 T C ---			TTGAGCAACAATGATTGCGAATTGGGCAGCTCCAAACCAAAAAATGATT[C/G]AGGGGCTCCACAG AGAGAGCATAAGGGGAAGACTTTTATAGGACAACTGTAGAAGTAAAGCAAGCAGACGTTTGATTG GTTACAGTTACACAGTTGCTTATTGGTCTATCTTATTGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTGGGCTGTGCTGA
stSG2141 b	173 A G ---			TTATTCAGGGGACAAGCTGCACAAAGGAATGTTCTCTATTATTTTAAACAAATGACTGCGGTGAC TGAATCTGACTGTGTGAATAATCTCAGAAATGGCAGCACCCTGGCATGGCGATGGTGCGAGTGGGT GCAGTCCCTGTGGTCTCTATTGCTTGAAGAGAGAAAG[A/G]AAGTCCCTATTATTATTTAAAGGC AGTTTTCAGAGCACTGGCATTCTGTGTTGCTCTG
stSG2141 a	113 C T ---			TTATTCAGGGGACAAGCTGCACAAAGGAATGTTCTCTATTATTTTAAACAAATGACTGCGGTGAC TGAATCTGACTGTGTGAATAATCTCAGAAATGGCAGCACCCTGG[C/T]ATGGCGATGGTGCGAGGTG GGTGAGTCCCTGTGGTCTCTATTGCTTGAAGAGAGAAAGTTCCCTATTATTATTATTTAAAGGC AGTTTTCAGAGCACTGGCATTCTGTGTTGCTCTG

stSG2148	50 A G ---	---	TGGGAACAACCGGCTATAGTCTGAGTCATATTTTAGACCGTGATTTTC[A/G]AAAGAAACAATAA ATGTGGATTAGAAAGGAACATCCATTACTGTATTTTCGATACTTGTGATGTTCCACAGACGAGCTC ATCAC
stSG2175	68 C T ---	---	CTCAATGAGGACTCCATCAGCCAAAGCGGTTATATGGCAGATGAGCTGTACAAATCTGTTGTGTGCT [C/T]GCCGCGTACTCAGCTAATGCTACCGGGTTGGAGCGCACACCGAGCCAGCCACCTTTTCCAT ACCTGGCAGAGGGAAGGAGTGGAGGACCA
stSG2189	41 C T ---	---	CAAGTGGTAAAGCTGGGATTTGAGCCTGATATTCACACTA[C/T]CTACATTCCTCCAGTATAATA GGAACCTCATCGCTAACTTTGAGCACTTAGTGTCTGAGTACTTCGTATAGGTATCTCAATCCTACTC CAGCTTTGCGAAG
stSG2200	49 T C ---	---	TGTTGATGACCATAGAGGATGCAAAGCTCCGGGCTGGTTCTGTATGATG[T/C]TTTATATTATGTAT AATGCTTACCTGATGATACCCAACTATTACTAGCCTTATAGATGAGGATGGATGGCAGCTTGGCTG GTCAAT
stSG2243	85 G T ---	---	CATTTCTGCTCCTGCTTCCCAGTACTACCCCGTCCAGCAACTGCCCTCTCGTATAAATAAGTATCAA GATGGTCAGTAGAAAAG[G/T]AGAGCATCTCTCAGCCCTGGAAGACAGTGTGGGAGCTTCAGCT
stSG2257	65 A C ---	---	TCAGTGATTGTAGGAGCTGGCTAAGTCATGTCTAACTCTGTGAGGAGGCTATCAGAAAGGGCAG[A/ C]GTGTGAGGAACTCTCGCCAAAGCACTGGGCTGTCTCCTCAGGCAGAAATTTCTCCT
stSG2306	67 A G ---	---	GTCATCAGCGTAGAGGTCAGTGTATAAACAAACAGTAGCTATATGATATTTGGAACTATTTTACA [A/G]TATGCTCCCATTTGGGTTTCCAAACTGATACAACCATGAGGTGAACACTTTCAGTGTTCACAG TTCTCCAGAGA
stSG2334	70 T G ---	---	GAAACTACCCACAGCATCATGTTAAAGAAGAGAGATGAAAGAAAAAATCCCCGCAAAAAACA AAAAAT[G/T]GCAGTGGGGGCTGTGGAGGGGTGAATG
stSG2339	63 T C ---	---	AGAGCAGAAATGGTGAATCAACAAGACCTCAATTTGCTTGACTGCAGAAGTAAGTGTGTGAC[T/C] GTTCTCAGAGTCAACATTACGGTGACTGTGTCTATTTCTGGCTGTCTCCTATTCATCA
stSG2465	76 C T ---	---	CAAGACTAAGAAGCCGCAACCGAGTGGTCCACTCAAAAAAGAGATTCTGTATCTACCTCAAAATG CAGAAACCA[C/T]TACAGATTAAAAAGAGAAACACACACACACTTTTGAGAAACTCGCCCTTCCTC ATCTTCAAAGTGTGGGTATGCA
stSG2549	140 T C ---	---	TTGCAGGCTGTATTCACAAATAACAAAGTCATGTATAGAGAATGTGAAATGATACTTGAAAAACCAA GATATATAAATATTGAAGTCATTTATGCCCTTTGATGACTGGGTTAAATATGCAAAGCAGCTAAAG GAATATT[C/T]ACACCCACCCCTTTTAACT
stSG2577	123 T G ---	---	AATTGCCAAATGGAAAATTCAGAGGATTTTAGACCAACTTTGCCCTGTTCATTCCCAGTTTGGT CCCAATATAGGCCCTTCTGCAAGAAGAGATCAATGCCGAACCGAACTGTGAAGCA[T/G]GAACAATC CCGGCCCCAGATTAAATTAT

stSG2577 a	121 C T	AATTGCCAAATGGAAATCCAGAGGATTTTAGACCAACTTGGCCCTGTGGCATTCGCCAGTTTGGT CCCAATATAGCCCTCTGCAAGAAGAGATCAATGCCGAACCGAACTGTGAAAG[G/T]ATGAACAATC COGGCCAGATTAATTAAT
stSG2700	58 G A	ATCTCTCGACTGCTTTAGTGGGAAAGGAATCAATTAATTAATGAAGTGTCCGGCCCC[G/A]AGTCAC TCAGCGTTTGGCGGAAATAAACCACTGTGCCAGAGCAGAGGAGGCTACTTGAGCCGGACACCA
stSG2724 b	101 T G	AAACAAGCTTTGTCAATTTCCACTACATTTTGTGTGCTTTTATTAATTAATTTGCAATGCTATAAT TTAATACTTATATCCAAATGCTTGCATAATCA[T/G]TTTTTTTAATCCTGGGTGTTGAAAGAAC
stSG2776 a	65 G A	GTGGCGATCTTTACTTTCCAGAAAGGGCGTAATATAAAACCTGTAGAAAGTCTCGAATATGC[G/ A]TATGGCCCTTTGGAGTTAGCCCCAGGAACCTCAACAAGGGACACTGCTGGCCAACCCACAAA ATATCCACTAATCCCGAATATAGTAACCTGCTTGTCGGAATG
stSG2791 b	109 G T	AAGGAAAGGTGGAGGGAAGGAAGGAATTAACAATGTTAGAAAGAGCAACTAAAGATTATTTTC TATTATCTCTGAACGGTAAGTAGCAATTTTAATAATATT[G/T]GGGTCCACTTAAATCTATTA AAGCAGAAAGTGTAAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAACCAATCAG
stSG2791 a	100 A G	AAGGAAAGGTGGAGGGAAGGAAGGAATTAACAATGTTAGAAAGAGCAACTAAAGATTATTTTC TATTATCTCTGAACGGTAAGTAGCAATTTTAATAATATT[G/T]GGGTCCACTTAAATCTATTA AAGCAGAAAGTGTAAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAACCAATCAG
			CCGCAATTTCAACACACATTTCTATGAAAACCTAAGGGTGGATCATGTACAAACACAAAAACAAGC TCCCTCCCTCCAAAACAA[C/T]GAACAAAAATAAGAAAAAGAAAAACCCATGAATGCCAGGTTTA ATTTTTTTCC
stSG2826	85 C T	ATGGGTGCATTGTAAAGGCAATTAATACTTTTCAGGCAGGGGCTGGCAATTTAATGAGCTGA TGTGTCCCAAGGGAGACGGCC[G/A]GGCTCACACATCCCATCAATACTCCTCCCAT
stSG2850	88 G A	ATACTCACGGGGGCTGAAGGGCAATGTGAAGAGTGACTGCAAGTCTCTGGCAATTTCTGTGGTGCAGC AAAT[C/G]CCCCCTTTATTTAAATGATCCAGACATCTGGGCAGCATAGCT
stSG3031	71 T C	GTCCCAACTCCTCCTCTTAGAGAAAAAACTGTGATTACCTCAACTTGAATATGAACCTGTGATTG AAAAAAGTCAAAAAC[G/A]TGAAGAAGCATCAAGCCAAAAGGCAAAACTGGCTGAGGC
stSG3058	81 G A	CAGCATCTCCAGAACATCTAGAACTGAACCATCTTGTCACTATTGAAAAACAAAGCCAAAGTTC CAATCCAAAATAATAATGAACGTGC[T/G]GATAAACATCTTCTTATGGTTCAGCCCTACTTT AGTT
stSG3092	94 T G	AAGAAGTACTTTGGTAGCTATTTAAATAAGAGGGGGTGGGAATGAATGTCGAGATACGAGCACCTG CATCTTTAGTCAATTTGTCAGTGGAGTC[A/G]TGGGGTGTCTAAGTGTCTGAACTGAAGTAG
stSG3230	95 A G	ACATCTCATCCAGTAAGATGAAGAAAGGAATATCTGAGAGCAAGCAGCCCTGCTCCAGGGGOC CAGGTATGTAGAGGCCAGTGGGGTGGCCACTGGTGTCTTACCACCCCTGCCATCCAGTCTG
stSG3245	160 G C	GCCCCAGTACCTACCTGGGAGGTT[G/C]TGTACTTGGCTAAGTACTTCATGCTTAT

stSG3265	42 T C ---	---	AGGTGAATGAGTTACTAAATGTAGCATTTATTTATAAGGAAT/CJGCAATGTGAATAGTTTCTCAG TTTTCAATTATGGAAGATGATGATTTTCCAGCCACATTCAGTGTATGTTTCTAAATAACACAATCGAC AGGACTGTCTGTTAGTACAATGGAGGACAGCTTTTTCAGGGCAATGGGATTTCTTGATAATGCTAA ATCTGCTTGTGAGCTGAATTTCTTGGGCTTTATGTGGCAGTGTGGTAAAAA
stSG3269 b	141 C T ---	---	TGTACTTACTGTGTCATCTATCCATTCCTTCCCTGAGCCTGGACTGCTCTCCAAAGGGAGACTAGG AGTGAAGGGAGGAGTCTCCCAAAGTTACCTTTAAGCTTGATAATTAGCTCCATAGCCATGCTAAA GCATGA/C/TJGTAGATCCCCAAGTCCCTGACACATTTTCTTAAGAACT
stSG3269 a	24 A G ---	---	TGTACTTACTGTGTCATCTATCC/CJGTTCCCTTCCCTGAGCCTGGACTGCTCTTCCAAAGGGAGACT AGGAGTGAAGGGAGGAGTCTCCCAAAGTTACCTTTAAGCTTGATAATTAGCTCCATAGCCATGCT AAAGCATGACTGTAGATCCCCAAGTCCCTGACACATTTTCTTCTAAGAACT
stSG3284	130 C T ---	---	TTAACTCAAGAACTTTTCAGTTACAGGAAGATTTATCTAATATTAAATGACTAAATTACAAAAGC ATAAAATGTTTGAAGCCATTTTAAAGTTGTTTGAATCCATATTAGCACTCAGACTTCCCCA[C/T] TCCCTAACCTTTGTTAATTGCTGTAAATGGGACATTTGTGTTTGATCTACCC
stSG3292	99 A T ---	---	GTCTCAAGTGAATCTGTAATACATTTTAACTGCTGACTTCAATCGGTACATGAGGCTTAGACATA CACATCATTTGGACAAGTGACTTAAATATCTAA/JTTCACAAATCAAAATAGCATTTTCTTAACITCAA TAAATGTCATATCTTTAGCTCTCACT/CJCCAGTGTATCCATTTCCCGAGCGTAGAGCTTTCTG TTCTGTAGATTTGCCTGTCTGGACATTTGATATAAATGAGTTGCTGTATCATGTTTCGACTTCTCTC ACCTAGCATGATGTTTCAAGACACATCCATGCTGTAGCATGCTGAGTGTGCTTCACTTCTTTAA GATCCCCAGTATTATTTCTAAATTTGAACCTTGTTTGTGGAATAAAAAATCTGAGGACCCTCAGAG GG[C/T]ATAAGGGAAACCTCTTTGTCTTAGTTCATAAGGACTTTCT
stSG3369	69 C T ---	---	CAAGACTGTAAGAACGTAGGCCCTTGAGAGTGAAGGAAGGATGCTCGAACTTCCCCAGGACTCAGG CTTCAGCTTCACAATCCCGAGGAAGGAATGACATTTCCAAACTGTCACTTTGTAGC/G/TJCTGGGT CAAAGTCTAAGAGGACAAATAAATAGAGACT
stSG3398	125 G T ---	---	TCTTACTCTGTTAACTCAGTCTGGAGTAAAGGATGCAATCACG/JGJCTCACTGTAGCCTGGACCTCC TGGGTTCAAGTGATCTCTCCACTCAGCCAACTGAGTAGCTGGCTGCAGGACAAAGTCAACATGCCTA CCTAAGTTTTGTAGAGACAG
stSG3416 a	43 A G ---	---	GTAAGACAAGGTTTTGCTATGTTGACCAGGCTGGCTTGAACTCCTTGGCTTCAAGCGACCGTACCA CCTTGGCCTCCCAAGTTGCTGATATTACAGGTGTAGCCACTGCCCGCCGACTTTTAAACTGAAT GTTGAAATCATTTCTGCTCTTTGCTGGTAACTGAT/JCAAGTTGCTTAACCTTTGTGAAACCAC TTTCTTATCTGTAAACAAATGGACAAACAGAACTTTTCTTCTCTCTC
stSG3424	173 T A ---	---	GTTTCATGTTAAAGATTAGGAAAGCTGTGGATGTGAGGGGTCAAGGTGATGTGAGGCGCTCACAGA ATGAGTGGCAGAGAGGGGCCCTT/A/GAAATAGCTTACTCTGTGTTTCTTATC
stSG3436	88 T A ---	---	

siSG3463	103 C T ---	---	GATACAGAAGATAGTGGTATGGATGGATAGTATGAAGGACAAATAATACAAATATATTTATTG AAATAACAAAAATGCATACACAGCTCAATGGGTAC[C/T]TGGAAACAACTTGCTTGACTATATTA CTGA
siSG3491	71 G A ---	---	CAAGATACTTCATTGTCTAAGTAGTGCAGTGTGGCAAAATATTTCTCAGGAACAAGGACGATTG AAGA[G/A]GTGGAATTACTGTGCAAGGAGTACTTTACCTCCAAATAGCCTGCAATTTAGCAGTCTGA ACAATCTCTAATCTTTACTGGCACCTGTGGATTCTATTAACACTCAATTTACTATTTCTGTGATG ACAGAAAAATAAGTTAAC
siSG3523	33 C T ---	---	TAGCCATCTTACTCTAGTTCTTTTGGGTTTTC[CT]GCATATATGTGTACAAACACACACACACC CCTAATCTCTCAATGCTCTTGGCATAAGTTTATCTCTTACTGGTCTC
siSG3536	213 A G ---	---	AGTACAAACACAGATTTAAAGAGCTCAGCAGTATTGACACGCTGGAAATTAATGGAGACATCCACTT ACTGGGAAGTAAGGAGCTGGTAGCCTACCTACACAGCTGCTACAAAACCAAAATACAGAATGGCTTC TGTGATACTGGCCTTGCTGAAACGCATCTCACTGTCATTCTATTGTTTATATTGTTAAATGAGCTTG TGCACCATAG[A/G]TCTGCTGGGTGTTCTCAGTCTTGCCATGAAGTATG
siSG3583	112 G A ---	---	GA AAAAGCTTAACATACGATCCATGTGCAAAACCCCAACAGGATCTACGAACTCTGGCATGATCCA CATCGCTACACATACCATGCTGGAAGTGACATCCACACAGGCAC[G/A]TAACATACACAGTACTGT CTAGTTATCAACACCTAC
siSG3586	60 G C ---	---	CCTAGTAACATAGTGAGACCTGCTCTACTAAAAATTTAAAAATCAGGTGGTGGTG[G/C]ACG CCTGTAGTCCCTACTTGGGAGGCTGAAGTAGGAGGACTGCTTGAAACCCAGGAGATGGAGGCTACAGT GAGTTATGATGGCGCATTGCACCTCCAGCTTGAGACTGTTTCAAAA
siSG3589	101 T C ---	---	ATATAGTGTGGTAGCATTATAAATCCTTTAAAAAGCAATCTGGCCATATCAAAGGCAAAAAAGT GTATATACCACCCCTGGCACAAAAACCCCAATGA[T/C]CCTATTCCAAGAATGTATCCAGATGAAA GTATCCAACAACAAAAAGCTATATACAC
siSG3590	70 A T ---	---	GAGAGATGAGCTATTTATCTTTTACTTAATGAAGATGTAAGAAATGATCTTCTGTTCTAAAAAAA AA[A/T]TTCTCTGATGCTCTTGACCCCTGTAGGAAACACATTTCAGTTTCTACACT
siSG3619	78 A C ---	---	CAGTGAGACTTCTCATTTTATAGCAATACATTTTGCAGCTTAAATTTCTTGAATTCATATACGCT TCTGTCAATTTA/CJAACAACTCCAGAGAAAACTGGGCTCTATATATTTAAG
siSG3644	40 T C ---	---	ACATATGTAAGTCCATTAGTAGCCATATTTAGGATGAGAT[C/G]GATTGAGAGGCGATGAACCAAGG ATCGGTAATAATCATTTATGAAATAATAAGTTATCTGGGGAACGGCCATTGTGCCAACATTTACTAA GTGCTCTACTA
siSG3646	70 G A ---	---	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAAATATATGATGATAACAATATATGCTTACT GGT[G/A]ATATTAACTTTGATACTTGGTTAAGATGGTGCTGCTAAATTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA

stSG3646 b	55 A G ---			CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATATATGATGATAACAATAA/GIATATGTCTT ACTGGTGATATAACCTTTGATACTTGTTAAGATGGTGCTGCTAATTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA
stSG3646 a	43 A T ---			CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATATATG[A/T]TGATAACAATAATATGTCTT ACTGGTGATATAACCTTTGATACTTGTTAAGATGGTGCTGCTAATTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA
stSG3693 b	85 A C ---			ATTGTTTCCCTGAACATTCCCGTGGTCTCCCTCTGAAAGCCGATGACCATCCAAACCCTGGACTCACCT GAAATATCCTACGAGGC[A/C]TCGCCCTCCGAGACTGACGATTATTAAACCACCCACACGGAAAAAGG
stSG3693 a	30 C T ---			ATTGTTTCCCTGAACATTCCCGTGGTCTCC[C/T]TCTGAAAGCCGATGACCATCCAAACCCTGGACTCA CCTGAAATATCCTACGAGGCATCGCCCTCCGAGACTGACGATTATTAAACCACCCACACGGAAAAAGG
stSG3698 b	145 G A ---			TCTTGCCCTTTGTGTACCCCTAGAGAGATGGCACCCCAATCCCGAGGGTTGCTCTCTGACTTCCACCAT TCACTGACTTTTATTGCCAGAGGAGCTCCAGGAAATCCACAGTTCTTGGAAAGAGAGGGGCTCTAAGTCT TTATTGGG[G/A]AGAATACCCACCCACCTTCCCTCACTGCAGA
stSG3698 a	51 C G ---			TCTTGCCCTTTGTGTACCCCTAGAGAGATGGCACCCCAATCCCGAGGGTTG[C/G]TCTCTGACTTCCA CCATTCACTGACTTTATTGCCAGAGGAGCTCCAGGAATCCACAGTTCTTGGAAAGAGAGGGGCTCTA AGTCTTTATTGGGAGATAACCCACCCACCTTCCCTCACTGCAGA
stSG3724	107 C T ---			ACGAGCTCATGTGCAGAGGGTCTCCTGCTGGATCCCACTGGAGCCATCCCTGGGCTAGACTTCT GTCTCCCTCACTTCTAAATGAGTGTCTCAGTGATGTGAAG[C/T]ACACAGGAGTCCCTCAGGGCAAAA GTGGCTATGCTGGTGCT
stSG3725	104 G A ---			GCCAAAACAAAAAGATCTTTGGAGTTTACTGACGGGCAGCAGTTAATAGCACAGTCAACAGCATTTAA ATCAAATATATTATACAGCCCAACAGCAACAGCCCC[G/A]AGCAGGAATCGGCACATAGTCATAA ATAACATCAGGGGTAAATAACGGCACATTTA
stSG3751	128 G A ---			CGGAAGAAAGAAACACAAATCCACAGGAACAATCTATGTTTCATACCTTTTAGAAAGATGATTTTG AGGGCTTCAGTATTTAAAGGGGAAAGCAGGCTGGAGGGGAAAGAGAGAGGATATGGTCCC[G/A]TT GCTGACTCCATGTGTTGCAAGAG
stSG3787	49 T A ---			TTCTGTGCAAAAGAATCCACATCATTTGTTGGTAGCAGAGGATCTCTTA[T/A]AAAGTTCCCTAAGA CACTGAGGGCATAAACCAAAACAAAATAAATAAGGAGTGATAGGCTAAAGCAGTATCTTCCCCT
stSG3880 b	115 G C ---			GACAAGAGGGAAGAGATGGGCCAGAGACAGGGCTGGGCAGCTGGGGTCCCTGAGTGCACAGGGC CACCACAGTCTGTGGGTCAAGGCCCTCTCTGGGGAGCAGGTCTA[G/C]GGCACGGAGGATGCAG GGCTGGGAGGGGACCCCACTCGGGGACCCAAAGGAGTCCATTCTGCCCCT

stSG3880	a	36 G C ---		GACAAGAGGGAAGAGATGGCCAGAGACCGGCTGTG/CJGGCAGCTGGGGTCCCTGAGTGCCAGG CGCCACCACAGTCCTGTGGGTCAAGGCCCTCCTCTGGGAGCAGGTCTAGGCACGGAGGATGCAG GGCTGGAGGGGACCCCAOCTCGGGGACCCAAAAGGAGTCATTCTGCCCC
stSG3895		44 A G ---		AATCAGCCATTGTACACATTGCAGCTATGTATTGTAGTTGTJA/GJTJTJTJTJTJTJTJTJTJTJT TACATGCCCTCATAGATATATTCAATTAGTGTATCACCATGGGAACAAGATGCTGATTCGTCAACTG AAAAAT
stSG3902		104 T C ---		TCTGTTGAGACTGGAGAGACCAGGTACCAAGCACCCGACTCTGGTGGGAACCTGGCTTCCTGATAACA TCATCTATTTCA CCTAAATGTGAAC TGCTTTCTTTTC/JJCAGCTCAATAGCTTAACATCTAATTC ATGTTTGCTCCCCTTTGCTGGACAAT
stSG3935		50 G A ---		GGGTGCTGACGGACAGGCACACCCAGCAGTTTCAACAAGCAAATTTGTCCQ/GAJTAGTGTGCAAGC TCCTCCCCAGTTTTCCACAGGCTGAGTACTATGGGTCACAACCTTCCTGGACGT
stSG40		25 A G ---		GAGGAAGAGGTTGAAGAAGTGTGAJA/GJAAATATATTTAAGATTTCTTGGGAGAAATCTCGTGC CCAAACCTGGTGATGGATCCCTTACTATTTAGAATAAGGAACAATAAACCCCTTGTGTATGTATCA CCCAA
stSG4009		32 A G ---		GTGTGGGCTGTCTGATGATGAATGGCGCGCTC/A/GJTACTCTTTACGGCTTACACTTTTATGCTCCT ATGAATTCCTGATGGGCTTTAAGGGCTGAACCATATCTGAAGGTTTTCCACACTGCTTACA
stSG4033		123 T C ---		AGAAAGCCTTGGGACAATGGCAGTGGCCCTTCTGAGTAAGACATGAATGCCATCTGGAGGATCCATT TGAAACTACAGTGCAGTAACCAAGA AACCTAATGTTTTCAAGCATAAAGGTACTTTT/CJGTGAAC AGGTGGGCAACAC
stSG4038	a	29 G A ---		GCTGAGACAGCTGTACAGCCACGCCCTGTG/JCGCAGGGCCCACTCTGTGCAATAAACATGTTCTGCC CATGTTCTCAGTCAGGAGGTTCAGGCTCCCGGAGAGCAOCTGAGGGTTCCATCACT
stSG406		53 T C ---		ACTGTGTTTCAACAGTATTGCGTTGTGACACTAGGAAAGCTAAACGAACAAAAT/CJGGTTTTAGTT TTGCTGAAGACTGGCCCTTATTAATGGACAGCTTTCCTCAACAAGAGATTATTAACCTTTTATCAGGTGTT AACATCTGTTTCAGGAACATGGCA
stSG4095	b	55 G T ---		ATCTGGGCTGAATTAGTCAAGCAGGTCAGATACTATTGTCTGCTAGATGTATTAGTGTATAAAAA GTTTGCTTCTGTAATACTTTTAAAGCTTGTCTATCTCATCTGTAAACCTATGTGTCTTGAGAATCAAG CCTTTGGACTAACCCAGGGCATTGCCCTTCATCCTGG
stSG4095	a	27 A C ---		ATCTGGGCTGAATTAGTCAAGCAGGTC/A/CJGATACTATTGTCTGCTAGATGATTAGGATAAAAA GTTTGCTTCTGTAATACTTTTAAAGCTTGTCTATCTCATCTGTAAACCTATGTGTCTTGAGAATCAAG CCTTTGGACTAACCCAGGGCATTGCCCTTCATCCTGG
stSG4120		65 G A ---		TGCATGTTCCACATCTTTCATAACAGCAAAATGTATAATAAACTTACGTACTTATGGATAATCAC[G/ AICTTTTTCCCTCAGAGAGCCCCACAGTTAAACACGTTCCAGCACACCATTAATCCACCGAGCT

siSG4128	54 A G ---				CTTGGCAGATAAGGACTCGTTTGGCAGATATGACTTTCCTTTGTGTACATTTCTT/GJGTATATATTT TACTTCTTCTGAAATGCCACATAATTTGCAATAATGATTCACCTCCTTAGCTCCCAAAAGCAAGTCC TTTATCAAATGCAAATGTTCCAGAGGG
siSG4209 b	128 G A ---			---	CACGAAACAGATGCAGCCTACACAGTGTGTAGGACCGAGGCTCACAACATCCACATGGCACAAGC AGGGCCGGCCACTCCAGGCAACGAAGCCACCCCGAACCTTGCAGAGCCGCACTCCCTC[G/A]GC AGGGGACCCACGGAGCGACAGGTCTTTGATGCCCTCCGAAGAGCTGAGCTCCATTCCA
siSG4209 a	65 G A ---			---	CACGAAACAGATGCAGCCTACACAGTGTGTAGGACCGAGGCTCACAACATCCACATGGCACAAG /A/CAGGGCCGGCCACTCCAGGCAACGAAGCCACCCCGAACCTTGCAGAGCCGCACTCCCTCGGC AGGGGACCCACGGAGCGACAGGTCTTTGATGCCCTCCGAAGAGCTGAGCTCCATTCCA
siSG4254 b	31 G A ---			---	CATTACCCAGAACGCCATGGAGGACCAAGC[G/A]CCACGGCCGGGACTCCCGGATGGCTGGGGG GCTATGGCTCTGACAAGAGATGAGCGAGGGCCGGGGCTGCTCTCTCCAGGGGAGACGTGAC TGGGGGGACCATGGCCGAAGAGAGGATGACCGGTGATG
siSG4301	81 T G ---			---	TGCAACAGCTCTGAGAGGAAATCCTTGGCAGATCAAAAGAGAGGGTAGTGGCTCCACACACTTTCCAT TTAAGCAAATAAATTT/GJAGCTTCTGAGTAGTTGTTCCAGTTTCACCCCAACATTTTG
siSG4331 b	71 T G ---			---	CTCACAAGGCCAACACAGAAAAGATACAAATACATTCATCCAGCTAATATTTAGTTTTATGACAC AGAGT/GJTTTTCAAACAAGTTTAAGTGTACCTGAAGAGCATGTTAAAAAGTTTAAGTTATCACTT GGAGACAGATTTCTGGCCCTCGCCCTTGATTTGATTTGAGGGGTGTC
siSG4340	76 G A ---			---	TTTTGCAACAACATGGATGGACCTGGAGGCCATTAAAGTGAAGTAATGATACAGAAAGTCAAAAACC ACATGTTCTC[G/A]TAAGTGGAGATAAACAATGTTGATACACCTGGACGTGGAGAGCAGAA
siSG4361 b	109 A C ---			---	TTCCCAACCATTTGAGTGACAGAGCTCAGTCAATGCAGAACTCAGGTTTGCATGACTCAAATTAGG AAGTCTTGGAATTTCCATAAGGGATAACTGCATCTTTTGACCTTCACAACCTAGAAAACGACTC AGCGACTTTTCTGTGAGCAAAATGTCGAGG
siSG4361 a	24 T C ---			---	TTCCCAACCATTTGAGTGACAGAGCTC/CJAGTCAATGCAGAACTCAGGTTTGCATGACTCAAATTAGG CACAAGTCTTGGAATTTCCATAAGGGATAACTGCATCTTTTGACCTTCACAACCTAGAAAACGACTC AGCGACTTTTCTGTGAGCAAAATGTCGAGG
siSG4376	73 A G ---			---	TTTCACTGCTACTGGTTTGGGTCTGAGTCCCTCAAACTCTGCTTGAAGTGTCTTCCAAAGGGGAG AACAG/GJCTGGAACCTCGGCTCTGCAAGAGCCATCTTCCAAAGCCATTTCTTCTCAGCTGC
siSG4381	50 T C ---			---	GAAAGCCACAACACTCCATAGCCAGAGAATGACAACATACGATTTTCTTTT/CJTCAGTCTTGTAGT ATCCACAGTAGTGTCTGTCCATGTACAAAGTGTCTGCCAGAACACCCCATTAATTCATGCC
siSG4410	79 A G ---			---	ACCAATGGTCTGCTATGTGATCCGATATTTTGGCCGATCTGAAATACTGCAAGGGCTTAACCAT TCAACACCCCG[G/J]TGACAACGAACCCAGTGGACTGTGAAACTCAGGCTGCAGGAGGGTGGCTTGT CAGCTGGGT

stSG443	65 C T ---	AGCAGATCAGTCAGCCACATTGTTCTCTCTCTCTTTAGGGAGAGGCTAGGAGTGAACACATCA/C/
stSG4430	54 A G ---	TJGTATGCAATGAGAAATAACCAACTGGTAGGATGGGGAGGGAGGGAGGCAATAGGCAC
a		AAATGGAATTCATCTCTGGCTGTCTCTCAGGTC
stSG4448	99 G A ---	ATGCACATTAAATGAATGGCCTAACTACTGGGAACTTTAGTAGTTCTATAAGGT/A/GJATTAAACATA
		GGTAGGATCCAGTTCCTATGACAGGCTGCTGAAGGAACAGATATAGGCATCAAGAGGGCAATTT
stSG4449	92 T C ---	CCCTCCCTCCCTTCCTTCCCTCCAGTCTTCCATACTGTTCCCTCCCTCCCTCCCTCCCTCCCTCCCT
		CGCTAGCCCTGCCCTCTGGGGTCACTGC/G/JTGGGTTAGGCCCCCAAAAA
		ATTAGCCATTCACTTGCACAAATTGCTTTACTGTAACTAAGAGTACTGTACTGATGATGTTTACAAT
		TAACTTTGGACAACCTAAACCTTA/T/CJTAGTGACATTGCTGTCTAATAATCAATACTTCATCATA
		GGCTGAACATAATTATTAAAGAGCAAAGTTACCCCTCCC
		CAGACATGAGGGATGCCCTGTCTCTCTGGGACAGAGCCCTA/C/AJAGATGATGTCCATGTTTTGTGT
stSG4467	42 C A ---	GAATGAAACTCAAACACTCTTCAGTTTTTAGAGTCAATTTCTGGTATCGAGCGACACACCGGAGGAG
		CACACCTGCTTCCAAAGGCTGCTGCTCTGCACACAGT
stSG4475	21 A C ---	ACATGTCAATTCCTGACCAGG/A/CJTATTAATAGTTTTATTAGAAGAAATGAGTTGAAGTGAGCGGA
		TTAAGAGACACAACTGGACTTTTGTTTTCTTTACTGTAGCACCCAGGTTTCATG
stSG4477	32 A G ---	GTAACTTCTGGGGTGGGGGTGAGACAAAC/A/GJATGAACCAATAATTAATTACAATTATACATT
		TCAAGGAGACTTTAATCTAGGTTAATGTGAACGCAGCCATCAATGTTTTGTCAGGAAAGGGAGA
		TGAAGTCTTGCTCTGGGCAACGTTTGGCCCTCATTCAGTCAGACATTGGC
		TGAATCAGAGCTGGGTGGGAGCTGCAGCGAGGGAGGCTGGGGCCAGATGAGCGCGCGGGGA
stSG4531	79 C T ---	CAGCAGGCGTG/C/JGCCACGTCTGGCGTTGGTAGAAGAGGACATAGGCTGCCCTGGACTCGATCT
stSG4550	86 G A ---	GATTCATTGACAGGGGAGACGCTGTGTCATCA
b		TGCATTAGGAAATGATACGGCATATTTGGGGGACAGAGAACAGGCTTGATGAGGACAGAGTCTATTT
stSG4550	85 C G ---	AAAAGACAGTGGCACC/G/AJCAATTGGAGGGGAAGCGGGGCGAGGTTTTAGAGAAC
a		TGCATTAGGAAATGATACGGCATATTTGGGGGACAGAGAACAGGCTTGATGAGGACAGAGTCTATTT
		AAAAGACAGTGGGAC/C/GJCAATTGGAGGGGAAGCGGGGCGAGGTTTTAGAGAAC
		AATCAGGCACAAGCTCGGGAGAGAAGCCAAAGCTCTCTGCAC/A/GJATGGGAGGGAGACAC
stSG4590	47 A G ---	CATTGAAAAAGGCATCGTTCTCTTCATGCAAGCGAGGCTGGCTCCACAGGCATGGTCTCCTTG
		AATCTGTATCACCCAGCGCTGGT/CJCAATGTACTAGTAGCTTTCCACAGGGATTTTTATACTATTTC
		CTATAAGGTTTTATCATGAATAAAAAAGCTCACAACCTCTTTTCAGCCATTGCAGATTTCACATTTATCT
stSG4623	22 T C ---	TAATATTCTGTTCAGATGCTCTGGAG
		TAAAAAAAACACCCCCCAAAAAACACCCAGAAAGTTTTGAGTTTTATGTTTTTCAGATTTAAAG
stSG4843	102 A C ---	GTATTTCTTTCTTAGCTTCTAAATTTTGAGTCAT/AJATCAGAAAGTCTCCCTACTCCAAGGTGA
		GAAAGGA

stSG4850	38 C T	---	GGAACTCTAACTGGGAATGGCCGAGGAGGAAGGGGCTC/TGTGCACTTGCAGGCCACGTCAGGAG AGCCAGCGGTGCTGTGCGGGAGGTTTCCAAAGGTGCTCCGTGAAGAGCATGGGCAAGTTGTCTGACAC TTGGTGGATTCTTGGGTCC
stSG4879	86 A G	---	AACTCTGAAGGGGGTGACCTCAACCCAGCCCTTGTCTGTGAGTGCTGCTTTTGCAGAATGGCCTG CCCCTGGGACTGGAGCAG[AG]CTTGGGTGAGCTCTAGGTGAGGGTGTGGAGGGGCATAGAAAT AAACCTTCC
stSG4885	104 G A	---	ACTGGACTGGCTGCTTGTAGCCGGCTGAGCGGCTGGGACTGCGGCTGACCACTCGCTCTTTCAG AGACTGCCCCCGGTGACCACGACTACGCTCTGCC[G/A]GTGGGAAAGCAGAGCAGGACC
stSG4896	112 C T	---	AAACAAATCAAAACCAATCCAGCAGTCTATGTACAGGGCCACTCCCTGCCCTCTCTGCCATAGAGA GGTTGGGGCAGCTGAGGAGTGTGGGGCTGGCACTTTTCTCTCAGCCACAGGCCCCCTGAGG AATTAATTGACTG
stSG4932	22 G A	---	ACAGTGCCGATGGTTACACAA[TG/A]TTGTAATGTATTTAATCCCACCTTACGAATGATTTAAATGA TAAATCTTATGTTTATTTTCATCACTACCAAAAGGCTGTGGTGCAAGGGTGTGGTTCTTGGTCTT
stSG4950	24 A G	---	TCATGACTCCCAGGAAAGGTCCT[AG/TC]TAGCTTCCCTCCCTACTTTCTCTACATGTCAGC ACTGTAATGTAGCTAAGATATAGTAAGGCATTGCTCCCTACCCCTACACTTCAAGG
stSG4957	136 G A	---	AGATACGGGCAAAACACTGGGATGGCTTCCCTGACAACTTAAGAGGTCCTCCGAGTTATATTCGGTT GGGAAACACTGACCCAGCCCTTATCTTCAAGGACTCTAGTCATTGGCAAGGAGGATTCATGAGCC CC[G/A]GTACACAGATGGGGCCCTGCTCTATATTCAAG
stSG4961	91 C T	---	GAAGTGCTCTGAGGAGGTGACTCTCCCTGGCTGACAGGGGAAGGCTTAGCAGAGCTTTGCTTAG AGGAGTAGATGAAAGGAAGTA[TC/T]AGAGAGGGCATTCAGGCCAAGTCAGCAACACAGACAA
stSG4967	72 A G	---	ACTGGTGCTCTCAGCAGATTCAAGGGTGTGTCAGGGCTGTTACCACAACTCAGTAGGAGTGCAA GGGCT[AG/T]ACCCCCGGAGCTAGACAGCCTGGGTTGAATCTCAACTTCTCCCTTTCTTGTGCTGTC AACCTTG
stSG4997	22 T C	---	CAAAGGAGAGTAGGAGCCCCAA[T/C]TTTAAATGGTTTCTCTCCCTCATGCTATTGATCCAAAA CTATATACAAATTTGTAGCAGTCTCTGTATAGTTATTACACATGTTTAGAAGGGAGGGGCAAGAA GGGATAGGGAGAATGGTGATCCAAAAT
stSG5312	37 C T	---	ACAGGTTCTACACTTTGAGCCTTTAGTGCAAAAACA[TC/T]ATGCCATGCGGGAAATAAAATGCTT ATCCAGTGGAGCGCTCCCTGATGCATTGAAATATTAGGATACTCAAGCAGAAGAC
stSG6345	107 G A	---	GCTCTGGTCAAGCAAAATCTCCAGGACAGAAAGCAACAGGACAGTAACACACATGTATGACCCTTA CAAGTGCTTTAAGATTTTAAAAATGTGATGTTTGTCCAC[G/A]TAGTTTCAGGCAATTAAGAATAT GCAACCCAGAGAAATTTCTGTGAAAAACATTTTGTCTTTTGGCCCTGTGTGGACAGAAAGGGTGGCCAA ATGGATTGAGTGATGAGCAGACATG

stSG6362	88 G C ...	---	TGTGAATGTACACTCAGGTCTAACAAATACCTATTATTTCTCTGGTTAAGAAGGTTTAGCAGGAGC CTCCAATGAGCACTGTATGTA/GCJAGAAAAGGGAAGGAGCAGGAGGAGGAACAGATCTGCACAGA AT
stSG8010	62 G T ...	---	CACATCTGTGTTTCTGGAGCAAGGGAAACCACAGAAAGGCAGGAGTTTGGGTGTGCACCTGG[G/T] GTCITTCAACTGGGTGGAAACCAACTGAGTCCTTGAAGTCTCGCTCTGAGGCTGCAGAAAGAAATAGA TGGCTT
stSG8022	53 G A ...	---	AGCTCTGACTCCCTGTTGACGTGACGTGATGTTGGTAGCCTGAAATGGACCAC[G/A]GTGGGAGTTAT TTACACCATGGAACTGGAAACTCTACAAATCAATCGGTTATTTCTTTATTTTCAGAGGGCAGGTT TATCAGCACACGCTGATCTCC
stSG8032	67 G C ...	---	TGATTGTTAGGGATAAGTGGCATTGTGTTTACAAATTACTTCCAAAGAATTCAGAAAAATTGTGTGTT G/CJTGGGAGGCAGGGTAGCAAGATAAAAAGAGGGAGGACAGCTGGGGTTGGTAAAA
stSG8064 b	46 C A ...	---	AGCTGGCTCTTCTCTGCGTGGTTCGGGAGGCTTACGTCCTCGCCCGTGGTCCCTGGGTGGCC TGCAGGACCAGGGGTGGGAACAATGCCAGGGAGAATTCCTGTACATCAACACAGGGAACA
stSG8064 a	23 G C ...	---	AGCTGGCTCTTCTCTGCGTGGTTCGGGAGGCTTACGTCCTCGCCCGTGGTCCCTGGGTGGCC TGCAGGACCAGGGGTGGGAACAATGCCAGGGAGAATTCCTGTACATCAACACAGGGAACA
stSG8072	59 A G ...	---	CACATCATCATCGAGTAGGTGAGGAGCAGGAGGGGTGGTCTTGTCTTAGGG[G/A]GTGGC AGAGGAGAAGGAAGTCCGAGTATTAGTGGCCGCATGCAGTTCAAGCCTGTGCTGTTCAAAA
stSG8100	40 A G ...	---	ATACACCCACACACCCCACTCAACCTTGTATCAAAATTCCTCAAGTGTAACTAAAGTATAAGAAAT ATCATGACTAGTTAAAGATAGCAATACCAATAGGTACAAAGTTCAAGTATTAGTATAACAAGTAT CTGAGTAACAAATGTCCTTGGAAATGGG
stSG8102	138 T C ...	---	AAGGCTCCTTGAAGCATGGTTTATTGTTCCATTAACTTGTCTCAGCTATACTGAAGTATGATT GACAAATAAACTTGCAATATTTGAGATGTACAGTGTGATGATACATGTATGTATACAAATGTGAAA TGAT/CJTGTGATAATCAATCAATTAATGGTATATGGTTAGGAAATGTGATGGT
stSG8105	110 A G ...	---	CAGTGGTTCTCAACTCCAGGTACACGAGGATGGTCTTGTGCTTGTAAATACACAGATGACTAGGCC CACCTGCGGAGTTCCTGTTGGAGTCTAGGCCTGAGAAATTC[G/J]TTCTAACAAAGTTCCCAAGTGA CCCTGAGGCTCTTGGACTGGGGAACATGCTTTGAG
stSG8130 b	96 T C ...	---	GTGTGTACATCATTTGGGAATGGAGGAAATAAATGACTGGTGGTGGCTTTTAAAGTTCAAATTT GACATTCAGACAAGCGGTGCCTGAGCCT/CJGTGCTGTCTTCAGATCTTCACAGCACAGTTCC
stSG8130 a	36 C G ...	---	GTGTGTACATCATTTGGGAATGGAGGAAATAAATGA/CJGTGGATGGTGGCTGCTTTTAAAGTTCA AATTGACATTCACAGACAAGCGGTGCCTGAGCCTGTGCTGTCTTCAGATCTTCACAGCACAGTTCC
stSG8145 b	124 T A ...	---	TTGTGGACTTCAAATCTTCTTCCTTCAGATTTTAAATGACATTATGCATGTACATATTTTAAATTT AGACACATTTTAGAGAACACAATTTGTGAACACAAATCAAGAAATGAATGAGATGTTT/AJCTGAAA TCTGATTCAAACACTTATCTTAAACTGACTTCTGTCAATCTCTGTCTGTGAAGG

[illegible]

ESTD-AT3a	--	--	---	---	AGACCTCAGTTTCTCTGTAAAGGGAAGTTTGTCTTGGATCTCCATGGGCCAGCCAGCACTG GTGCCCTGTGAGTCTGTATCAGGTAGAGGAGATGGACACAGGTGGAGGAAATTTGAAAGGGCATTG GAATTCAGAGCAAGAGACAGATATTAGAGCTGGGGAATGTGG
ESTD-B3AR	--	--	---	---	GGCTGCCAGGGTTCCGTGGAGGCGGCCCTAGCCGGGGCCCTGCTGGCGCTGGCGTGTGGCCACC GTGGAGGCAACCTGCTGGTTCATCGTGGCCATCGCCGGACTCCGAGACTCCAGACCATGACCAACGT GTTCTGACTTCGCTGGCCGCGACCGACCTGGTGATGGGACTCTGTTGGTGGCGCGGGGCCACCTTT GGCC
ESTD-BA511	--	--	---	---	GGGCAACATAGTGAAACCCCATCTCTACAAAAAATACAAAAATTAGCCAGGTGTGGTAGCAAGTGC CTGTAGTCCAGCTACTTGGGAGGCTGAAGTGGGAGGATCCCTTAAGCCTGGGAGGTGGAGGCTGCAG TGAGCCAAGATGGTGCACCTGCA
ESTD-BCL2	--	--	---	---	AGCTGGATTAAACTCTCTTTCTCTGGGGCCGTGGGTGGAGCTGGGGGAGAGGTGCCGTT GGCCCGGTTGCTTTCTCTGGGAAGGATGGCGACGCTGGGAGAACAGGTACGACAAACCGGAG ATAGTGATGAAGTACATCCATTATAAGCTGTGCGAGAGGGCTACGAGTGGGATCGGGAGATGTGG GGCGCGCCCCCGGGGGCGCCCGCCACCGGSCATCTTCTCTCTCCCA
ESTD-BCR	--	--	---	---	CAGTGGCTGAGTGGACGATGACATTTCAGAAACCCATAGAGCCCCGGGAGACTCATCTGCGCAAGA GACCAAGAGGTGAGCTTCTGTTGTCGGGAAAGGGAGGCGAGGTGACAAGCTAACTCTGCTTCAA ATCAACCATCCGGTGGACACTGTGTGGCTGCCATCTGCCCTGGCACA
ESTD-BRCA1a	--	--	---	---	AAGAAGAAAACTAGAAACAGTTAAAGTGTCTAATAATGCTGAAGACCCCAAGATCTCATGTTAA GTGGAGAAAGGTTTGCAAACTGAAAGATCTGTAGAGATGACAGTATTTCACTGGTACCTGGTAC TGATTATGGCACTCAGGAAAGTATCTCGTTACTGGAAATTAGCACTCTAGGGAAAGGCCAAAAACAGAA CCAAATAAAT
ESTD-BRCA1b	--	--	---	---	ACTAAATGTAAAGAAAAATCTGCTAGAGGAAAAACTTTGAGGAACATTCAATGTCACCTGAAAGAGAA ATGGGAAATGAGAACATTCGAAGTACAGTGAGGCAACAATTAGCCGTAATAACATTAGAGAAAAATGTT TTTAAAGAAGCCAGCTCAAGCAATATTAAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTA TTAATGAAA
ESTD-BRCA1c	--	--	---	---	ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTAGATGATGGTGAATAAAGGAAGATAC TAGTTTTGCTGAAATGACATTAGGAAAGTTTCTGCTGTTTTAGCAAAAGCGTCCAGAAAGGAGAG CTTAGCAGGAGTCTAGCCCTTCACCCATACACATTTGGCTCAGGGTTACCGAAGAGGGGCCAAGA AATTAGAGTCTCAGAAAGAGAACTTATCTAGTGAGGATGAAGAGCTTCCC
ESTD-C1R	--	--	---	---	ACACAGGTGCTGGCACTGGGGCTGGGGATCCTCTCCCTAAATTTGCTCCGGGAAGCACATTTCATCAA CCCAGTCAGTTTGGGGACAGCCATGCACCTGAGCCTCTGGTAGCCTTTCAACCATGCATTCCTCTAA GCTCTGCAAAAT

ESTD-C7	--	--	--	---	---	---	ATATCGTGGCCTTAGTTACCTAGAGCTGGACAATCTGCTGGA
ESTD-CB22	--	--	--	---	---	---	GGCAAGTTTTATTGATAGAGAGGAATCAATAATGGCAATAGGAGAGACATCACCTGGGAATGTTAG GCAGTGCTTAAGTGGGATGAGACACAATGGCAGTCCCAACCCATAGGGCGATACAAAAGAC AGGCAAGGAAGGGTAGAACCATCAAGAGGAATAGGCTGGTACCCCAAGCAAGGAGGACCTAG TAACATAATTGTGCTTCAATTATGGTCTTTCCGGGCTTCTCTCACACAC
ESTD-CB23	--	--	--	---	---	---	TAGAACCATCAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCTAGTAACATAATTGTGC TTCATTATGGTCTTTCCGGGCTTCTCTCACACATACACAGAGCCCTACAGGACCAGACAGCT CTCAGAGCAACCCTAGCCCATACCTCTTCCCTTTCCAGAGGACCTGAAAAACGTGTCCCAACCCGA GGTCGCTGTGTTGAGCCATCAGAAGCAGAGATCTCCACACCCAAAA
ESTD-CB24	--	--	--	---	---	---	ACCAGACCAGACAGCTCTCAGAGCAACCTAGCCCCATTACCTCTTCCCTTCCAGAGGACCTGAA AAACGTGTTCCACCCGAGTGGCTGTGTTTGAGCCATCAGAAGCAGAGATCTCCACACCCAAAAAG GCCACACTGGTATGCTGGCCACAGGCTTTACCCGACACAGTGGAGCTGAGCTGGTGGGTGAATGG GAAGAGGTGCACAGTGGGTGACACAGACCCGAGCCCTCAAGGAG
ESTD-CB25	--	--	--	---	---	---	GTTTTCTTCAGACTGTGGCTTACCTCCGGTAAGTGAGTCTCTCTTTTCTCTATCTTTGCGCGTC TCTGCTCTCGAACCCAGGCGATGGAGATCCAGGACACAGGCGTGAGGGAGGCGAGAGCCACCTG TGCACAGGTACCTACATGCTCTGTTCTGTCAACAGAGTCTTACAGCAAGGGTCTGCTGTGCCACC ATCCTCTATGAGATCTTGCTAGGGAAGGCGACCTTGTATGCGGTG
ESTD-CB27	--	--	--	---	---	---	TTTTCTGTTTCCCTGAAGATTGAGCTCCCAACCCCAAGTAGGTAAGCTAAACCAATAAAAAAT TGTTGTTGGGCTGGTTGCTATTCAGGAGTCTGTGGAGTCTGCTCATCACTGACCTATCTCTGA TTTAGGGAAGCAGCATTCCTTGGACATCTGAAGTGACAGCCCTCTTCTCTCCACCCCAATGCTGCT TTCTCCTGTTCACTGATGAAGTCTCTCAACACCATTTCCATACC
ESTD-COL2A1c	--	--	--	---	---	---	AGAATGTATATAGTCTCAAACTGGCCATCTCCATTTTCAGTCCAAAAGTTATACAGTAGACAACA GTGGTGACATACGTTGCTATTATGCTCTCTTTCCTGTCACTTTCAAGGTGTTCAAGGTGGAAGGT GAACAGGTCCCGCTGGTCTCCAGGCTTCCAGGTAAGTCAACTCAAGCATATACATACTGCCTTTG GTCAGCCTATTGAGCTGTAATCACCATAACCGTACCT
ESTD-COL2A1d	--	--	--	---	---	---	TGAGAGAACACCTAGTCTCCATCTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTTGGGACCTGGAACACTGGACTTCTTCTACTGACGACAGCAAGACTTACCC AAGAGAGATTAAATGGCAAGATATACAATACAAATTTTATTGACCAACACTATCATATGGAACAGC ATT
ESTD-CPT2	--	--	--	---	---	---	GCCGCAATGCCCGGGAGTTCTCCAATGTGTGGAGAAGGCCCTTAGAAGACATGTTTGTATGCCTTAGAA GGCAATCCCATCAAAAGTTAACTTCTGGGCAGATGAAAGCTACCATCACTTCTCATCATGAAAC TGGGAGGCCGGGCATAGTCTCATGCTGTATCCAGCATTTTGAGAGGCTGAGCGGGTGGATCAC TTGAGGTGAGGATTGAGACCAACCTGGCCAACT

[illegible]

ESTD- D7S399	..	--	---	---	---	---	TGAATCTTAATTGCTATCTCTACAAAATGTATAAATCCTGAATCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCAGTCTCCTACATCATCCTTTACAAAACATTTTCATCCATGGACTCCATAGTAG AATATTTGAAGAAACAAACATGACAAACATTTTC
ESTD-DM	--	--	---	---	---	---	GTGGGACACCGAGGCTCCAGGCTGGGCGCTTGACGTGTGCTCAAGCAGCTGCTGGCGCTCCACT TCCATGGGTGTGGGCGCTGGACCTCACTGTCCCTGGGAGAGGAGGAGTGGGAGGGAGACA GAATGCTGATTATCTGTGGAGAACAGAACCTTCTGGCGCTGTGGGTAGGGGAGCTGCTTCCAAGACC TCCTGATTTGAGGAAGGGAGCAGCAGAGCGAAGAGAACAGAGT
ESTD- DRD1	--	--	---	---	---	---	TCCCAGCCCTATCGGTCATATTGGACTATGACACTGACGTCTCTCTGGAGAAGATCCAAACCCATCAC ACAAAACGGTCAGCACCCCAACCTGAACCTCGCAGATGAATCTGCCACACATGCTCATCCCAAAAGCT AGAGGAGATTGCTCTGGGGCTCGCTATTAAAGAACTAAGGTAC
ESTD- DRD2	--	--	---	---	---	---	TCTGCTTTGTGTCAGGAGGCTGCCCGCGGAGCCAGGAGCTGGAGATGGAGATGCTCTCCAGCACCA GCCCACCGAGAGACCGGTACAGCCCCATCCCACCCAGCCACCACTGACTCTCCCGACCCCG TCCCACACGGTCTCCACAGCACTCCGACAGCCCCGCCAACCCAGAGAGAATGGGCATGCCAAAG ACCACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD- DRD3	--	--	---	---	---	---	AAGACGATGGCCAGGATGAGCGCGCAGTAGGAGAGGGGCATAGTAGGCATGTGGCGGGCGCTGGCTGG CACCTGTGGAGTTCTCTGCCCCACAGGTGTAGTTTCAAGTGGCCACTCAGCTGGCTCAGAGATGCCATA GCCCAGAGGGAGGTGCGTGATGCCAAGGGCTTCTGTGAGGAGA
ESTD- ERBB2	--	--	---	---	---	---	TCTTTAGGATCCGCATCTCGGCTGTTGGGCATCGCTCCGCTAGGTGTACGCGGCTCCACACAGCTGG GGTGAGGGGGTGGTGGGTGAGTCCCGGGGGCGGTGCAGACCCACCGGGCTGGGAGGACTTCAOCC CGCCTCACCTCCGTTCTCGCAGCAGTCTCCGCATCGTGTACT
ESTD- ETS2	--	--	---	---	---	---	ACTCACAGTGTCTTTAAGTGAATGGTCGAGAAAGAGGACCCAGGAAGCCGCTCCTGGCGCCTGGCA GTCCGTGGGACGGGATGGTTCTGGCTGTTTGGATTCTCAAGGAGCGAGCATGTGCTGGACACACAC AGACTATTTTAGATTTCTTTTGCCTTTTGCACCCAGGAACGCAATGCAAAAACCTCTTTGAGAGG GTAGGAGGGTGGGAAGGAACAACCATGTCATTTCAAGAGTTAGTTTG
ESTD-F2	--	--	---	---	---	---	GATAAGTACACTGAGGCCCCAGGAGGTTATTGCCTAGTAGCCCCAACTGTGCATGCACGCTTAACCTCT GCACCAATGGCCTCCAGGCCCGTAGGGGAACCTGGGGGATCTAGGGGATGGGTGAGGAATGGCCG AGCCAGTCCCGCCGGTGGCTGGTCCCAACAGAGGAGGCCGTGGAGGAGGACAGGAGATGGGC TGGATGAG
ESTD-F9	--	--	---	---	---	---	AGATCCTGATGATTTTTTCTCTATTTTTTCTAAATGTTTTTACAGTTTGAAGTTTTAGATTTATGCCCA TGCTCCATTTTGAAGTTAATTTTGTAAAGTATGATGTTTAAAGTCAACCTCATTTTTTTTTTCCATA GGTATGTCCAAATTTATCCAGCACAAATTTGTTAAACAAAAAAC

ESTD- GODH	--	--	---	---	CGCAGACGGTCAGTGTGGGTGCGGAGTGTGGAGGGAAGGAGGAGGAAGTGGGGTTTAGGGACT TTCCGGGTGACTTCCCGTTCTGTGCTTGCAGAGAAAGCGGGAGAACACAGAGCCAACTGGCTAA GTGTAAAGGACCTCTGTGTCGACCGTGTGTTCTGTGTCGCCCTGTTAGCTGTCTGTGCGGACGTGCA CTCTGTCCCGGAAATTCGAGAGCT
ESTD-GCK	--	--	---	---	GTTTTATGCATGGCAGCTTAATGACAGGATGGTCAGCCCTGCTGAGGCCACTCCTGGTCACCATGAC AACCACAGGCCCTCTCAGGAACACAGTAAGCCCTGGCAGGAGATCCCCACCCACACCTGGCTGG AGCAGGAATGCCGAGCGGCTGAGCCCGAGGGAAGCAGGCTAGGATGTGAGAGACACAGTCACC TGCAGCCTAATTACTCAAAGCTGTCCCAGGTCACAG
ESTD- GNAT2	--	--	---	---	GACCTGAGTACCTCCCTAGTGAGCAAGATGTCTCCGATCCAGGGTCAAAACCACAGGCATATTG AAACCAAGTTTCCGTCAAAGACTTGAATTCAGGTAAGTCATGGTTCCTAGG
ESTD- GPPK2L	--	--	---	---	AGTCTTCATCTGCGGTGTCCAGGTAGATCCCTTTCACCGCCGAGAACTGCTCGATATC
ESTD- HRAS	--	--	---	---	CTGGGCTCGCCCGCAGCAGCTGCTGGCACCTGGACGGCGGCGCCAGGCTCACTCTATAGTGGGTGG TATTCGTCCACAAAATGCATCTGGATCAGCT
ESTD- HSD3B1	--	--	---	---	TTGGAAGTTCTCCACTGTTAOCACGTCTATGTTGGCAATGTGGCCTGGGCCACATCTGGCCCTTG AGGCCCTGCAGGACCCCAAGAGGCCCAAGCATCCGAGGACAGTCTACTATATCTCAGATGACA CGCTCACCAAGCTATGATAACCTTAATTACACCTGAGCAAGAGTTCGGCCTCCGGCTTGATTCC AGATGGAGCTTCTTTATCCCTGATGATGATTGGATTGGCTTCTGCTG
ESTD-HT2	--	--	---	---	GGGCTAAATTTCCGAGCAACTTTGCATAGACTGTTTTATTGACTTGACAGGATTGCTAGAGATAGG CAGGGAGAGGAAGATGTTACAGTTTGTGAGAGAGAAATAAAGATAACCTGGGGTTTTCTGTGC TTTGCTTCTCACATCCCTGGGGAGTTAATAGCTGCAATTTTCAAGAACGGTATACAGGGACAGCA AAGCGCAGTCGTGAAGTTTCAAAACAAGACACACCTT
ESTD-HT4	--	--	---	---	ACCAACGAGCCCGGATACAGACACTCTTAAGTTTGCCTAAGGCTCATTCAATCATTAGGCATTTT CTGATAAAGTGGTCTTGGTGCTTCTATCGGCAAGAAATGCGTACTATTTGAATAGTAGAGGTAA ACCACAGCCCGAAGAGTCACTGAGACTGGCAGCTCTGCAGCAGGCGTGAACCCCGTAGCCCTAAA TGACAGCCGAAGAGGCGCGAAGACATGCAGATGTGC
ESTD-HT5	--	--	---	---	AACACACAAGCCCGCAGGAGAAATTGAACCTCGGACCCCTGGTTTACAAGACCAGTGTCTAACCCCT GAGCTATGGAGCCCTCGTCTGCTGTTGGTTTTCTTCCTTCTATAGATTGATGTTATGCTOCTA GCATTCGGGCTACCGAATAGGATGTAGCTTGAGTAAATTCAGGATATTCCTTACAAAATGAAA ACATTTCTGCTCTGTAATCCCTCGAAAAGGTTCT
ESTD- IGFBP1	--	--	---	---	ACCCAGTGGAGCCCGCTCATTGACGGTCTTGGCAGGAGGTGCCCTGGGAGAAGGAAGATGTTC CAGGGCACACATAGCTTAGTGGAGACTC

ESTD- IGHV4-6	--	--	---	---	---	TTTACTATTTCAATGGATACAGAAATGTGGAGTCACTATATCTATGAACAAAAATTCAGATTT CAGTGTTAAGTAATGTTGCCTACATTTGTGTGAGTGACGGGAGTGGTGATCCGAGAGTGTGGTGGG TGCACGGACATAATGATTCAGAAAGCAATATGAAAGATGAGTATCTATGGATACGAACTGAAAGT ATGTAATACTTCACAAAATACTAATAAACGGAGTTGAATATAAAACCCA
ESTD-IL1A	--	--	---	---	---	CAAAGTAAGCACCCTAAATGTTAGCTATTACTATCATATTATTATTATTTATTTATTTTGG AGATGGAGTCTGGCTCTGCACCCAGGCTGGAGTGGAGTGGCACAATCTCGGCTCACTGCAAGCTCTG CCCTCTGGGTTATGCCATCTCTGCTCAGCTCAGCTCCCGAGTAGCTGGGAATACAGGCACCCGCCACT GTTCCCGGCTAATTTTGTATTTTGTAGTAGAGACGGAGTTCAACCGT
ESTD-IL1B	--	--	---	---	---	CCACTACAGATGGATAAATGGGTACAATGAAGGCCCAATAGCCCTCCCTGTCTGTATTGAGGGTGT GGGTCTCTACCTTGGGTGCTCTCTGCTCAGGAGCTCTGTGCAATTGCAGG
ESTD- KRT10	--	--	---	---	---	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTCCATGTGAGTGTACCTTTTGGCAATATT AAAGGAAGAAAATGCATTTAAAGTAAGTCTAAGGTTTTTCCATTAAACCACATATTACTTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGCTGCTTTTAAATAGTCTC TGCCAGATACATCTCCCTATATAAGTTATAACCAAGTATTGATA
ESTD- KRT8	--	--	---	---	---	ACCTCACCCCTCCCTTAGCCGTTGGAAGCAGGAAATCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGCTGACATGAGACCTCAGACAGAACTTTCTAGAGTT TGCTAGAGTCAAGGTCAAGACTAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCATAG GCTGCCTATCTCTCCGCTCAGGTTACCACGTCAACATTGACACA
ESTD- LF79	--	--	---	---	---	GGGTGATTTGAGGCTCAGTTAATATTTCAAAATTTGTAACCGTAGCAAACTGCATTGGTATTAGA AAAATAAAAATTTCCAATATGTAGTGTGTATACCTGCCTCTGCCATGCAGCATCATAGCCTGT GGGAACCGAGGGCTTCCCTTACCCACAGA
ESTD- LMP2	--	--	---	---	---	TACACACTTTCCTTACCCATTCACTGAAAACGACTCGCAAACTGGAGCCTTGTAGGAATGGAGTTGA CCTTCCCAAAAGCCACTATGATAAGCTATTGGTG
ESTD-LPL	--	--	---	---	---	TGTCAGTGTCCCTAGGGCACCTCAOCCACTCCAGCTTCTCAGCTCTGGCTGTCTGCTGCTGCA AGGTTTTGCTTAATCTCAATTCATGTCTCTTCATCTTTTAGCAGCTGTGGGTTTTGTTGTTTC TTCTGTTTTGCTTAGTATCTGACTACTTTTTTAATTATAAAAGAGATGTATCTAAACAAAATAGAG ATTGTTATCAGAAGTTCACAACATTTATTAATAATTTTTCACCTG
ESTD-MCC	--	--	---	---	---	TTGTCAGGAGTGTGCTGCTGCTGCCCTCCAGCTCTGTCCCTAGCCGAACCTCAGGACAACGTGCAG CATCCATGTAGGAGAGCCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAACAGCATGCATCCCCGAA TCTCAGGAAGTCTCTGCTTTCCAAGGTTTTGGTCTAAGTTGCTGATTACCCCGGATTTTCTGACGATC TTTCAACTGCTAGAGCATCTGGTCCCTGTTTAGCATGG
ESTD-NF1	--	--	---	---	---	ATTATCCAGATGAATTTACAAAACATATACCAGATCCACAGACTGATATGGCTGGT

ESTD-RDS	--	--	--	---	---	CCCGAGGAATCTGAGAGCGAGAGCGGGCTGGCTGCTGGAGAAGAGCGTGC CGGAGACCTGGAAGG CCTTCTGGAGAGTGTGAAGAAGCTGGGCAAGGGCAACAGGTGGAAGCGAGGGCGCAGACGCAGG CCAGGCCAGAGGCTGGCTGAGGGCCCTGGGGCCCTCCCTCCCGAACACTGAGAAATAGTGCAC CCAGAAACGTTGGATCTCCCTCATCCAACTCCGAAAGTCTGAA
ESTD- RYR1	--	--	--	---	---	CTTGTGACGGGAGGTACGTCTCCGCTCTTTTCATGGACATATGGATGAGTGTCTGACCATTTCCC CTGCTGACAGTGTATGACAGCGCAGACTTGTCTACTATGAGAGGGAGCTGTGTGCACACTATGCCCC TCCCTCTGGAGGCTGGAGCCACTGAGAAATCAGCTGGAGTGGAGCCACCTGTGGAACCCCAACCCCTGCCTCC CCGAGTCCGGCATGTACTACCGGGCAGTACCTAGCGCTCACCGAGG
ESTD- SPTB	--	--	--	---	---	TGAAACACCCCTGTGGTCCGGAGCCAGGTGTGTTCTCCTGGGAGCCTGAGGAGTTGTGTGTGTG CAGTCCCCCGGCCACCTGCTGTTGAGCCTGGACATACACTTCACTTCCCTTTGGCCCCGAGAAGAC ATTTACCCACTGGCCATGTCCCTGGCCTGTTGTGCACACCTCTGTGAACCCCAACCCCTGCCTCC
ESTD- SSA1	--	--	--	---	---	CCACCCCAAGCCAGTTCTAGCAAGGGCAGGAC TTCACTTTGTGGATTGTTCTTTTGTGTGCGAGCACCTTTTCAACATGATGTGATCCCATTTGTCCAAG TTTGCTTTGGCTGCTGCTGTGGGATATTGAAAGAGATCTTTGCCAGTCCCAATGTCTAGAGAG TTTTCCCAATGTTTCTGTAATAGTTTCATAGTTGAGGCCCTAGATTAAAGTCTTTAATCCATTTTG ATTGATTCTGTA
ESTD-TAT	--	--	--	---	---	AAATGGTCAGGACCCTGATCCACAAGAAGTGGTACCATTTTCATAGGGCCCATCAGTTTCAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTCATTCATCTTAAATGACTTGTGGGACAGGATCA ATTCTCTCACCCTAGAACGTTGTTTACAACCTTTCTCCAGTATGGATGGGATTATGATGGGGG GAGAAGCAAAATTTAAATAGGACCCCATGAGACATCA
ESTD- THRB	--	--	--	---	---	TGCGGCTTCTCCTCGGAGGGTAGACTTCTTACTTGGCTGTGATTTCOAAGAGAAGAGTCCCAAG CACACGAAACAGAAAGTTGCAGATCCCATGAGGCCAGTCTCAATCACACAGGATCATTTCATCCA CACTGGATTGGCCCAACAAGTCTGAGTGCCAGCCAGGACTCAACGGTCCCTGTAGATGGG
ESTD- TNFA	--	--	--	---	---	TTCTGCATCCTGTCTGGAAGTTAGAAGGAAACAGACCACAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGGTTTGGAGGGCATGAGGACGGGTTGAGCCTCCAGGGTCTACACACAAATCAGTCAGTG GCCAGAAAGACCCCTCAGAAATCGAGCAGGAGGATGGGAGTGTGAGGGGTATCCTTGTATGCTT GTGTGCCCAACTTCCAAATCCCGCCCGCGATGG
ESTD-TYR	--	--	--	---	---	TAGTGAAGTTTTCATCTCTGCTGAGCTTCTGGATTCTTGTCCACCGCAACAAGAGAGTCTATGC CAAGCAGAAAGCTGGTCTTCATGGGCAAAATCAATCTCTCCAGATTTTCAGATCCCCCAAGCA GTGCATCCATTGACACATAATAATGCATCCAGACAAAGAGGTCAATAATTGATGTCTCGTTAAACAT GGGTGTTGATCCATTTTTCATTTGGCCATAGGTCCCTATGGGATGACA

ESTD- TYRP1	--	--	--	---	---	AGTAGTGGATGAAGCTAACCCAGCCTCTCCCTCACTGATCAATGCTATGCTGAAGAATATGAA AACTCCAGAATCCTAATCAGTCTGTGGTCTAACAAATGCCCTACTCTCTTAATGATTAGTATCACAA AACCACCTGGTTGAATATAATAGATTGAGTTAATACGTATTTCTTTCACTTTATTACCTTCTTTCT AATACAAGCATATGTTAGAAATTAAGTTCTAGGCATACTT
ESTD- VB12	--	--	--	---	---	TCCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCAAGACACAAAGGTACAGAGACAGGAACACCCAGTG ACTCTGAGATGTCACCAGACTGAGAACCCACCGTTATATGTACTGGTATCGACAAGACCCCGGGCATG GGCTGAGGCTGATCCATTACTCATAT
ESTD-WVF	--	--	--	---	---	AGGTAGGAAAAGCAAGAGTTGATTAGTGAAGGAGAGAATGGACCTACCTTCCACACTGTCTTTGG TCCCCTAGAGTCTG
ESTD-WT1	--	--	--	---	---	AAGACCTACGTGAATGTTACATGTGCTTAAAGCCTCCCTTCTCTTACTCTCTGCTGCAGGATGTG CGACGTGTCCTGGAGTAGCCCCGACTCTTGACGGTCGGCATCTGAGACCAGTGAGAAACGCCCTT CATGTGCTTACCCAGGCTGCAA
ESTD- s14544	--	--	--	---	---	TGGGAAGTTAGAGCCTATATTAATTACGGAATTACTAAGGCAGGACACAGAGGCTTAATTGAAAA TATCCCAAAGTTGAAATGTCAGTTCGCTGTGTGGTTAGATGCAGGATTTATATGATCCGTTAACC TCT
EST71770 6	--	--	--	---	---	AGCACCACTCTCAGCTCAAGCCTCAGCACCAAGATGCTGTTCTATAAGGATGACGTGCTGTTTACAA CATCTCCTCCATGAAGAGCACAGAGAGTTATTTATCTGAAGTCCGGATCTATGACTCAGGGACAT ATAATGTACTGTGATTGTGAACAACAAGAGAAAAACCCTGCAGAGTACCAGCTGTTGGTGAAGG AGTGCCCACTCCAGGCTGACACTGGACAAGAAAGAGGCCATCCAAGG
EST52418 6	--	--	--	---	---	CAATTACAGGGTCAACTGCTATGATGTGTTTGGAGCCCACTACCCCTTTGGTGGCTACAAGATGTCG GGGAGTGGCCGGGAGTTGGCGAGTAGCGGCTGCAGGCATACACTAAAGTGAAAACTGTGAGTGTGG
EST13586 3	--	--	--	---	---	CCCACTCTATTGGCCAGCCCCAGGGACAGAGCTGATCCTTGAACCTTAAAGTTCCACATTGCCAGGA CCAGTGAGCAGCAACAGGGCCAGGGCTGGCTTATCAGCCTCCAGCCAGACCCCTGGCTGCAGACAT AAATAGGCCCTGCAAGAGCTGGCTGCTTAGAGACTGCGAGAGGAGGTGCGTCTGCTGCTGCCCGG GTCACTC
EST51976 7	--	--	--	---	---	AGGCAGAACTGGGCCCCCATCGGGGGACGTGGAAAGGCCACTTGAGCTTCTGGAGAAGGACCTGA GGGACAAAGGTCAACTCCTTTCTCAGCACCTTCAAGGAGAAAGAGAGCCAGGACAGACTCTCTCCCT CCCTGAGCTGGAGCAACAGCAGGAACAGCAGCAGGAGGAGCAGCAGGAGCAGGTGCAGATGCTGGCC CCTTTGGAGAGCTGAGCTGCCCTGGTGC

-301-

EST11458 6	--	--	---	---	---	CCACITTTGGTAGTCCAGTGTGACTCATCCACAATGATTTCTCCAGTGTCTCATCTTGTCTCGAGTTTT CTCTGCCATGTTGCTATTGCAGGACGGACCTGTCCCAAGCCAGATGATTTACCATTTTCCACAGTGGT CCCATTAAACAATCTATGAGCCAGGAGAGATACGATTTCTCGAAGCCGGGCTATGTGTCC CGAGGAGGATGAGAAATTTATCTGCCCTCTCACAGGACTGTGGCC
EST39852 8	--	--	---	---	---	CGGTCTTCTCCAGGTATTGTGCAGAGGCCGAGATGACCTCTATGTCTCAGATGCATTCCATAAG GCATTCTTGAGGTGAGTACACCTTCCCACCTCTTACGGTACAGAAAGAGATGCATGAACAGCA GGAACACGTGGAAAGGCCTGTTTCCAGTGTAAAGGCATGCAAAAGGCCCTCCACAGGCTGCTATAAT ACAGCCCT
EST62448 0	--	--	---	---	---	ACCTGGTGTCTGGTGTGGGTGAACCTGGTCTCTTGGCATTGCCGGCCCTCTCGGGGCCGGTGG TCCTCTGGTGTCTGGGTAGTCTCTGGAGTCAACGGTCTCTCTAGTGAAGCTGGTGTGATGGCAACC CTGGGAACGATGTTCCCTCCAGGTGCGGATGGTCAACCCGGACACAAGGGAGAGCGGTTACCCCTGG CAATAT
EST36027 2	--	--	---	---	---	AGTGACTTCCAGGAAATGGCTACCCCACTTGCTTCATGCGCCTGTGGCCAACTATGCCTCTCAGA ACATCACTACCTACTGCAAGAACAGCAATTGCATACATGATGAGGAGACTGGAACCTGAAAAAGG CTGTCACTTACAGGGCTCTAATGATGTTGAACCTGTGCTGAGGGCAACAGAGGTTCACTTACACT GTTCTTGTAGATGGCTGCTCTAAAAGACAAATGAATGGGGAAGACAA
EST12274 0	--	--	---	---	---	CCCCAGTTGACAGCCACTGCTCTAGACTAAGTTTCTTCTTCCAAATAGAGCCCTACCAAAGTGTAT TACATAAAGAAGTCAAGTGGTTTACTCTCATGACCAAAATATTCTTCCCTCTTCCCTAGGATGAGGTGA TAGTAAATGACCGATGGGTGAGAACTGTTCTGTCAACCATGGAGGATACATAACTGTGAAGATAA ATTCAAGCCACAGAGCTTGCCAGATC
EST76807 EST44438 7	--	--	---	---	---	ATGCTAAGGGGATCGGACATGAAGGACCCCTGTAGCCGATTGTCTATCTCCAGCGGCCCTGTCATC CAGCTCACTCATCAATGGGGCCAGTCAGGCCAGGCACTGGCTCCGGAGGACTCAACCACTGCCCCCT GCTGCCATGTGGACTGGTGCAAGTTGAGGACTTCTTG GCAGCCAGGAGCCGCTGCAACCATGCCCGCATAGATGCGGACCTCAAGCTCGACTTCAAGGACGTCT GCTCCGACCTAAGCGGAGCAGCCTCAAGAGCCGAGCCGAGGTGGG
EST12839 3	--	--	---	---	---	TGCAAAACACACAAAATCTTCTCCAGATGCCCTATGGCTGTGGAGAGCAGAAATATGGTCCCTTTGCT CCTAACATCTATGTACTGGATTATCTAAATGAACACAGCAGCTTACTCCAGAGATCAAGTCCAAAGG CCATTGGCTATCTCAACACTGGTGAGTGATTAATCTGAGTAAGGAACTTGAATGTTATTCAACTGG ATTTCCAGTAGGTTTCAGTTACTTATGAATATATATGATACCTTAGCTTAG
EST54419 8	--	--	---	---	---	CTTCTGCCTAATTTGAATGATATTGTTGCTGTGGGACCTGAGCACTTTTATGGCACAAATGATCACTA TTTTCTTGACCCCTACTTACAATCCTGGGAGATGATTTTGGTTTAGCGTGGTGTGATGTTGTCTACTA TAGTCCAAGTGAA

EST10398 2	--	--	--	---	---	TGCTGGGTGGCAAGGCTGCAAAAGGAGGCAAGGAGGAGGCTTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTCTATCTACTTGATGATGTTACATTTGGGGCTTGACTTTCCACACGGAGAAG CATTGTTTTCTCGGGCCAAAGGATCTACCAATAGTGCTATTAGGCATTG
EST36751 7	--	--	--	---	---	CCAAAGTCGTTCAATTTAGCTTTGACAGGTTTAACTCGATTACTTTTCTATTCAAATCTCTGTAAAA TTGAAATATGAACCTAGTTTTCTGATCTATGGTTTCAAGTTAAACAG
EST40562	--	--	--	---	---	CACGTGAAAGGAGCTATTTTGGAGGCTTTAAGAGTAAAGATCTGCCCAAACCTTGTGGCTGAC TTTATGGCTAAGAAAGTTTCACTGGATGCATTAATAACAAATATTACCTTTTGAATAAATAATG AAGGATTTGACCTGCTCGCTCTGGAAGAGTATCCGTACCGTCTGACGTTTGAACAAATACAGAT GCCTTCCCTGTAGCAGTTTACGCTCTCTACCCCTA
EST18288 3	--	--	--	---	---	GCTCTATACCCCTGTGGTCTCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGTGAGAA GATTGACAGGTTTCATGACGGCTGTGACAGGATGGAAGACTGGCTGCTCCCTGACGGGAGCCAGTGTGG ACAGCACCCCTGGCTTCAACACCTACGTCACCTTCCAAAGTAAGGCAAAACCTCTCTGCTGGCTCTGGC CCTAGGACTTAGTATCC
EST70523 3	--	--	--	---	---	TTCCGCGAGCCCCCATCTCTGGACCCCTGGTCCCCCTCAGGGGCAACCCCGGCGCACTCAACGCTCT CGCTCTCGGTAACATCCGCGCGGCGGCTCTTGAGCACATAGCCTGGACCGTTTCCGTATAGGAGG ACCGTGTAGGCTTCTGCTCCGCGGCTTGGCAGGGCCAGCCCTGCAGAGAGAGGGTCCCTGTGGT TGAGCTGAACACAGCTGTGGAGTGTCTCCACAGT
EST58707 7	--	--	--	---	---	CAGTGTATCTGGAAGCCTACAGGACACCAAAATACCTTAATCATCAATTGGTTACAGGAGCTTT AAGTTCAGCATCTTTGGCTCACATGAAGGCAAAATCCGAGAGACCTAGAGATACACGAGACCGA ATGTATCAATGGACATTCAGCAGGAACCTTCAACGATACCTGCTCTGGTAGGCCAGGTTTATAGCA CACTTGTCACCTACATTTCTGATTGGTGGACTCTTGTGCTAAGAAACCTT
EST74167 6	--	--	--	---	---	AGACCATGAAGGAGTTGAAGGCTACAATCGGAACCTGGAGGAACAACCTGACCCCGGTGGCGGAGG AGACGCGGGCACGCTGTCCAGGAGCTGCAGGCGCGGCGGCGGCTGGCGGCGGACATGGAGGA CGTGCAGGCGGCTGTGTCAGTACCGCGGCGAGGTGACGCCCATGCTGCGCCAGAGCACCGAGGAGC TGCGGGTGGGCTCGCTCCACCTGGCAAGCTGCGTAAAGCGGCTCCTC
EST43211 8	--	--	--	---	---	CGCTGGTGCAGTACCGCGGCGAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGAGCTGCGGGTGOG CCTGCGCTCCACCTGCGCAAGCTGCGTAAGCGGCTCTCCGCGATGCCGATGACCTGCAGAAAGCGC TGCCAGTGTACAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG GGGCGGCTGGTGAACAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTC
EST36770 4	--	--	--	---	---	TGTAGCCAAAGTCACCTGCATCATCTTTGGCTGCTGGAGGCTTGGCCAGTTTGCAGCTATAATCC ATCGAAATGATTTTTCATTGAGAACACCAATATTACAGTTTGTCTTCCATTATGAGTCCCAAAAT TCAACCTCCCGATAGGCTGGGCTGACCAAAATATACTGGGTTTCTGTTTCTTCTGATCAT TCTTACAAGTTATACCTTATTGGAAGGCCCTAAAGAGGCTTATG

EST65258 8							TGCCCATCACGCGCGGAGACATGGCTTGCCACAGCTCTTGAGGATGTCACCAATTAAACCAGAAAT CCAGTTATTTCCACCCCTCAAAATGACAGCCATGCCCGCGGTGCTTCTGGGGCTCGTCGGGGGG ACAGCTCCACTCTGACTGGCACAGCTTTGCATGGAGACTTGAGGAGGGGCTTGAGGTTGGTGAG GTTAGGTGCGTGTTCCTGTGCAAGTCAGGACATCAGTCTGATTAA
EST38216 3							ATGCAGGATGAAGGTGGACAGGGGAGAGAGGGCCAACTGTCATCCAGGCCCTGCAGATGTCGCTG GACTATGGTTTGTGACCCCACTGACCTCCATGAGCATCAGGG
							ATACTAGTACAAGTGGTAATTTTGTACATTACACTAAATATTAGCAATTTGTTTAGCATTACCTAA TTTTTTCCTGCTCCATGCAGACTGTAGCTTTACCTTAAATGCTTATTTTAAATGACAGTGGAAAG TTTTTTTTCCTCGAAGTGCAGTATCCAGAGTTTGGTTTTTGAACCTAGCAATGCCTGTGAAAAA GAACTGAATACCTAAGATTCTGTCTGGGGTTTTTGGTGCATGCA
EST62782 --							GAGATCGGTGTGTGAGTTATTAGGCATGGTTACCTGTGATTCTCCCAATCTTGCGTTCCACCGATG GAACTCCGGCAATCTGACACGTGTGCACCCAGGCTGTACCCCAATTAGTGAACATGGCTTCGAG AGAGTTGAACAGATTCTCGAAGACAGCAGCGGGATGGGGCAGGAGAGCTGCCCTGGATGAA
EST68308 5							GGAAGAGATTTAAGAAGCTTGATTTGGACAATCTGTTCTTTGAGTGTGGAAGAGTTTCATGCTCT GCCTGAGTTACACAGAACTCTTTAGTACAGCGAGTAATAGATATTCGACACAGATGGGAATGGA GAAGTAGACTTTAAAGTAAAGTAGTATTTTTTA
EST54045 6							GGAATATTAAATATTTTAAATACCTCCATTTTGCTTATCCTTTTAGTGAAGATGATACCTGCAA AAGACATGGCTAAAGTATGATGTGATGTGCAATTTGTTTCTTACAAAATCGGATGGGAATCT GTTAAGTAACTACTGTTTGGCTTGGAAATGGATTTTAAATGTTGACTTTTATCAT
EST52908 0							ATCACAGTCTCTGGTCTCTGGCCATCATTTCTCTGGGAGAGATGGATGGTGTCTGCAAGCCCTTTGG CAATGTGAGATTGTATG
EST19590 --							AGGAGAAGCTGAGGAGGGGAAGAGAGACAAAGATGACATTGATGAGTGAAGATGTCGGCTCAGGAT GCCGGAATGAC
EST76136 --							TGAAGCTTCTGCCCAGCTTGCAATGTTTCTAGGAGAACCCGCGTCATACCTTTATCTATAGCCTTCCCC TAGGTCCT
EST58607 0							CTCTGGATGGTTACAGGTGGCAGGCACAAAGCCAGTCCATCCTGTAGTCATCATAGTTGTGGCTCC CAAGTTGCTCTCCTCACTGGAGAACAAAGGACAGCCACATGGCGGGATGGCGGGGAGTTCTGGT TGCGGCCACGCTGTGGCTCTGTTGTGAACGGTAGCCTTTGGGTTGCGATGCCTAAACCTTTGTTTCT TGCCAAAGGAGGGGGGGTGCCATGCTGAGATGTAGATGCGGCC
							Legend: 1=Marker 2=PM Position 3=Reference Allele 4=Altered Allele 5=SNP Forward Primer 6=SNP Reverse Primer 7=Sequence

-305-

EQUIVALENTS

While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that

5 various changes in form and details may be made therein without departing from the spirit and scope of the invention as defined by the appended claims. Those skilled in the art will recognize or be able to ascertain using no more than routine experimentation, many equivalents to the

10 specific embodiments of the invention described specifically herein. Such equivalents are intended to be encompassed in the scope of the claims.

-306-

CLAIMS

WE CLAIM:

1. A nucleic acid segment shown in column 7 of the Table,
or a portion thereof which includes a polymorphic site,
5 or the complement of the segment or portion thereof.
2. The nucleic acid segment of claim 1 that is DNA.
3. The nucleic acid segment of claim 1 that is RNA.
4. The segment of claim 1 that is less than 100 bases.
5. The segment of claim 1 that is less than 50 bases.
- 10 6. The segment of claim 1 that is less than 20 bases.
7. The segment of claim 1, wherein the polymorphic site is
biallelic.
8. The segment of claim 1, wherein the polymorphic form
occupying the polymorphic site is the reference base
15 for the fragment listed in the Table, column 3.
9. The segment of claim 1, wherein the polymorphic form
occupying the polymorphic site is an alternative form
for the fragment listed in the Table, column 4.
10. An allele-specific oligonucleotide that hybridizes to a
20 segment of a fragment shown in the Table, column 7 or
its complement.
11. The allele-specific oligonucleotide of claim 10 that is
a probe.

-307-

12. The allele-specific oligonucleotide of claim 10,
wherein a central position of the probe aligns with the
polymorphic site of the fragment.
13. The allele-specific oligonucleotide of claim 10 that is
5 a primer.
14. The allele-specific oligonucleotide of claim 13,
wherein the 3' end of the primer aligns with the
polymorphic site of the fragment.
15. The allele-specific oligonucleotide of Claim 10, which
10 is selected from the group consisting of the nucleotide
sequences of the Table, column 5.
16. The allele-specific oligonucleotide of Claim 10, which
is selected from the group consisting of the nucleotide
sequences of the Table, column 6.
- 15 17. An isolated nucleic acid comprising a sequence of the
Table, column 7 or the complement thereof, wherein the
polymorphic site within the sequence or complement is
occupied by a base other than the reference base shown
in the Table, column 3.
- 20 18. A method of analyzing a nucleic acid, comprising
obtaining the nucleic acid from an individual; and
determining a base occupying any one of the polymorphic
sites shown in the Table.
19. The method of claim 18, wherein the determining
25 comprises determining a set of bases occupying a set of
the polymorphic sites shown in the Table.

-308-

20. The method of claim 18, wherein the nucleic acid is obtained from a plurality of individuals, and a base occupying one of the polymorphic positions is determined in each of the individuals, and the method
5 further comprising testing each individual for the presence of a disease phenotype, and correlating the presence of the disease phenotype with the base.